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(54) Title: MANIPULATION OF FLAVONOID BIOSYNTHESIS IN PLANTS

(57) Abstract: The present invention relates to nucleic acids and nucleic acid fragments encoding amino acid sequences for flavonoid biosynthetic enzymes in plants, and the use thereof for the modification of flavonoid biosynthesis in plants. More particularly, the flavonoid biosynthetic enzyme is selected from the group consisting of chalcone isomerase (CHI), chalcone synthase (CHS), chalcone reductase (CHR), dihydroflavonol 4 reductase (DFR), leucoanthocyanidin reductase (LCR), flavonoid 3', 5' hydroxylase (3',5'H), flavanone 3-hydroxylase (F3H), flavonoid 3'-hydroxylase (F3'H), phenylalanine ammonia-lyase (PAL) and vestitone reductase (VR), and functionally active fragments and variants thereof.

MANIPULATION OF FLAVONOID BIOSYNTHESIS IN PLANTS

The present invention relates to nucleic acids and nucleic acid fragments encoding amino acid sequences for flavonoid biosynthetic enzymes in plants, and the use thereof for the modification of flavonoid biosynthesis in plants.

- 5 Flavonoids constitute a relatively diverse family of aromatic molecules that are derived from phenylalanine and malonyl-coenzyme A (CoA, via the fatty acid pathway). These compounds include six major subgroups that are found in most higher plants: the chalcones, flavones, flavonols, flavandiols, anthocyanins and condensed tannins (or proanthocyanidins). A seventh group, the aurones, is
10 widespread, but not ubiquitous.

- Some plant species also synthesize specialised forms of flavonoids, such as the isoflavonoids that are found in legumes and a small number of non-legume plants. Similarly, sorghum, maize and gloxinia are among the few species known to synthesize 3-deoxyanthocyanins (or phlobaphenes in the polymerised form).
15 The stilbenes which are closely related to flavonoids, are synthesised by another group of unrelated species that includes grape, peanut and pine.

- Besides providing pigmentation to flowers, fruits, seeds, and leaves, flavonoids also have key roles in signalling between plants and microbes, in male fertility of some species, in defense as antimicrobial agents and feeding
20 deterrents, and in UV protection.

Flavonoids also have significant activities when ingested by animals, and there is great interest in their potential health benefits, particularly for compounds such as isoflavonoids, which have been linked to anticancer benefits, and stilbenes that are believed to contribute to reduced heart disease.

- 25 The major branch pathways of flavonoid biosynthesis start with general phenylpropanoid metabolism and lead to the nine major subgroups: the colorless chalcones, aurones, isoflavonoids, flavones, flavonols, flavandiols, anthocyanins, condensed tannins, and phlobaphene pigments. The enzyme phenylalanine

ammonia-lyase (PAL) of the general phenylpropanoid pathway will lead to the production of cinnamic acid. Cinnamate-4-hydroxylase (C4H) will produce p-coumaric acid which will be converted through the action of 4-coumaroyl:CoA-ligase (4CL) to the production of 4-coumaroyl-CoA and malonyl-CoA. The first committed step in flavonoid biosynthesis is catalyzed by chalcone synthase (CHS), which uses malonyl CoA and 4-coumaroyl CoA as substrates. Chalcone reductase (CHR) balances the production of 5-hydroxy- or 5-deoxyflavonoids. The next enzyme, chalcone isomerase (CHI) catalyses ring closure to form a flavanone, but the reaction can also occur spontaneously. Other enzymes in the pathway are: flavanone 3-hydroxylase (F3H), dihydroflavonol 4-reductase (DFR), flavonoid 3'-hydroxylase (F3'H) and flavonoid 3', 5' hydroxylase (F3'5'H).

The *Arabidopsis* BANYULS gene encodes a DFR-like protein that may be a leucoanthocyanidin reductase (LCR) that catalyzes an early step in condensed tannin biosynthesis. Condensed tannins are plant polyphenols with protein-precipitating and antioxidant properties, synthesized by the flavonoid pathway. Their chemical properties include protein binding, metal chelation, anti-oxidation, and UV-light absorption. As a result condensed tannins inhibit viruses, microorganisms, insects, fungal pathogens, and monogastric digestion. Moderate amounts of tannins improve forage quality by disrupting protein foam and conferring protection from rumen pasture bloat. Bloat is a digestive disorder that occurs on some highly nutritious forage legumes such as alfalfa (*Medicago sativa*) and white clover (*Trifolium repens*). Moderate amounts of tannin can also reduce digestion rates in the rumen and can reduce parasitic load sufficiently to increase the titre of amino acids and small peptides in the small intestine without compromising total digestion.

Vestitone reductase (VR) is the penultimate enzyme in medicarpin biosynthesis. Medicarpin, a phytoalexin, has been associated with plant resistance to fungal pathogens.

While nucleic acid sequences encoding some flavonoid biosynthetic enzymes CHI, CHS, CHR, DFR, LCR, F3'5'H, F3H, F3'H, PAL and VR have been isolated for certain species of plants, there remains a need for materials useful in

modifying flavonoid biosynthesis; in modifying protein binding, metal chelation, anti-oxidation, and UV-light absorption; in modifying plant pigment production; in modifying plant defense to biotic stresses such as viruses, micro-organisms, insects or fungal pathogens; in modifying forage quality, for example by disrupting
5 protein foam and/or conferring protection from rumen pasture bloat, particularly in forage legumes and grasses, including alfalfa, medics, clovers, ryegrasses and fescues, and for methods for their use.

It is an object of the present invention to overcome, or at least alleviate, one or more of the difficulties or deficiencies associated with the prior art.

10 In one aspect, the present invention provides substantially purified or isolated nucleic acids or nucleic acid fragments encoding the flavonoid biosynthetic enzymes CHI, CHS, CHR, DFR, LCR, F3'5'H, F3H, F3'H, PAL and VR from a clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species and functionally active fragments and variants thereof.

15 The present invention also provides substantially purified or isolated nucleic acids or nucleic acid fragments encoding amino acid sequences for a class of proteins which are related to CHI, CHS, CHR, DFR, LCR, F3'5'H, F3H, F3'H, PAL and VR and functionally active fragments and variants thereof. Such proteins are referred to herein as CHI-like, CHS-like, CHR-like, DFR-like, LCR-like, F3'5'H-like,
20 F3H-like, F3'H-like, PAL-like and VR-like, respectively.

The individual or simultaneous enhancement or otherwise manipulation of CHI, CHS, CHR, DFR, LCR, F3'5'H, F3H, F3'H, PAL and/or VR or like gene activities in plants may enhance or otherwise alter flavonoid biosynthesis; may enhance or otherwise alter the plant capacity for protein binding, metal chelation,
25 anti-oxidation or UV-light absorption; may enhance or reduce or otherwise alter plant pigment production; may modify plant defense to biotic stresses such as viruses, micro-organisms, insects or fungal pathogens; and/or may modify forage quality, for example by disrupting protein foam and/or conferring protection from rumen pasture bloat.

The individual or simultaneous enhancement or otherwise manipulation of CHI, CHS, CHR, DFR, LCR, F3'5'H, F3H, F3'H, PAL and/or VR or like gene activities in plants has significant consequences for a range of applications in, for example, plant production and plant protection. For example, it has applications in

5 increasing plant tolerance and plant defense to biotic stresses such as viruses, micro-organisms, insects and fungal pathogens; in improving plant forage quality, for example by disrupting protein foam and in conferring protection from rumen pasture bloat; in reducing digestion rates in the rumen and reducing parasitic load; in the production of plant compounds leading to health benefits, such as

10 isoflavonoids, which have been linked to anticancer benefits, and stilbenes that are believed to contribute to reduced heart disease.

Methods for the manipulation of CHI, CHS, CHR, DFR, LCR, F3'5'H, F3H, F3'H, PAL and/or VR or like gene activities in plants, including legumes such as clovers (*Trifolium* species), lucerne (*Medicago sativa*) and grass species such as

15 ryegrasses (*Lolium* species) and fescues (*Festuca* species) may facilitate the production of, for example, forage legumes and forage grasses and other crops with enhanced tolerance to biotic stresses such as viruses, micro-organisms, insects and fungal pathogens; altered pigmentation in flowers; forage legumes with enhanced herbage quality and bloat-safety; crops with enhanced isoflavonoid

20 content leading to health benefits.

The clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species may be of any suitable type, including white clover (*Trifolium repens*), red clover (*Trifolium pratense*), subterranean clover (*Trifolium subterraneum*), alfalfa (*Medicago sativa*), Italian or annual ryegrass (*Lolium multiflorum*), perennial ryegrass (*Lolium perenne*), tall fescue (*Festuca arundinacea*), meadow fescue (*Festuca pratensis*) and red fescue (*Festuca rubra*).

25 Preferably the species is a clover or a ryegrass, more preferably white clover (*T. repens*) or perennial ryegrass (*L. perenne*). White clover (*Trifolium repens* L.) and perennial ryegrass (*Lolium perenne* L.) are key pasture legumes and grasses,

30 respectively, in temperate climates throughout the world. Perennial ryegrass is also an important turf grass.

The nucleic acid or nucleic acid fragment may be of any suitable type and includes DNA (such as cDNA or genomic DNA) and RNA (such as mRNA) that is single- or double-stranded, optionally containing synthetic, non-natural or altered nucleotide bases, and combinations thereof.

- 5 The term "isolated" means that the material is removed from its original environment (eg. the natural environment if it is naturally occurring). For example, a naturally occurring nucleic acid present in a living plant is not isolated, but the same nucleic acid separated from some or all of the coexisting materials in the natural system, is isolated. Such nucleic acids could be part of a vector and/or
- 10 such nucleic acids could be part of a composition, and still be isolated in that such a vector or composition is not part of its natural environment.

- Such nucleic acids or nucleic acid fragments could be assembled to form a consensus contig. As used herein, the term "consensus contig" refers to a nucleotide sequence that is assembled from two or more constituent nucleotide
- 15 sequences that share common or overlapping regions of sequence homology. For example, the nucleotide sequence of two or more nucleic acids or nucleic acid fragments can be compared and aligned in order to identify common or overlapping sequences. Where common or overlapping sequences exist between two or more nucleic acids or nucleic acid fragments, the sequences (and thus their
- 20 corresponding nucleic acids or nucleic acid fragments) can be assembled into a single contiguous nucleotide sequence.

- In a preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encoding a CHI or CHI-like protein includes a nucleotide sequence selected from the group consisting of
- 25 (a) sequences shown in Figures 1, 3, 4, 6, 7, 9, 10, 12, 122 and 127 hereto (Sequence ID Nos: 1, 3 to 7, 8, 10 to 12, 13, 15 and 16, 17, 19 to 22, 307, and 309, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encoding a CHS or CHS-like protein includes a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 13, 15, 16, 18, 19, 21, 22, 24, 25, 27, 28, 30, 31, 33, 34, 137, 142, 147, 152, 157 and 162 hereto (Sequence ID Nos: 23, 25 to 63, 64, 66 to 68, 69, 71 to 77, 78, 80 to 90, 91, 93 and 94, 95, 97 to 100, 101, 103 to 105, 106, 313, 315, 317, 319, 321, and 323, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encoding a CHR or CHR-like protein includes a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 36, 38, 40, 41, 43 and 132 hereto (Sequence ID Nos: 108, 110, 112 to 116, 117, 119 to 134, and 311, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encoding a DFR or DFR-like protein includes a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 44, 46, 47, 49, 50, 52, 54, 55, 57, 59, 61, 62, 64, 101, 103, 104, 106, 117 and 167 hereto (Sequence ID Nos: 135, 137 to 146, 147, 149 to 152, 153, 155, 157 and 158, 159, 161, 163, 165 to 167, 168, 170 to 184, 286, 288 to 292, 293, 295 to 297, 305, and 325, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encoding an LCR or LCR-like protein includes a nucleotide sequence selected from the group

consisting of (a) sequences shown in Figures 65 and 67 hereto (Sequence ID Nos: 185 and 187 to 193, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and

5 (c).

In a still further preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encoding an F3'5'H or F3'5'H-like protein includes a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 68, 70 and 72 hereto

10 (Sequence ID Nos: 194, 196, and 198 to 201, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a further preferred embodiment of this aspect of the invention, the

15 substantially purified or isolated nucleic acid or nucleic acid fragment encoding an F3H or F3H-like protein includes a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 73, 75, 76, 78, 107, 109, 111 and 172 hereto (Sequence ID Nos: 202, 204 to 244, 245, 247, 298, 300 to 302, 303, and 327, respectively); (b) complements of the sequences recited in (a); (c)

20 sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a still further preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encoding an F3'H or F3'H-like protein includes a nucleotide sequence selected from the group

25 consisting of (a) sequences shown in Figures 80 and 82 hereto (Sequence ID Nos: 249, and 251 and 252, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encoding an PAL or PAL-like protein includes a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 83, 85, 86, 88, 89, 91, 93, 95, 97, 177, 182 and 187 hereto (Sequence ID Nos: 253, 255 to 257, 258, 260 to 267, 268, 270, 272, 274, 276 and 277, 329, 331, and 333, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a still further preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encoding an VR or VR-like protein includes a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 98, 100 and 192 hereto (Sequence ID Nos: 278, 280 to 285, and 335, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

By "functionally active" in relation to nucleic acids it is meant that the fragment or variant (such as an analogue, derivative or mutant) encodes a polypeptide which is capable of modifying flavonoid biosynthesis in a plant. Such variants include naturally occurring allelic variants and non-naturally occurring variants. Additions, deletions, substitutions and derivatizations of one or more of the nucleotides are contemplated so long as the modifications do not result in loss of functional activity of the fragment or variant. Preferably the functionally active fragment or variant has at least approximately 80% identity to the relevant part of the above mentioned nucleotide sequence, more preferably at least approximately 90% identity, even more preferably at least approximately 95% identity, most preferably at least approximately 98% homology. Such functionally active variants and fragments include, for example, those having nucleic acid changes which result in conservative amino acid substitutions of one or more residues in the corresponding amino acid sequence. Preferably the fragment has a size of at least

10 nucleotides, more preferably at least 15 nucleotides, most preferably at least 20 nucleotides.

Nucleic acids or nucleic acid fragments encoding at least a portion of several CHI, CHS, CHR, DFR, LCR, F3'5'H, F3H, F3'H, PAL and VR have been
5 isolated and identified. The nucleic acids or nucleic acid fragments of the present invention may be used to isolate cDNAs and genes encoding homologous proteins from the same or other plant species. Isolation of homologous genes using sequence-dependent protocols, such as methods of nucleic acid hybridisation, and methods of DNA and RNA amplification as exemplified by various uses of nucleic
10 acid amplification technologies (e.g. polymerase chain reaction, ligase chain reaction), is well known in the art.

For example, genes encoding other CHI or CHI-like, CHS or CHS-like, CHR or CHR-like, DFR or DFR-like, LCR or LCR-like, F3'5'H or F3'5'H-like, F3H or F3H-like, F3'H or F3'H-like, PAL or PAL-like and VR or VR-like proteins, either as
15 cDNAs or genomic DNAs, may be isolated directly by using all or a portion of the nucleic acids or nucleic acid fragments of the present invention as hybridisation probes to screen libraries from the desired plant employing the methodology well known to those skilled in the art. Specific oligonucleotide probes based upon the nucleic acid sequences of the present invention may be designed and synthesized
20 by methods known in the art. Moreover, the entire sequences may be used directly to synthesize DNA probes by methods known to the skilled artisan such as random primer DNA labelling, nick translation, or end-labelling techniques, or RNA probes using available *in vitro* transcription systems. In addition, specific primers may be designed and used to amplify a part or all of the sequences of the present
25 invention. The resulting amplification products may be labelled directly during amplification reactions or labelled after amplification reactions, and used as probes to isolate full-length cDNA or genomic fragments under conditions of appropriate stringency.

In addition, short segments of the nucleic acids or nucleic acid fragments of
30 the present invention may be used in amplification protocols to amplify longer nucleic acids or nucleic acid fragments encoding homologous genes from DNA or

RNA. For example, polymerase chain reaction may be performed on a library of cloned nucleic acid fragments wherein the sequence of one primer is derived from the nucleic acid sequences of the present invention, and the sequence of the other primer takes advantage of the presence of the polyadenylic acid tracts to the 3' end of the mRNA precursor encoding plant genes. Alternatively, the second primer sequence may be based upon sequences derived from the cloning vector. For example, those skilled in the art can follow the RACE protocol [Frohman *et al.* (1988) *Proc. Natl. Acad. Sci. USA* 85:8998, the entire disclosure of which is incorporated herein by reference] to generate cDNAs by using PCR to amplify 5 copies of the region between a single point in the transcript and the 3' or 5' end. Using commercially available 3' RACE and 5' RACE systems (BRL), specific 3' or 5' cDNA fragments may be isolated [Ohara *et al.* (1989) *Proc. Natl. Acad. Sci. USA* 86:5673; Loh *et al.* (1989) *Science* 243:217, the entire disclosures of which are incorporated herein by reference]. Products generated by the 3' and 5' RACE 15 procedures may be combined to generate full-length cDNAs.

In a second aspect of the present invention there is provided a substantially purified or isolated polypeptide from a clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species, selected from the group consisting of CHI and CHI-like, CHS and CHS-like, CHR and CHR-like, DFR and DFR-like, 20 LCR and LCR-like, F3'5'H and F3'5'H-like, F3H and F3H-like, F3'H and F3'H-like, PAL and PAL-like, VR and VR-like; and functionally active fragments and variants thereof.

The clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species may be of any suitable type, including white clover (*Trifolium repens*), red clover (*Trifolium pratense*), subterranean clover (*Trifolium subterraneum*), alfalfa (*Medicago sativa*), Italian or annual ryegrass (*Lolium multiflorum*), perennial ryegrass (*Lolium perenne*), tall fescue (*Festuca arundinacea*), meadow fescue (*Festuca pratensis*) and red fescue (*Festuca rubra*). Preferably the species is a clover or a ryegrass, more preferably white clover (*T. repens*) or perennial ryegrass (*L. perenne*). 30

In a preferred embodiment of this aspect of the invention, the substantially purified or isolated CHI or CHI-like polypeptide includes an amino acid sequence selected from the group consisting of the sequences shown in Figures 2, 5, 8, 11, 123 and 128 hereto (Sequence ID Nos: 2, 9, 14, 18, 308, and 310, respectively),
5 and functionally active fragments and variants thereof.

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated CHS or CHS-like polypeptide includes an amino acid sequence selected from the group consisting of the sequences shown in Figures 14, 17, 20, 23, 26, 29, 32, 35, 138, 143, 148, 153, 158 and 163 hereto
10 (Sequence ID Nos: 24, 65, 70, 79, 92, 96, 102, 107, 314, 316, 318, 320, 322, and 324, respectively), and functionally active fragments and variants thereof.

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated CHR or CHR-like polypeptide includes an amino acid sequence selected from the group consisting of the sequences shown in
15 Figures 37, 39, 42 and 133 hereto (Sequence ID Nos: 109, 111, 118, and 312, respectively), and functionally active fragments and variants thereof.

In a still further preferred embodiment of this aspect of the invention, the substantially purified or isolated DFR or DFR-like polypeptide includes an amino acid sequence selected from the group consisting of the sequences shown in
20 Figures 45, 48, 51, 53, 56, 58, 60, 63, 102, 105, 118 and 168 hereto (Sequence ID Nos: 136, 148, 54, 156, 160, 162, 164, 169, 287, 294, 306, and 326, respectively), and functionally active fragments and variants thereof.

In a still further preferred embodiment of this aspect of the invention, the substantially purified or isolated LCR or LCR-like polypeptide includes an amino
25 acid sequence shown in Figure 66 hereto (Sequence ID No: 186), and functionally active fragments and variants thereof.

In a still further preferred embodiment of this aspect of the invention, the substantially purified or isolated F3'5'H or F3'5'H-like polypeptide includes an amino acid sequence selected from the group consisting of the sequences shown

in Figures 69 and 71 hereto (Sequence ID Nos: 195 and 197, respectively), and functionally active fragments and variants thereof.

In a still further preferred embodiment of this aspect of the invention, the substantially purified or isolated F3H or F3H-like polypeptide includes an amino acid sequence selected from the group consisting of the sequences shown in
5 Figures 74, 77, 79, 108, 112 and 173 hereto (Sequence ID Nos: 203, 246, 248, 299, 304, and 328, respectively), and functionally active fragments and variants thereof.

In a still further preferred embodiment of this aspect of the invention, the
10 substantially purified or isolated F3'H or F3'H-like polypeptide includes an amino acid sequence shown in Figure 81 hereto (Sequence ID No: 250), and functionally active fragments and variants thereof.

In a still further preferred embodiment of this aspect of the invention, the substantially purified or isolated PAL or PAL-like polypeptide includes an amino
15 acid sequence selected from the group consisting of the sequences shown in Figures 84, 87, 90, 92, 94, 96, 178, 183 and 188 hereto (Sequence ID Nos: 254, 259, 269, 271, 273, 275, 330, 332, and 334, respectively), and functionally active fragments and variants thereof.

In a still further preferred embodiment of this aspect of the invention, the
20 substantially purified or isolated VR or VR-like polypeptide includes an amino acid sequence shown in Figures 99 and 193 hereto (Sequence ID Nos: 279 and 336, respectively), and functionally active fragments and variants thereof.

By "functionally active" in relation to polypeptides it is meant that the fragment or variant has one or more of the biological properties of the proteins
25 CHI, CHI-like, CHS, CHS-like, CHR, CHR-like, DFR, DFR-like, LCR, LCR-like, F3'5'H, F3'5'H-like, F3H, F3H-like, F3'H, F3'H-like, PAL, PAL-like, VR and VR-like, respectively. Additions, deletions, substitutions and derivatizations of one or more of the amino acids are contemplated so long as the modifications do not result in loss of functional activity of the fragment or variant. Preferably the functionally

active fragment or variant has at least approximately 60% identity to the relevant part of the above mentioned amino acid sequence, more preferably at least approximately 80% identity, even more preferably at least approximately 90% identity most preferably at least approximately 95% homology. Such functionally
5 active variants and fragments include, for example, those having conservative amino acid substitutions of one or more residues in the corresponding amino acid sequence. Preferably the fragment has a size of at least 10 amino acids, more preferably at least 15 amino acids, most preferably at least 20 amino acids.

In a further embodiment of this aspect of the invention, there is provided a
10 polypeptide recombinantly produced from a nucleic acid or nucleic acid fragment according to the present invention. Techniques for recombinantly producing polypeptides are well known to those skilled in the art.

Availability of the nucleotide sequences of the present invention and deduced amino acid sequences facilitates immunological screening of cDNA
15 expression libraries. Synthetic peptides representing portions of the instant amino acid sequences may be synthesized. These peptides may be used to immunise animals to produce polyclonal or monoclonal antibodies with specificity for peptides and/or proteins including the amino acid sequences. These antibodies may be then used to screen cDNA expression libraries to isolate full-length cDNA
20 clones of interest.

A genotype is the genetic constitution of an individual or group. Variations in genotype are important in commercial breeding programs, in determining parentage, in diagnostics and fingerprinting, and the like. Genotypes can be readily described in terms of genetic markers. A genetic marker identifies a
25 specific region or locus in the genome. The more genetic markers, the finer defined is the genotype. A genetic marker becomes particularly useful when it is allelic between organisms because it then may serve to unambiguously identify an individual. Furthermore, a genetic marker becomes particularly useful when it is based on nucleic acid sequence information that can unambiguously establish a
30 genotype of an individual and when the function encoded by such nucleic acid is known and is associated with a specific trait. Such nucleic acids and/or nucleotide

sequence information including single nucleotide polymorphisms (SNPs), variations in single nucleotides between allelic forms of such nucleotide sequence, may be used as perfect markers or candidate genes for the given trait.

Applicants have identified a number of SNPs of the nucleic acids or nucleic acid fragments of the present invention. These are indicated (marked with grey on the black background) in the figures that show multiple alignments of nucleotide sequences of nucleic acid fragments contributing to consensus contig sequences. See for example, Figures 3, 6, 9, 12, 15, 18, 21, 24, 27, 30, 33, 40, 43, 46, 49, 54, 61, 64, 67, 72, 75, 82, 85, 88, 97, 100, 103, 106 and 109 hereto (Sequence ID Nos: 3 to 7, 10 to 12, 15 and 16, 19 to 22, 25 to 63, 66 to 68, 71 to 77, 80 to 90, 93 and 94, 97 to 100, 103 to 105, 112 to 116, 119 to 134, 137 to 146, 149 to 152, 157 and 158, 165 to 167, 170 to 184, 187 to 193, 198 to 201, 204 to 244, 251 and 252, 255 to 257, 260 to 267, 276 and 277, 280 to 285, 288 to 292, 295 to 297, and 300 to 302, respectively).

Accordingly, in a further aspect of the present invention, there is provided a substantially purified or isolated nucleic acid or nucleic acid fragment including a single nucleotide polymorphism (SNP) from a nucleic acid or nucleic acid fragment according to the present invention or complements or sequences antisense thereto, and functionally active fragments and variants thereof.

In a still further aspect of the present invention there is provided a method of isolating a nucleic acid or nucleic acid fragment of the present invention including a SNP, said method including sequencing nucleic acid fragments from a nucleic acid library.

The nucleic acid library may be of any suitable type and is preferably a cDNA library.

The nucleic acid or nucleic acid fragments may be isolated from a recombinant plasmid or may be amplified, for example using polymerase chain reaction.

The sequencing may be performed by techniques known to those skilled in the art.

In a still further aspect of the present invention, there is provided use of the nucleic acids or nucleic acid fragments of the present invention including SNPs,
5 and/or nucleotide sequence information thereof, as molecular genetic markers.

In a still further aspect of the present invention there is provided use of a nucleic acid or nucleic acid fragment of the present invention, and/or nucleotide sequence information thereof, as a molecular genetic marker.

More particularly, nucleic acids or nucleic acid fragments according to the
10 present invention and/or nucleotide sequence information thereof may be used as a molecular genetic marker for quantitative trait loci (QTL) tagging, QTL mapping, DNA fingerprinting and in marker assisted selection, particularly in clovers, alfalfa, ryegrasses and fescues. Even more particularly, nucleic acids or nucleic acid fragments according to the present invention and/or nucleotide sequence
15 information thereof may be used as molecular genetic markers in plant improvement in relation to plant tolerance to biotic stresses such as viruses, micro-organisms, insects, fungal pathogens; in relation to forage quality; in relation to bloat safety; in relation to condensed tannin content; in relation to plant pigmentation. Even more particularly, sequence information revealing SNPs in
20 allelic variants of the nucleic acids or nucleic acid fragments of the present invention and/or nucleotide sequence information thereof may be used as molecular genetic markers for QTL tagging and mapping and in marker assisted selection, particularly in clovers, alfalfa, ryegrasses and fescues.

In a still further aspect of the present invention there is provided a construct
25 including a nucleic acid or nucleic acid fragment according to the present invention.

The term "construct" as used herein refers to an artificially assembled or isolated nucleic acid molecule which includes the gene of interest. In general a construct may include the gene or genes of interest, a marker gene which in some

cases can also be the gene of interest and appropriate regulatory sequences. It should be appreciated that the inclusion of regulatory sequences in a construct is optional, for example, such sequences may not be required in situations where the regulatory sequences of a host cell are to be used. The term construct includes
5 vectors but should not be seen as being limited thereto.

In a still further aspect of the present invention there is provided a vector including a nucleic acid or nucleic acid fragment according to the present invention.

The term "vector" as used herein encompasses both cloning and
10 expression vectors. Vectors are often recombinant molecules containing nucleic acid molecules from several sources.

In a preferred embodiment of this aspect of the invention, the vector may include a regulatory element such as a promoter, a nucleic acid or nucleic acid fragment according to the present invention and a terminator; said regulatory
15 element, nucleic acid or nucleic acid fragment and terminator being operatively linked.

By "operatively linked" is meant that said regulatory element is capable of causing expression of said nucleic acid or nucleic acid fragment in a plant cell and said terminator is capable of terminating expression of said nucleic acid or nucleic
20 acid fragment in a plant cell. Preferably, said regulatory element is upstream of said nucleic acid or nucleic acid fragment and said terminator is downstream of said nucleic acid or nucleic acid fragment.

The vector may be of any suitable type and may be viral or non-viral. The vector may be an expression vector. Such vectors include chromosomal, non-
25 chromosomal and synthetic nucleic acid sequences, eg. derivatives of plant viruses; bacterial plasmids; derivatives of the Ti plasmid from *Agrobacterium tumefaciens*, derivatives of the Ri plasmid from *Agrobacterium rhizogenes*; phage DNA; yeast artificial chromosomes; bacterial artificial chromosomes; binary bacterial artificial chromosomes; vectors derived from combinations of plasmids

and phage DNA. However, any other vector may be used as long as it is replicable, integrative or viable in the plant cell.

The regulatory element and terminator may be of any suitable type and may be endogenous to the target plant cell or may be exogenous, provided that they are functional in the target plant cell.

Preferably the regulatory element is a promoter. A variety of promoters which may be employed in the vectors of the present invention are well known to those skilled in the art. Factors influencing the choice of promoter include the desired tissue specificity of the vector, and whether constitutive or inducible expression is desired and the nature of the plant cell to be transformed (eg. monocotyledon or dicotyledon). Particularly suitable constitutive promoters include the Cauliflower Mosaic Virus 35S (CaMV 35S) promoter and derivatives thereof, the maize Ubiquitin promoter, and the rice Actin promoter.

A variety of terminators which may be employed in the vectors of the present invention are also well known to those skilled in the art. The terminator may be from the same gene as the promoter sequence or a different gene. Particularly suitable terminators are polyadenylation signals, such as the CaMV 35S polyA and other terminators from the nopaline synthase (*nos*), the octopine synthase (*ocs*) and the *rbcS* genes.

The vector, in addition to the regulatory element, the nucleic acid or nucleic acid fragment of the present invention and the terminator, may include further elements necessary for expression of the nucleic acid or nucleic acid fragment, in different combinations, for example vector backbone, origin of replication (*ori*), multiple cloning sites, spacer sequences, enhancers, introns (such as the maize Ubiquitin *Ubi* intron), antibiotic resistance genes and other selectable marker genes [such as the neomycin phosphotransferase (*npt2*) gene, the hygromycin phosphotransferase (*hph*) gene, the phosphinothricin acetyltransferase (*bar* or *pat*) gene and the gentamycin acetyl transferase (*aacC1*) gene], and reporter genes [such as beta-glucuronidase (*GUS*) gene (*gusA*) and green fluorescent protein

(gfp)]. The vector may also contain a ribosome binding site for translation initiation. The vector may also include appropriate sequences for amplifying expression.

As an alternative to use of a selectable marker gene to provide a phenotypic trait for selection of transformed host cells, the presence of the vector in transformed cells may be determined by other techniques well known in the art, such as PCR (polymerase chain reaction), Southern blot hybridisation analysis, histochemical GUS assays, northern and Western blot hybridisation analyses.

Those skilled in the art will appreciate that the various components of the vector are operatively linked, so as to result in expression of said nucleic acid or nucleic acid fragment. Techniques for operatively linking the components of the vector of the present invention are well known to those skilled in the art. Such techniques include the use of linkers, such as synthetic linkers, for example including one or more restriction enzyme sites.

The constructs and vectors of the present invention may be incorporated into a variety of plants, including monocotyledons (such as grasses from the genera *Lolium*, *Festuca*, *Paspalum*, *Pennisetum*, *Panicum* and other forage and turfgrasses, corn, oat, sugarcane, wheat and barley), dicotyledons (such as *Arabidopsis*, tobacco, clovers, medics, eucalyptus, potato, sugarbeet, canola, soybean, chickpea) and gymnosperms. In a preferred embodiment, the constructs and vectors may be used to transform monocotyledons, preferably grass species such as ryegrasses (*Lolium* species) and fescues (*Festuca* species), more preferably perennial ryegrass, including forage- and turf-type cultivars. In an alternate preferred embodiment, the constructs and vectors may be used to transform dicotyledons, preferably forage legume species such as clovers (*Trifolium* species) and medics (*Medicago* species), more preferably white clover (*Trifolium repens*), red clover (*Trifolium pratense*), subterranean clover (*Trifolium subterraneum*) and alfalfa (*Medicago sativa*). Clovers, alfalfa and medics are key pasture legumes in temperate climates throughout the world.

Techniques for incorporating the constructs and vectors of the present invention into plant cells (for example by transduction, transfection or

transformation) are well known to those skilled in the art. Such techniques include *Agrobacterium* mediated introduction, electroporation to tissues, cells and protoplasts, protoplast fusion, injection into reproductive organs, injection into immature embryos and high velocity projectile introduction to cells, tissues, calli, immature and mature embryos. The choice of technique will depend largely on the type of plant to be transformed.

Cells incorporating the constructs and vectors of the present invention may be selected, as described above, and then cultured in an appropriate medium to regenerate transformed plants, using techniques well known in the art. The culture conditions, such as temperature, pH and the like, will be apparent to the person skilled in the art. The resulting plants may be reproduced, either sexually or asexually, using methods well known in the art, to produce successive generations of transformed plants.

In a further aspect of the present invention there is provided a plant cell, plant, plant seed or other plant part, including, e.g. transformed with, a construct, vector, nucleic acid or nucleic acid fragment of the present invention.

The plant cell, plant, plant seed or other plant part may be from any suitable species, including monocotyledons, dicotyledons and gymnosperms. In a preferred embodiment the plant cell, plant, plant seed or other plant part may be from a monocotyledon, preferably a grass species, more preferably a ryegrass (*Lolium* species) or fescue (*Festuca* species), even more preferably perennial ryegrass, including both forage- and turf-type cultivars. In an alternate preferred embodiment the plant cell, plant, plant seed or other plant part may be from a dicotyledon, preferably forage legume species such as clovers (*Trifolium* species) and medics (*Medicago* species), more preferably white clover (*Trifolium repens*), red clover (*Trifolium pratense*), subterranean clover (*Trifolium subterraneum*) and alfalfa (*Medicago sativa*).

The present invention also provides a plant, plant seed or other plant part, or a plant extract derived from a plant cell of the present invention.

The present invention also provides a plant, plant seed or other plant part, or a plant extract derived from a plant of the present invention.

In a further aspect of the present invention there is provided a method of modifying flavonoid biosynthesis in a plant; said method including introducing
5 into said plant an effective amount of a nucleic acid or nucleic acid fragment, construct and/or a vector according to the present invention.

In a further aspect of the present invention there is provided a method of modifying protein binding, metal chelation, anti-oxidation, and/or UV-light absorption in a plant, said method including introducing into said plant an effective
10 amount of a nucleic acid or nucleic acid fragment, construct and/or a vector according to the present invention.

In a further aspect of the present invention there is provided a method of modifying pigment production in a plant, said method including introducing into said plant an effective amount of a nucleic acid or nucleic acid fragment, construct
15 and/or a vector according to the present invention.

In a further aspect of the present invention there is provided a method of modifying plant defense to biotic stresses such as viruses, micro-organisms, insects and fungal pathogens, said method including introducing into said plant an effective amount of a nucleic acid or nucleic acid fragment, construct and/or a
20 vector according to the present invention.

In a further aspect of the present invention there is provided a method of modifying forage quality of a plant by disrupting protein foam and/or conferring protection from rumen pasture bloat, said method including introducing into said plant an effective amount of a nucleic acid or nucleic acid fragment, construct
25 and/or a vector according to the present invention.

By "an effective amount" it is meant an amount sufficient to result in an identifiable phenotypic trait in said plant, or a plant, plant seed or other plant part derived therefrom. Such amounts can be readily determined by an appropriately

skilled person, taking into account the type of plant, the route of administration and other relevant factors. Such a person will readily be able to determine a suitable amount and method of administration. See, for example, Maniatis et al, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, the entire disclosure of which is incorporated herein by reference.

Using the methods and materials of the present invention, flavonoid biosynthesis, protein binding, metal chelation, anti-oxidation, UV-light absorption, tolerance to biotic stresses such as viruses, micro-organisms, insects and fungal pathogens; pigmentation in for example flowers and leaves; herbage quality and bloat-safety; and/or isoflavonoid content leading to health benefits, may be increased or otherwise modified, for example by incorporating additional copies of a sense nucleic acid or nucleic acid fragment of the present invention. They may be decreased or otherwise modified, for example by incorporating an antisense nucleic acid or nucleic acid fragment of the present invention.

The present invention will now be more fully described with reference to the accompanying Examples and drawings. It should be understood, however, that the description following is illustrative only and should not be taken in any way as a restriction on the generality of the invention described above.

In the Figures

Figure 1 shows the consensus contig nucleotide sequence of TrCH1a (Sequence ID No: 1).

Figure 2 shows the deduced amino acid sequence of TrCH1a (Sequence ID No: 2).

Figure 3 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCH1a (Sequence ID Nos: 3 to 7).

Figure 4 shows the consensus contig nucleotide sequence of TrCH1b (Sequence ID No: 8).

Figure 5 shows the deduced amino acid sequence of TrCH1b (Sequence ID No: 9).

Figure 6 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCH1b (Sequence ID Nos: 10 to 12).

Figure 7 shows the consensus contig nucleotide sequence of TrCH1c (Sequence ID No: 13).

Figure 8 shows the deduced amino acid sequence of TrCH1c (Sequence ID No: 14).

Figure 9 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCH1d (Sequence ID Nos: 15 to 16).

Figure 10 shows the consensus contig nucleotide sequence of TrCH1d (Sequence ID No: 17).

Figure 11 shows the deduced amino acid sequence of TrCH1d (Sequence ID No: 18).

Figure 12 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCH1d (Sequence ID Nos: 19 to 22).

Figure 13 shows the consensus contig nucleotide sequence of TrCHSa (Sequence ID No: 23).

Figure 14 shows the deduced amino acid sequence of TrCHSa (Sequence ID No: 24).

Figure 15 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCHSa (Sequence ID Nos: 25 to 63).

Figure 16 shows the consensus contig nucleotide sequence of TrCHSb (Sequence ID No: 64).

Figure 17 shows the deduced amino acid sequence of TrCHSb (Sequence ID No: 65).

- 5 Figure 18 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCHSb (Sequence ID Nos: 66 to 68).

Figure 19 shows the consensus contig nucleotide sequence of TrCHSc (Sequence ID No: 69).

- 10 Figure 20 shows the deduced amino acid sequence of TrCHSc (Sequence ID No: 70).

Figure 21 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCHSc (Sequence ID Nos: 71 to 77).

- 15 Figure 22 shows the consensus contig nucleotide sequence of TrCHSd (Sequence ID No: 78).

Figure 23 shows the deduced amino acid sequence of TrCHSd (Sequence ID No: 79).

- 20 Figure 24 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCHSd (Sequence ID Nos: 80 to 90).

Figure 25 shows the consensus contig nucleotide sequence of TrCHSe (Sequence ID No: 91).

- 25 Figure 26 shows the deduced amino acid sequence of TrCHSe (Sequence ID No: 92).

Figure 27 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCHSe (Sequence ID Nos: 93 and 94).

Figure 28 shows the consensus contig nucleotide sequence of TrCHSf (Sequence ID No: 95).

Figure 29 shows the deduced amino acid sequence of TrCHSf (Sequence ID No: 96).

Figure 30 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCHSf (Sequence ID Nos: 97 to 100).

Figure 31 shows the consensus contig nucleotide sequence of TrCHSg (Sequence ID No: 101).

Figure 32 shows the deduced amino acid sequence of TrCHSg (Sequence ID No: 102).

Figure 33 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCHSg (Sequence ID Nos: 103 to 105).

Figure 34 shows the consensus contig nucleotide sequence of TrCHSh (Sequence ID No: 106).

Figure 35 shows the deduced amino acid sequence of TrCHSh (Sequence ID No: 107).

Figure 36 shows the nucleotide sequence of TrCHRa (Sequence ID No: 108).

Figure 37 shows the deduced amino acid sequence of TrCHRa (Sequence ID No: 109).

Figure 38 shows the consensus contig nucleotide sequence of TrCHRB (Sequence ID No: 110).

Figure 39 shows the deduced amino acid sequence of TrCHRB (Sequence ID No: 111).

- 5 Figure 40 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCHRB (Sequence ID Nos: 112 to 116).

Figure 41 shows the consensus contig nucleotide sequence of TrCHRC (Sequence ID No: 117).

- 10 Figure 42 shows the deduced amino acid sequence of TrCHRC (Sequence ID No: 118).

Figure 43 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCHRC (Sequence ID Nos: 119 to 134).

- 15 Figure 44 shows the consensus contig nucleotide sequence of TrDFRa (Sequence ID No: 135).

Figure 45 shows the deduced amino acid sequence of TrDFRa (Sequence ID No: 136).

- 20 Figure 46 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrDFRa (Sequence ID Nos: 137 to 146).

Figure 47 shows the consensus contig nucleotide sequence of TrDFRb (Sequence ID No: 147).

- 25 Figure 48 shows the deduced amino acid sequence of TrDFRb (Sequence ID No: 148).

Figure 49 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrDFRb (Sequence ID Nos: 149 to 152).

Figure 50 shows the nucleotide sequence of TrDFRc (Sequence ID No: 153).

- 5 Figure 51 shows the deduced amino acid sequence of TrDFRc (Sequence ID No: 154).

Figure 52 shows the consensus contig nucleotide sequence of TrDFRd (Sequence ID No: 155).

- 10 Figure 53 shows the deduced amino acid sequence of TrDFRd (Sequence ID No: 156).

Figure 54 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrDFRd (Sequence ID Nos: 157 and 158).

Figure 55 shows the nucleotide sequence of TrDFRe (Sequence ID No: 159).

- 15 Figure 56 shows the deduced amino acid sequence of TrDFRe (Sequence ID No: 160).

Figure 57 shows the nucleotide sequence of TrDFRf (Sequence ID No: 161).

Figure 58 shows the deduced amino acid sequence of TrDFRf (Sequence ID No: 162).

- 20 Figure 59 shows the consensus contig nucleotide sequence of TrDFRg (Sequence ID No: 163).

Figure 60 shows the deduced amino acid sequence of TrDFRg (Sequence ID No: 164).

Figure 61 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrDFRg (Sequence ID Nos: 165 to 167).

Figure 62 shows the consensus contig nucleotide sequence of TrDFRh (Sequence
5 ID No: 168).

Figure 63 shows the deduced amino acid sequence of TrDFRh (Sequence ID No: 169).

Figure 64 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrDFRh (Sequence ID Nos: 170 to
10 184).

Figure 65 shows the consensus contig nucleotide sequence of TrLCRa (Sequence ID No: 185).

Figure 66 shows the deduced amino acid sequence of TrLCRa (Sequence ID No: 186).

15 Figure 67 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrLCRa (Sequence ID Nos: 187 to 193).

Figure 68 shows the nucleotide sequence of TrF3'5'Ha (Sequence ID No: 194).

Figure 69 shows the deduced amino acid sequence of TrF3'5'Ha (Sequence ID
20 No: 195).

Figure 70 shows the consensus contig nucleotide sequence of TrF3'5'Hb (Sequence ID No: 196).

Figure 71 shows the deduced amino acid sequence of TrF3'5'Hb (Sequence ID No: 197).

Figure 72 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrF3'5'Hb (Sequence ID Nos: 198 to 201).

Figure 73 shows the consensus contig nucleotide sequence of TrF3Ha (Sequence ID No: 202).

Figure 74 shows the deduced amino acid sequence of TrF3Ha (Sequence ID No: 203).

Figure 75 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrF3Ha (Sequence ID Nos: 204 to 244).

Figure 76 shows the nucleotide sequence of TrF3Hb (Sequence ID No: 245).

Figure 77 shows the deduced amino acid sequence of TrF3Hb (Sequence ID No: 246).

Figure 78 shows the nucleotide sequence of TrF3Hc (Sequence ID No: 247).

Figure 79 shows the deduced amino acid sequence of TrF3Hc (Sequence ID No: 248).

Figure 80 shows the consensus contig nucleotide sequence of TrF3'Ha (Sequence ID No: 249).

Figure 81 shows the deduced amino acid sequence of TrF3'Ha (Sequence ID No: 250).

Figure 82 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrF3'Ha (Sequence ID Nos: 251 and 252).

Figure 83 shows the consensus contig nucleotide sequence of TrPALa (Sequence ID No: 253).

Figure 84 shows the deduced amino acid sequence of TrPALa (Sequence ID No: 254).

- 5 Figure 85 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrPALa (Sequence ID Nos: 255 to 257).

Figure 86 shows the consensus contig nucleotide sequence of TrPALb (Sequence ID No: 258).

- 10 Figure 87 shows the deduced amino acid sequence of TrPALb (Sequence ID No: 259).

Figure 88 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrPALb (Sequence ID Nos: 260 to 267).

- 15 Figure 89 shows the nucleotide sequence of TrPALc (Sequence ID No: 268).

Figure 90 shows the deduced amino acid sequence of TrPALc (Sequence ID No: 269).

Figure 91 shows the nucleotide sequence of TrPALd (Sequence ID No: 270).

- 20 Figure 92 shows the deduced amino acid sequence of TrPALd (Sequence ID No: 271).

Figure 93 shows the nucleotide sequence of TrPALe (Sequence ID No: 272).

Figure 94 shows the deduced amino acid sequence of TrPALe (Sequence ID No: 273).

Figure 95 shows the consensus contig nucleotide sequence of TrPALf (Sequence ID No: 274).

Figure 96 shows the deduced amino acid sequence of TrPALf (Sequence ID No: 275).

- 5 Figure 97 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrPALf (Sequence ID Nos: 276 and 277).

Figure 98 shows the consensus contig nucleotide sequence of TrVRa (Sequence ID No: 278).

- 10 Figure 99 shows the deduced amino acid sequence of TrVRa (Sequence ID No: 279).

Figure 100 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrVRa (Sequence ID Nos: 280 to 285).

- 15 Figure 101 shows the consensus contig nucleotide sequence of LpDFRa (Sequence ID No: 286).

Figure 102 shows the deduced amino acid sequence of LpDFRa (Sequence ID No: 287).

- 20 Figure 103 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpDFRa (Sequence ID Nos: 288 to 292).

Figure 104 shows the consensus contig nucleotide sequence of LpDFRb (Sequence ID No: 293).

- 25 Figure 105 shows the deduced amino acid sequence of LpDFRb (Sequence ID No: 294).

Figure 106 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpDFRb (Sequence ID Nos: 295 to 297).

Figure 107 shows the consensus contig nucleotide sequence of LpF3Ha
5 (Sequence ID No: 298).

Figure 108 shows the deduced amino acid sequence of LpF3Ha (Sequence ID No: 299).

Figure 109 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpF3Ha (Sequence ID Nos: 300 to
10 302).

Figure 110 shows a plasmid map of the cDNA encoding perennial ryegrass F3OH.

Figure 111 shows the full nucleotide sequence of perennial ryegrass F3OH cDNA (Sequence ID No: 303).

Figure 112 shows the deduced amino acid sequence of perennial ryegrass F3OH
15 cDNA (Sequence ID No: 304).

Figure 113 shows plasmid maps of sense and antisense constructs of LpF3OH in pDH51 transformation vector.

Figure 114 shows plasmid maps of sense and antisense constructs of LpF3OH in pPZP221:35S² binary transformation vector.

20 Figure 115 shows screening by Southern hybridisation for RFLPs using LpF3OH as a probe.

Figure 116 shows a plasmid map of the cDNA encoding white clover BANA.

Figure 117 shows the full nucleotide sequence of white clover BANA cDNA (Sequence ID No: 305).

Figure 118 shows the deduced amino acid sequence of white clover BANA cDNA (Sequence ID No: 306).

Figure 119 shows plasmid maps of sense and antisense constructs of TrBANA in pDH51 transformation vector.

- 5 Figure 120 shows plasmid maps of sense and antisense constructs of TrBANA in pPZP221:35S² binary transformation vector.

Figure 121 shows a plasmid map of the cDNA encoding white clover CH1a.

Figure 122 shows the full nucleotide sequence of white clover CH1a cDNA (Sequence ID No: 307).

- 10 Figure 123 shows the deduced amino acid sequence of white clover CH1a cDNA (Sequence ID No: 308).

Figure 124 shows plasmid maps of sense and antisense constructs of TrCH1a in pDH51 transformation vector.

- 15 Figure 125 shows plasmid maps of sense and antisense constructs of TrCH1a in pPZP221:35S² binary transformation vector.

Figure 126 shows a plasmid map of the cDNA encoding white clover CH1d.

Figure 127 shows the full nucleotide sequence of white clover CH1d cDNA (Sequence ID No: 309).

- 20 Figure 128 shows the deduced amino acid sequence of white clover CH1d cDNA (Sequence ID No: 310).

Figure 129 shows plasmid maps of sense and antisense constructs of TrCH1d in pDH51 transformation vector.

Figure 130 shows plasmid maps of sense and antisense constructs of TrCHId in pPZP221:35S² binary transformation vector.

Figure 131 shows a plasmid map of the cDNA encoding white clover CHRc.

Figure 132 shows the full nucleotide sequence of white clover CHRc cDNA
5 (Sequence ID No: 311).

Figure 133 shows the deduced amino acid sequence of white clover CHRc cDNA (Sequence ID No: 312).

Figure 134 shows plasmid maps of sense and antisense constructs of TrCHRc in pDH51 transformation vector.

10 Figure 135 shows plasmid maps of sense and antisense constructs of TrCHRc in pPZP221:35S² binary transformation vector.

Figure 136 shows a plasmid map of the cDNA encoding white clover CHSa1.

Figure 137 shows the full nucleotide sequence of white clover CHSa1 cDNA (Sequence ID No: 313).

15 Figure 138 shows the deduced amino acid sequence of white clover CHSa1 cDNA (Sequence ID No: 314).

Figure 139 shows plasmid maps of sense and antisense constructs of TrCHSa1 in pDH51 transformation vector.

Figure 140 shows plasmid maps of sense and antisense constructs of TrCHSa1 in
20 pPZP221:35S² binary transformation vector.

Figure 141 shows a plasmid map of the cDNA encoding white clover CHSa3.

Figure 142 shows the full nucleotide sequence of white clover CHSa3 cDNA (Sequence ID No: 315).

Figure 143 shows the deduced amino acid sequence of white clover CHSa3 cDNA (Sequence ID No: 316).

Figure 144 shows plasmid maps of sense and antisense constructs of TrCHSa3 in pDH51 transformation vector.

- 5 Figure 145 shows plasmid maps of sense and antisense constructs of TrCHSa3 in pPZP221:35S² binary transformation vector.

Figure 146 shows a plasmid map of the cDNA encoding white clover CHSc.

Figure 147 shows the full nucleotide sequence of white clover CHSc cDNA (Sequence ID No: 317).

- 10 Figure 148 shows the deduced amino acid sequence of white clover CHSc cDNA (Sequence ID No: 318).

Figure 149 shows plasmid maps of sense and antisense constructs of TrCHSc in pDH51 transformation vector.

- 15 Figure 150 shows plasmid maps of sense and antisense constructs of TrCHSc in pPZP221:35S² binary transformation vector.

Figure 151 shows a plasmid map of the cDNA encoding white clover CHSd2.

Figure 152 shows the full nucleotide sequence of white clover CHSd2 cDNA (Sequence ID No: 319).

- 20 Figure 153 shows the deduced amino acid sequence of white clover CHSd2 cDNA (Sequence ID No: 320).

Figure 154 shows plasmid maps of sense and antisense constructs of TrCHSd2 in pDH51 transformation vector.

Figure 155 shows plasmid maps of sense and antisense constructs of TrCHSd2 in pPZP221:35S² binary transformation vector.

Figure 156 shows a plasmid map of the cDNA encoding white clover CHSf.

Figure 157 shows the full nucleotide sequence of white clover CHSf cDNA
5 (Sequence ID No: 321).

Figure 158 shows the deduced amino acid sequence of white clover CHSf cDNA (Sequence ID No: 322).

Figure 159 shows plasmid maps of sense and antisense constructs of TrCHSf in pDH51 transformation vector.

10 Figure 160 shows plasmid maps of sense and antisense constructs of TrCHSf in pPZP221:35S² binary transformation vector.

Figure 161 shows a plasmid map of the cDNA encoding white clover CHSh.

Figure 162 shows the full nucleotide sequence of white clover CHSh cDNA (Sequence ID No: 323).

15 Figure 163 shows the deduced amino acid sequence of white clover CHSh cDNA (Sequence ID No: 324).

Figure 164 shows plasmid maps of sense and antisense constructs of TrCHSh in pDH51 transformation vector.

Figure 165 shows plasmid maps of sense and antisense constructs of TrCHSh in
20 pPZP221:35S² binary transformation vector.

Figure 166 shows a plasmid map of the cDNA encoding white clover DFRd.

Figure 167 shows the full nucleotide sequence of white clover DFRd cDNA (Sequence ID No: 325).

Figure 168 shows the deduced amino acid sequence of white clover DFRd cDNA (Sequence ID No: 326).

Figure 169 shows plasmid maps of sense and antisense constructs of TrDFRd in pDH51 transformation vector.

- 5 Figure 170 shows plasmid maps of sense and antisense constructs of TrDFRd in pPZP221:35S² binary transformation vector.

Figure 171 shows a plasmid map of the cDNA encoding white clover F3Ha.

Figure 172 shows the full nucleotide sequence of white clover F3Ha cDNA (Sequence ID No: 327).

- 10 Figure 173 shows the deduced amino acid sequence of white clover F3Ha cDNA (Sequence ID No: 328).

Figure 174 shows plasmid maps of sense and antisense constructs of TrF3Ha in pDH51 transformation vector.

- 15 Figure 175 shows plasmid maps of sense and antisense constructs of TrF3Ha in pPZP221:35S² binary transformation vector.

Figure 176 shows a plasmid map of the cDNA encoding white clover PALa.

Figure 177 shows the full nucleotide sequence of white clover PALa cDNA (Sequence ID No: 329).

- 20 Figure 178 shows the deduced amino acid sequence of white clover PALa cDNA (Sequence ID No: 330).

Figure 179 shows plasmid maps of sense and antisense constructs of TrPALa in pDH51 transformation vector.

Figure 180 shows plasmid maps of sense and antisense constructs of TrPALa in pPZP221:35S² binary transformation vector.

Figure 181 shows a plasmid map of the cDNA encoding white clover PALb.

Figure 182 shows the full nucleotide sequence of white clover PALb cDNA
5 (Sequence ID No: 331).

Figure 183 shows the deduced amino acid sequence of white clover PALb cDNA (Sequence ID No: 332).

Figure 184 shows plasmid maps of sense and antisense constructs of TrPALb in pDH51 transformation vector.

10 Figure 185 shows plasmid maps of sense and antisense constructs of TrPALb in pPZP221:35S² binary transformation vector.

Figure 186 shows a plasmid map of the cDNA encoding white clover PALf.

Figure 187 shows the full nucleotide sequence of white clover PALf cDNA (Sequence ID No: 333).

15 Figure 188 shows the deduced amino acid sequence of white clover PALf cDNA (Sequence ID No: 334).

Figure 189 shows plasmid maps of sense and antisense constructs of TrPALf in pDH51 transformation vector.

Figure 190 shows plasmid maps of sense and antisense constructs of TrPALf in
20 pPZP221:35S² binary transformation vector.

Figure 191 shows a plasmid map of the cDNA encoding white clover VRa.

Figure 192 shows the full nucleotide sequence of white clover VRa cDNA (Sequence ID No: 335).

Figure 193 shows the deduced amino acid sequence of white clover VRa cDNA (Sequence ID No: 336).

Figure 194 shows plasmid maps of sense and antisense constructs of TrVRa in pDH51 transformation vector.

- 5 Figure 195 shows plasmid maps of sense and antisense constructs of TrVRa in pPZP221:35S² binary transformation vector.

Figure 196 shows A, infiltration of Arabidopsis plants; B, selection of transgenic Arabidopsis plants on medium containing 75 µg/ml gentamycin; C, young transgenic Arabidopsis plants; D, E, two representative results of real-time PCR
10 analysis of Arabidopsis transformed with chimeric genes involved in flavonoid biosynthesis.

Figure 197 shows the genetic map detailing the relation of perennial ryegrass genes involved in flavonoid biosynthesis.

EXAMPLE 1

- 15 **Preparation of cDNA libraries, isolation and sequencing of cDNAs coding for CHI, CHI-like, CHS, CHS-like, CHR, CHR-like, DFR, DFR-like, LCR, LCR-like, F3'5'H, F3'5'H-like, F3H, F3H-like, F3'H, F3'H-like, PAL, PAL-like, VR and VR-like proteins from white clover (*Trifolium repens*) and perennial ryegrass (*Lolium perenne*)**

20

cDNA libraries representing mRNAs from various organs and tissues of white clover (*Trifolium repens*) and perennial ryegrass (*Lolium perenne*) were prepared. The characteristics of the white clover and perennial ryegrass libraries, respectively, are described below (Tables 1 and 2).

TABLE 1

cDNA libraries from white clover (*Trifolium repens*)

Library	Organ/Tissue
01wc	Whole seedling, light grown
02wc	Nodulated root 3, 5, 10, 14, 21 & 28 day old seedling
03wc	Nodules pinched off roots of 42 day old rhizobium inoculated plants
04wc	Cut leaf and stem collected after 0, 1, 4, 6 & 14 h after cutting
05wc	Inflorescences: <50% open, not fully open and fully open
06wc	Dark grown etiolated
07wc	Inflorescence – very early stages, stem elongation, < 15 petals, 15-20 petals
08wc	seed frozen at -80°C, imbibed in dark overnight at 10°C
09wc	Drought stressed plants
10wc	AMV infected leaf
11wc	WCMV infected leaf
12wc	Phosphorus starved plants
13wc	Vegetative stolon tip
14wc	stolon root initials
15wc	Senescing stolon
16wc	Senescing leaf

TABLE 2

5

cDNA libraries from perennial ryegrass (*Lolium perenne*)

Library	Organ/Tissue
01rg	Roots from 3-4 day old light-grown seedlings
02rg	Leaves from 3-4 day old light-grown seedlings
03rg	Etiolated 3-4 day old dark-grown seedlings
04rg	Whole etiolated seedlings (1-5 day old and 17 days old)
05rg	Senescing leaves from mature plants

Library	Organ/Tissue
06rg	Whole etiolated seedlings (1-5 day old and 17 days old)
07rg	Roots from mature plants grown in hydroponic culture
08rg	Senescent leaf tissue
09rg	Whole tillers and sliced leaves (0, 1, 3, 6, 12 and 24 h after harvesting)
10rg	Embryogenic suspension-cultured cells
11rg	Non-embryogenic suspension-cultured cells
12rg	Whole tillers and sliced leaves (0, 1, 3, 6, 12 and 24 h after harvesting)
13rg	Shoot apices including vegetative apical meristems
14rg	Immature inflorescences including different stages of inflorescence meristem and inflorescence development
15rg	Defatted pollen
16rg	Leaf blades and leaf sheaths (<i>rbcL</i> , <i>rbcS</i> , <i>cab</i> , <i>wir2A</i> subtracted)
17rg	Senescing leaves and tillers
18rg	Drought-stressed tillers (pseudostems from plants subjected to PEG-simulated drought stress)
19rg	Non-embryogenic suspension-cultured cells subjected to osmotic stress (grown in media with half-strength salts) (1, 2, 3, 4, 5, 6, 24 and 48 h after transfer)
20rg	Non-embryogenic suspension-cultured cells subjected to osmotic stress (grown in media with double-strength salts) (1, 2, 3, 4, 5, 6, 24 and 48 h after transfer)
21rg	Drought-stressed tillers (pseudostems from plants subjected to PEG-simulated drought stress)
22rg	Spikelets with open and maturing florets
23rg	Mature roots (specific subtraction with leaf tissue)

The cDNA libraries may be prepared by any of many methods available. For example, total RNA may be isolated using the Trizol method (Gibco-BRL, USA) or the RNeasy Plant Mini kit (Qiagen, Germany), following the

5 manufacturers' instructions. cDNAs may be generated using the SMART PCR

- cDNA synthesis kit (Clontech, USA), cDNAs may be amplified by long distance polymerase chain reaction using the Advantage 2 PCR Enzyme system (Clontech, USA), cDNAs may be cleaned using the GeneClean spin column (Bio 101, USA), tailed and size fractionated, according to the protocol provided by Clontech. The
- 5 cDNAs may be introduced into the pGEM-T Easy Vector system 1 (Promega, USA) according to the protocol provided by Promega. The cDNAs in the pGEM-T Easy plasmid vector are transfected into *Escherichia coli* Epicurian coli XL10-Gold ultra competent cells (Stratagene, USA) according to the protocol provided by Stratagene.
- 10 Alternatively, the cDNAs may be introduced into plasmid vectors for first preparing the cDNA libraries in Uni-ZAP XR vectors according to the manufacturer's protocol (Stratagene Cloning Systems, La Jolla, CA, USA). The Uni-ZAP XR libraries are converted into plasmid libraries according to the protocol provided by Stratagene. Upon conversion, cDNA inserts will be contained in the
- 15 plasmid vector pBluescript. In addition, the cDNAs may be introduced directly into precut pBluescript II SK(+) vectors (Stratagene) using T4 DNA ligase (New England Biolabs), followed by transfection into *E. coli* DH10B cells according to the manufacturer's protocol (GIBCO BRL Products).
- Once the cDNA inserts are in plasmid vectors, plasmid DNAs are prepared
- 20 from randomly picked bacterial colonies containing recombinant plasmids, or the insert cDNA sequences are amplified via polymerase chain reaction using primers specific for vector sequences flanking the inserted cDNA sequences. Plasmid DNA preparation may be performed robotically using the Qiagen QiaPrep Turbo kit (Qiagen, Germany) according to the protocol provided by Qiagen. Amplified insert
- 25 DNAs are sequenced in dye-terminator sequencing reactions to generate partial cDNA sequences (expressed sequence tags or "ESTs"). The resulting ESTs are analyzed using an Applied Biosystems ABI 3700 sequence analyser.

EXAMPLE 2**DNA sequence analyses**

- The cDNA clones encoding CHI, CHI-like, CHS, CHS-like, CHR, CHR-like, DFR, DFR-like, LCR, LCR-like, F3'5'H, F3'5'H-like, F3H, F3H-like, F3'H, F3'H-like, PAL, PAL-like, VR and VR-like proteins were identified by conducting BLAST (Basic Local Alignment Search Tool; Altschul *et al.* (1993) *J. Mol. Biol.* 215:403-410) searches. The cDNA sequences obtained were analysed for similarity to all publicly available DNA sequences contained in the eBioinformatics nucleotide database using the BLASTN algorithm provided by the National Center for Biotechnology Information (NCBI). The DNA sequences were translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the SWISS-PROT protein sequence database using BLASTx algorithm (v 2.0.1) (Gish and States (1993) *Nature Genetics* 3:266-272) provided by the NCBI.
- The cDNA sequences obtained and identified were then used to identify additional identical and/or overlapping cDNA sequences generated using the BLASTN algorithm. The identical and/or overlapping sequences were subjected to a multiple alignment using the CLUSTALw algorithm, and to generate a consensus contig sequence derived from this multiple sequence alignment. The consensus contig sequence was then used as a query for a search against the SWISS-PROT protein sequence database using the BLASTx algorithm to confirm the initial identification.

EXAMPLE 3

- Identification and full-length sequencing of cDNAs encoding perennial ryegrass F3OH and white clover BANA, CH1a, CH1d, CHRc, CHS1, CHS3, CHSc, CHSd2, CHSf, CHSh, DFRd, F3Ha, PALa, PALb, PALf and VRa proteins**

To fully characterise for the purposes of the generation of probes for hybridisation experiments and the generation of transformation vectors, a set of

cDNAs encoding perennial ryegrass F3OH and white clover BANA, CH1a, CH1d, CHRC, CHS1, CHS3, CHS5, CHS2, CHSf, CHSh, DFRd, F3Ha, PALa, PALb, PALf and VRa proteins was identified and fully sequenced.

Full-length cDNAs were identified from our EST sequence database using relevant published sequences (NCBI databank) as queries for BLAST searches. Full-length cDNAs were identified by alignment of the query and hit sequences using Sequencher (Gene Codes Corp., Ann Arbor, MI 48108, USA). The original plasmid was then used to transform chemically competent XL-1 cells (prepared in-house, CaCl₂ protocol). After colony PCR (using HotStarTaq, Qiagen) a minimum of three PCR-positive colonies per transformation were picked for initial sequencing with M13F and M13R primers. The resulting sequences were aligned with the original EST sequence using Sequencher to confirm identity and one of the three clones was picked for full-length sequencing, usually the one with the best initial sequencing result.

Sequencing was completed by primer walking, i.e. oligonucleotide primers were designed to the initial sequence and used for further sequencing. In most cases the sequencing could be done from both 5' and 3' end. The sequences of the oligonucleotide primers are shown in Table 2. In some instances, however, an extended poly-A tail necessitated the sequencing of the cDNA to be completed from the 5' end.

Contigs were then assembled in Sequencher. The contigs include the sequences of the SMART primers used to generate the initial cDNA library as well as pGEM-T Easy vector sequence up to the EcoRI cut site both at the 5' and 3' end.

Plasmid maps and the full cDNA sequences of perennial ryegrass F3OH and white clover BANA, CH1a, CH1d, CHRC, CHS1, CHS3, CHS5, CHS2, CHSf, CHSh, DFRd, F3Ha, PALa, PALb, PALf and VRa proteins were obtained (Figures 110, 116, 121, 126, 131, 136, 141, 146, 151, 156, 161, 166, 171, 176, 181, 186 and 191).

TABLE 2

List of primers used for sequencing of the full-length cDNAs

gene name	clone ID	sequencing primer	primer sequence (5'>3')
LpF3OH	08rg1YsF07	08rg1YsF07.f1	TTGAGAGCTTCGTCGACC
		08rg1YsF07.r1	AACTCCTCGTAGTACTCC
TrCHRC	11wc1IsD03	11wc1IsD03.f1	TTCAATTGGAGTACTTGG
		11wc1IsD03.r1	ACTCCTTGTTCATATAACC
TrCHSa1	02wc2FsD07	02wc2FsD07.f1	ACATGGTGGTGGTTGAGG
		02wc2FsD07.f2	TGCTGCACTCATGTTGG
		02wc2FsD07.f3	ACATTGATAAGGCATTGG
TrCHSa3	05wc1RsB06	05wc1RsB06.f1	AGGAGGCTGCAGTCAAGG
		05wc1RsB06.f2	TGCCTGAAATTGAGAAACC
		05wc1RsB06.f3	AAAGCTAGCCTTGAAGCC
TrCHSc	07wc1TsE12	07wc1TsE12.f1	TCGGACATAACTCATGTGG
		07wc1TsE12.f2	TTGGGTGGAGAAATAAGG
		07wc1TsE12.r1	TGGACATTATTGTTTGC
		07wc1TsE12.r2	TATCATGTCTGGAAATGC
TrCHSd2	07wc1XsD03	07wc1XsD03.f1	TTTATGTGAGTACATGGC
		07wc1XsD03.f2	AGCAGCTGTGATTGTAGG
		07wc1XsD03.f3	TGAGAAAGCTCTTGTGTAGG
TrCHSf	07wc1UsD07	07wc1UsD07.f1	AGATTGCATCAAAGAATGG
		07wc1UsD07.r1	GGTCCAAAAGCCAATCC
TrCHSh	13wc2IsG04	13wc2IsG04.f1	TAAGACGAGACATAGTGG
		13wc2IsG04.r1	TATTCACTAAGCACATGC
TrDFRd	12wc1CsE09	12wc1CsE09.f1	TTACCTCGTCTGTCTCG
		12wc1CsE09.r1	AACACACACATGTCTACC
TrF3Ha	07wc1LsG03	07wc1LsG03.f1	TGAAGGATTGGAGAGAGC
		07wc1LsG03.r1	TACACAGTTGCATCTGG
TrPALa	04wc1UsB03	04wc1UsB03.f1	ATCGGAATCTGCTAGAGC
		04wc1UsB03.f2	TGTTGGTTCTGGTTTAGC
		04wc1UsB03.r1	TTCATATGCAATCCTTGC
		04wc1UsB03.r2	TCTTGGTTGTGTTGTTCC

TrPALb	05wc1PsH02	05wc1PsH02.f1	TGGGACTGATAGTTATGG
		05wc1PsH02.f2	TCTTGCTCTTGTAAATGG
		05wc1PsH02.r1	AGCACCATTCCACTCTCC
		05wc1PsH02.r2	TTCTCTTCGCTACTTGGC
TrPALf	13wc2AsD12	13wc2AsD12.f1	ATAGTGGTGTGAGGGTGG
		13wc2AsD12.f2	TCTTGTTAATGGTACTGC
		13wc2AsD12.r1	ATTTATCGCACTCTTCGC
		13wc2AsD12.r2	AAAGTGAAGACATGAGC
TrVRa	11wc1NsA07	11wc1NsA07.f1	AAGAACAGTGGATGGAGC
		11wc1NsA07.r1	TCAACTCATCTACTGATAG

EXAMPLE 4

Development of transformation vectors containing chimeric genes with cDNA sequences from perennial ryegrass F3OH and white clover BANA,

- 5 **CH1a, CH1d, CHRc, CHSa1, CHSa3, CHSc, CHSd2, CHSf, CHSh, DFRd, F3Ha, PALa, PALb, PALf and VRa**

- To alter the expression of the proteins involved in flavonoid biosynthesis, protein binding, metal chelation, anti-oxidation, UV-light absorption, tolerance to biotic stresses such as viruses, micro-organisms, insects and fungal pathogens;
- 10 pigmentation in for example flowers and leaves; herbage quality and bloat-safety and isoflavonoid content leading to health benefits, perennial ryegrass F3OH and white clover BANa, CH1a, CH1d, CHRc, CHSa1, CHSa3, CHSc, CHSd2, CHSf, CHSh, DFRd, F3Ha, PALa, PALb, PALf and VRa, through antisense and/or sense suppression technology and for over-expression of these key enzymes in
- 15 transgenic plants, a set of sense and antisense transformation vectors was produced.

- cDNA fragments were generated by high fidelity PCR using the original pGEM-T Easy plasmid cDNA as a template. The primers used (Table 3) contained recognition sites for appropriate restriction enzymes, for example EcoRI and XbaI,
- 20 for directional and non-directional cloning into the target vector. After PCR amplification and restriction digest with the appropriate restriction enzyme (usually

XbaI), the cDNA fragments were cloned into the corresponding site in pDH51, a pUC18-based transformation vector containing a CaMV 35S expression cassette. The orientation of the constructs (sense or antisense) was checked by DNA sequencing through the multi-cloning site of the vector. Transformation vectors containing chimeric genes using full-length open reading frame cDNAs encoding perennial ryegrass F3OH and white clover BANA, CH1a, CH1d, CHRc, CHSa1, CHSa3, CHSc, CHSd2, CHSf, CHSh, DFRd, F3Ha, PALa, PALb, PALf and VRa proteins in sense and antisense orientations under the control of the CaMV 35S promoter were generated (Figures 113, 119, 124, 129, 134, 139, 144, 149, 154, 159, 164, 169, 174, 179, 184, 189 and 194).

TABLE 3

List of primers used to PCR-amplify the open reading frames

gene name	clone ID	primer	primer sequence (5'→3')
LpF3OH	08rg1YsF07	08rg1YsF07f	GAATTCTAGAAGCAGAAAGTACGGACATCAGC
		08rg1YsF07r	GAATTCTAGAACCATATGGCGACACATCG
TrBANa	05wc2XsG02	05wc2XsG02f	GGATCCTCTAGAGCACTAGTGTGTATAAGTTTCTTGG
		05wc2XsG02r	GGATCCTCTAGACCCCTTAGTCTTAAATACTCG
TrCH1a	06wc2AsF12	06wc2AsF12f	GAATTCTAGAGATCTGAAACAACATAGTCACC
		06wc2AsF12r	GAATTCTAGATCAATCTTGTGCTGCAATGC
TrCH1d	12wc1FsG04	12wc1FsG04f	GAATTCTAGAAGTTCAACGAGATCAATGG
		12wc1FsG04r	GAATTCTAGATTCCGCTTGGTCTTTATTGTC
TrCHRc	11wc1IsD03	11wc1IsD03f	GAATTCTAGAACATGGGTAGTGTGAAATTC
		11wc1IsD03r	GAATTCTAGAAGATATTGAGTGAGCTTAAGG
TrCHSa1	02wc2FsD07	02wc2FsD07f	GACGTCGACATTACATACATAGCAGGAAC
		02wc2FsD07r	GACGTCGACAGTCTCTCATCTCATATAGC
TrCHSa3	05wc1RsB06	05wc1RsB06f	GAATTCTAGAAGATATGGTGAGTGTAGCTG
		05wc1RsB06r	GAATTCTAGAATCACACATCTTATATAGCC
TrCHSc	07wc1TsE12	07wc1TsE12f	GAATTCTAGAAGAAGAAATATGGGAGACGAAGG
		07wc1TsE12r	GAATTCTAGAAGACTTCATGCACACAAGTTCC
TrCHSd2	07wc1XsD03	07wc1XsD03f	GAATTCTAGAATAACCTATCAGTACTCACC
		07wc1XsD03r	GAATTCTAGAATCTAGGCAATTTAAGTGGC

TrCHSf	07wc1UsD07	07wc1UsD07f	GAATTCTAGATGATTTCATTTGTTTCCATAAC
		07wc1UsD07r	GAATTCTAGAACATATTCATCTTCCTATCAC
TrCHSh	13wc2IsG04	13wc2IsG04f	GAATTCTAGATCCAAATTCGTACCTCACC
		13wc2IsG04r	GAATTCTAGATAGTTACATCTCTCGGCAGG
TrDFRd	12wc1CsE09	12wc1CsE09f	GACGTCGACACAACAGTCTTCCACTTGAGC
		12wc1CsE09r	GACGTCGACTCTATACTCTGGTAACTATAGG
TrF3Ha	07wc1LsG03	07wc1LsG03f	GAATTCTAGAACACACACACACAAACACC
		07wc1LsG03r	GAATTCTAGAACCAAGCAGCTTAATACACG
TrPALa	04wc1UsB03	04wc1UsB03f	AGTACTGCAGAGATATGGAACTAGTAGCAGCAGC
		04wc1UsB03r	AGTACTGCAGTAGCAAAACAGTCCCAACTCC
TrPALb	05wc1PsH02	05wc1PsH02f	AGTACTGCAGATAATGGAGGGAATTACCAATGG
		05wc1PsH02r	AGTACTGCAGTGCTAATTAACATATTGGTAGAGG
TrPALf	13wc2AsD12	13wc2AsD12f	AGTACTGCAGATAATGGAGGGAATTACCAATGG
		13wc2AsD12r	AGTACTGCAGTGCTAATTAACATATTGGTAGAGG
TrVRa	11wc1NsA07	11wc1NsA07f	AGTACTGCAGATAAGAGAGTCAAAAATGGC
		11wc1NsA07r	AGTACTGCAGAACACATACTTAGAGATAGCC

EXAMPLE 5

Development of binary transformation vectors containing chimeric genes with cDNA sequences from perennial ryegrass F3OH and white clover BANa,

- 5 **CHla, CHld, CHRc, CHSa1, CHSa3, CHSc, CHSd2, CHSf, CHSh, DFRd, F3Ha, PALa, PALb, PALf and VRa**

- To alter the expression of the proteins involved in flavonoid biosynthesis, protein binding, metal chelation, anti-oxidation, UV-light absorption, tolerance to biotic stresses such as viruses, micro-organisms, insects and fungal pathogens;
- 10 pigmentation in for example flowers and leaves; herbage quality and bloat-safety and isoflavonoid content leading to health benefits, perennial ryegrass F3OH and white clover BANa, CHla, CHld, CHRc, CHSa1, CHSa3, CHSc, CHSd2, CHSf, CHSh, DFRd, F3Ha, PALa, PALb, PALf and VRa, through antisense and/or sense suppression technology and for over-expression of these key proteins in
- 15 transgenic plants, a set of sense and antisense binary transformation vectors was produced.

cDNA fragments were generated by high fidelity PCR using the original pGEM-T Easy plasmid cDNA as a template. The primers used (Table 3) contained recognition sites for appropriate restriction enzymes, for example EcoRI and XbaI, for directional and non-directional cloning into the target vector. After PCR

5 amplification and restriction digest with the appropriate restriction enzyme (usually XbaI), the cDNA fragments were cloned into the corresponding site in a modified pPZP binary vector (Hajdukiewicz *et al.*, 1994). The pPZP221 vector was modified to contain the 35S² cassette from pKYLX71:35S² as follows. pKYLX71:35S² was cut with ClaI. The 5' overhang was filled in using Klenow and the blunt end was A-

10 tailed with Taq polymerase. After cutting with EcoRI, the 2kb fragment with an EcoRI-compatible and a 3'-A tail was gel-purified. pPZP221 was cut with HindIII and the resulting 5' overhang filled in and T-tailed with Taq polymerase. The remainder of the original pPZP221 multi-cloning site was removed by digestion with EcoRI, and the expression cassette cloned into the EcoRI site and the 3' T

15 overhang restoring the HindIII site. This binary vector contains between the left and right border the plant selectable marker gene *aaaC1* under the control of the 35S promoter and 35S terminator and the pKYLX71:35S²-derived expression cassette with a CaMV 35S promoter with a duplicated enhancer region and an *rbcs* terminator.

20 The orientation of the constructs (sense or antisense) was checked by restriction enzyme digest. Transformation vectors containing chimeric genes using full-length open reading frame cDNAs encoding perennial ryegrass F3OH and white clover BANA, CH1a, CH1d, CHRc, CHSa1, CHSa3, CHSc, CHSd2, CHSf, CHSh, DFRd, F3Ha, PALa, PALb, PALf and VRa proteins in sense and antisense

25 orientations under the control of the CaMV 35S² promoter were generated (Figures 114, 120, 125, 130, 135, 140, 145, 150, 155, 160, 165, 170, 175, 180, 185, 190 and 195).

EXAMPLE 6

Production and analysis of transgenic Arabidopsis plants carrying chimeric perennial ryegrass F3OH and white clover BANa, CH1a, CH1d, CHRc, CHSa1, CHSa3, CHSc, CHSd2, CHSf, CHSh, DFRd, F3Ha, PALa, PALb, PALf and VRa genes involved in flavonoid biosynthesis

A set of transgenic Arabidopsis plants carrying chimeric perennial ryegrass and white clover genes involved in flavonoid biosynthesis, protein binding, metal chelation, anti-oxidation, UV-light absorption, tolerance to biotic stresses such as viruses, micro-organisms, insects and fungal pathogens; pigmentation in for example flowers and leaves; herbage quality and bloat-safety and isoflavonoid content leading to health benefits, were produced.

pPZP221-based transformation vectors with *LpF3OH* and *TrBANa*, *TrCH1a*, *TrCH1d*, *TrCHRc*, *TrCHSa1*, *TrCHSa3*, *TrCHSc*, *TrCHSd2*, *TrCHSf*, *TrCHSh*, *TrDFRd*, *TrF3Ha*, *TrPALa*, *TrPALb*, *TrPALf* and *TrVRa* cDNAs comprising the full open reading frame sequences in sense and antisense orientations under the control of the CaMV 35S promoter with duplicated enhancer region (35S²) were generated as detailed in Example 6.

Agrobacterium-mediated gene transfer experiments were performed using these transformation vectors.

The production of transgenic Arabidopsis plants carrying the perennial ryegrass F3OH and white clover BANa, CH1a, CH1d, CHRc, CHSa1, CHSa3, CHSc, CHSd2, CHSf, CHSh, DFRd, F3Ha, PALa, PALb, PALf and VRa cDNAs under the control of the CaMV 35S promoter with duplicated enhancer region (35S²) is described here in detail.

Preparation of Arabidopsis plants

Seedling punnets were filled with Debco seed raising mixture (Debco Pty. Ltd.) to form a mound. The mound was covered with two layers of anti-bird netting secured with rubber bands on each side. The soil was saturated with water and

enough seeds (*Arabidopsis thaliana* ecotype Columbia, Lehle Seeds #WT-02) sown to obtain approximately 15 plants per punnet. The seeds were then vernalised by placing the punnets at 4 °C. After 48 hours the punnets were transferred to a growth room at 22 °C under fluorescent light (constant illumination, 55 $\mu\text{mol m}^{-2}\text{s}^{-1}$) and fed with Miracle-Gro (Scotts Australia Pty. Ltd.) once a week. Primary bolts were removed as soon as they appeared. After 4 – 6 days the secondary bolts were approximately 6 cm tall, and the plants were ready for vacuum infiltration.

Preparation of *Agrobacterium*

Agrobacterium tumefaciens strain AGL-1 were streaked on LB medium containing 50 $\mu\text{g/ml}$ rifampicin and 50 $\mu\text{g/ml}$ kanamycin and grown at 27 °C for 48 hours. A single colony was used to inoculate 5 ml of LB medium containing 50 $\mu\text{g/ml}$ rifampicin and 50 $\mu\text{g/ml}$ kanamycin and grown over night at 27 °C and 250 rpm on an orbital shaker. The overnight culture was used as an inoculum for 500 ml of LB medium containing 50 $\mu\text{g/ml}$ kanamycin only. Incubation was over night at 27 °C and 250 rpm on an orbital shaker in a 2 l Erlenmeyer flask.

The overnight cultures were centrifuged for 15 min at 5500 xg and the supernatant discarded. The cells were resuspended in 1 l of infiltration medium [5% (w/v) sucrose, 0.03% (v/v) Silwet-L77 (Vac-In-Stuff, Lehle Seeds #VIS-01)] and immediately used for infiltration.

Vacuum Infiltration

The *Agrobacterium* suspension was poured into a container (Décor Telfresh storer, #024) and the container placed inside the vacuum desiccator (Bel Art, #42020-0000). A punnet with *Arabidopsis* plants was inverted and dipped into the *Agrobacterium* suspension and a gentle vacuum (250 mm Hg) was applied for 2 min. After infiltration, the plants were returned to the growth room where they were kept away from direct light overnight. The next day the plants were returned to full direct light and allowed to grow until the siliques were fully developed. The plants were then allowed to dry out, the seed collected from the siliques and either

stored at room temperature in a dry container or used for selection of transformants.

Selection of transformants

Prior to plating the seeds were sterilised as follows. Sufficient seeds for one
5 150 mm petri dish (approximately 40 mg or 2000 seeds) were placed in a 1.5 ml
microfuge tube. 500 μ l 70% ethanol were added for 2 min and replaced by 500 μ l
sterilisation solution (H_2O :4% chlorine:5% SDS, 15:8:1). After vigorous shaking,
the tube was left for 10 min after which time the sterilisation solution was replaced
with 500 μ l sterile water. The tube was shaken and spun for 5 sec to sediment the
10 seeds. The washing step was repeated 3 times and the seeds were left covered
with approximately 200 μ l sterile water.

The seeds were then evenly spread on 150 mm petri dishes containing
germination medium (4.61 g Murashige & Skoog salts, 10 g sucrose, 1 ml 1 M
KOH, 2 g Phytigel, 0.5 g MES and 1 ml 1000x Gamborg's B-5 vitamins per litre)
15 supplemented with 250 μ g/ml timetin and 75 μ g/ml gentamycin. After vernalisation
for 48 hours at 4 °C the plants were grown under continuous fluorescent light (55
 μ mol m⁻²s⁻¹) at 22 °C to the 6 – 8 leaf stage and transferred to soil.

Preparation of genomic DNA

3 – 4 leaves of Arabidopsis plants regenerated on selective medium were
20 harvested and freeze-dried. The tissue was homogenised on a Retsch MM300
mixer mill, then centrifuged for 10 min at 1700xg to collect cell debris. Genomic
DNA was isolated from the supernatant using Wizard Magnetic 96 DNA Plant
System kits (Promega) on a Biomek FX (Beckman Coulter). 5 μ l of the sample (50
 μ l) were then analysed on an agarose gel to check the yield and the quality of the
25 genomic DNA.

Analysis of DNA using real-time PCR

Genomic DNA was analysed for the presence of the transgene by real-time
PCR using SYBR Green chemistry. PCR primer pairs (Table 4) were designed

- using MacVector (Accelrys). The forward primer was located within the 35S² promoter region and the reverse primer within the transgene to amplify products of approximately 150 - 250 bp as recommended. The positioning of the forward primer within the 35S² promoter region guaranteed that homologous genes in
- 5 Arabidopsis were not detected.

- 5 μ l of each genomic DNA sample was run in a 50 μ l PCR reaction including SYBR Green on an ABI (Applied Biosystems) together with samples containing DNA isolated from wild type Arabidopsis plants (negative control), samples containing buffer instead of DNA (buffer control) and samples containing
- 10 the plasmid used for transformation (positive plasmid control).

Plants were obtained after transformation with all chimeric constructs and selection on medium containing gentamycin. The selection process and two representative real-time PCR analyses are shown in Figure xx.

TABLE 4

- 15 **List of primers used for Real-time PCR analysis of Arabidopsis plants transformed with chimeric perennial ryegrass genes involved in flavonoid biosynthesis**

construct	primer 1 (forward)	primer 2 (reverse)
pPZP221LpF3OHsense	TTGGAGAGGACACGCTGAAATC	AGGAGAGGGTTGGACATCGC
pPZP221LpF3OHanti	CATTTCATTGGAGAGGACACGC	ACGAGGAGTTCTGGAAGATGGG
pPZP221TrBANasense	TTGGAGAGGACACGCTGAAATC	GCAACAAACCAGTGCCACC
pPZP221TrBANaanti	TCATTTGGAGAGGACACGCTG	GATGATTGCCCCAGCAAGG
pPZP221TrCHIsense	CATTTCATTGGAGAGGACACGC	CAAGGTTCTCGACTTGGATTGC
pPZP221TrCHIanti	TCATTTGGAGAGGACACGCTG	AGATTACCTGCCTTGTGAACGAG
pPZP221TrCHIsense	TCATTTGGAGAGGACACGCTG	GACGGTAGGAGGGAATAGATTGTTCT
pPZP221TrCHIanti	TCATTTGGAGAGGACACGCTG	CCAGGTTATCCGAGTATTCAACG
pPZP221TrCHRCsense	CCACTATCCTTCGCAAGACCC	TCCCATTCCAACCACAGGC
pPZP221TrCHRCanti	TCATTTGGAGAGGACACGCTG	CAAGCCAGGACTCAGTGACCTATG
pPZP221TrCHSa1sense	TCATTTGGAGAGGACACGCTG	CTGGTCAACACGATTGCTGG
pPZP221TrCHSa1anti	TCATTTGGAGAGGACACGCTG	AACCACAGGAGGAGCTTGACTG

pPZP221TrCHSa3sense	CATTTCATTGGAGAGGACACGC	AACACGGTTTGGTGGATTTC
pPZP221TrCHSa3anti	TCATTGGAGAGGACACGCTG	ACAACCTGGAGAAGGACITGATTGG
pPZP221TrCHScsense	TTGGAGAGGACACGCTGAAATC	ACAAGTTGGTGAGGGAATGCC
pPZP221TrCHScanti	TCATTGGAGAGGACACGCTG	GGGATTGATACTTGCTTTTGAGAC
pPZP221TrCHSd2sense	CCCACTATCCTTCGCAAGACC	AGTTGCAGTGCCGATTGCC
pPZP221TrCHSd2anti	CATTTCATTGGAGAGGACACGC	AAGATGGACTTGCCACAACAGG
pPZP221TrCHSfsense	CATTTCATTGGAGAGGACACGC	TCGTTGCCTTTCCCTGAGTAGG
pPZP221TrCHSfanti	TCATTGGAGAGGACACGCTG	GATTGGCTTTTGGACCAAGG
pPZP221TrCHShsense	TCATTGGAGAGGACACGCTG	CGGTCACCAATTTTTTGTGGAGG
pPZP221TrCHShanti	TCATTGGAGAGGACACGCTG	TGTTGTGTTGGTGTGGACCG
pPZP221TrDFRdsense	CATTTCATTGGAGAGGACACGC	ATTGAGATTTGGACGCTGGC
pPZP221TrDFRdanti	CATTTCATTGGAGAGGACACGC	CGCAACCTGGATTGTTGAGAGC
pPZP221TrF3Hasense	TCATTGGAGAGGACACGCTG	TCTTCCTTAACGAACTTGACTCG
pPZP221TrF3Haanti	TCATTGGAGAGGACACGCTG	GAACAACAACCTAGGGACTTGGAGG
pPZP221TrPALasense	ATGACGCACAATCCCACTATCC	TTGCCTCAGCAGCCACACC
pPZP221TrPALaanti	GGAGAGGACACGCTGAATCAC	TGCCAAAAGAGGTTGAAAGTGC
pPZP221TrPALbsense	ATCCCACTATCCTTCGCAAGACCC	AATGACTCCCCATCAACGACTCCG
pPZP221TrPALbanti	TTGGAGAGGACACGCTGAAATC	GACAAATTTGTTACAGCTATGTGCC
pPZP221TrPALfsense	ATCCCACTATCCTTCGCAAGACCC	CACCATACGCTTCACCTCATCC
pPZP221TrPALfanti	TCATTGGAGAGGACACGCTG	TTGTTAGAGAGGAGTTAGGAACCGC
pPZP221TrVRasense	CCACTATCCTTCGCAAGACCC	GCTTACATCCCTTACGTTCTGG
pPZP221TrVRaanti	CCACTATCCTTCGCAAGACCC	AAAAGCTCGTGGACGCTGG

EXAMPLE 7

Genetic mapping of perennial ryegrass genes involved in flavonoid biosynthesis, protein binding, metal chelation, anti-oxidation, UV-light

- 5 absorption, tolerance to biotic stresses such as viruses, micro-organisms, insects and fungal pathogens; pigmentation in for example flowers and leaves; herbage quality and bloat-safety and isoflavonoid content leading to health benefits

- 10 The cDNAs representing genes involved in flavonoid biosynthesis, protein binding, metal chelation, anti-oxidation, UV-light absorption, tolerance to biotic stresses such as viruses, micro-organisms, insects and fungal pathogens;

- pigmentation in for example flowers and leaves; herbage quality and bloat-safety and isoflavonoid content leading to health benefits, were amplified by PCR from their respective plasmids, gel-purified and radio-labelled for use as probes to detect restriction fragment length polymorphisms (RFLPs). RFLPs were mapped in the F_1 (first generation) population, $NA_6 \times AU_6$. This population was made by crossing an individual (NA_6) from a North African ecotype with an individual (AU_6) from the cultivar Aurora, which is derived from a Swiss ecotype. Genomic DNA of the 2 parents and 114 progeny was extracted using the 1 x CTAB method of Fulton et al. (1995).
- Probes were screened for their ability to detect polymorphism using the DNA (10 μ g) of both parents and 5 F_1 progeny restricted with the enzymes *DraI*, *EcoRI*, *EcoRV* or *HindIII*. Hybridisations were carried out using the method of Sharp et al. (1988). Polymorphic probes were screened on a progeny set of 114 individuals restricted with the appropriate enzyme (Figure 115).
- RFLP bands segregating within the population were scored and the data was entered into an Excel spreadsheet. Alleles showing the expected 1:1 ratio were mapped using MAPMAKER 3.0 (Lander et al. 1987). Alleles segregating from, and unique to, each parent, were mapped separately to give two different linkage maps. Markers were grouped into linkage groups at a LOD of 5.0 and ordered within each linkage group using a LOD threshold of 2.0.
- Loci representing genes involved in flavonoid biosynthesis mapped to the linkage groups as indicated in Table 5 and in Figure 197. These gene locations can now be used as candidate genes for quantitative trait loci associated with flavonoid biosynthesis, protein binding, metal chelation, anti-oxidation, UV-light absorption, tolerance to biotic stresses such as viruses, micro-organisms, insects and fungal pathogens; pigmentation in for example flowers and leaves; herbage quality and bloat-safety and isoflavonoid content leading to health benefits.

TABLE 5

Map locations of ryegrass genes involved in flavonoid biosynthesis across two genetic linkage maps of perennial ryegrass

Probe	Polymorphic	Mapped with	Locus	Linkage group	
				NA ₆	AU ₆
<i>LpDFRb</i>	Y	<i>Hind</i> III	<i>LpDFRb</i>	6	6

5

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Finally, it is to be understood that various alterations, modifications and/or additions may be made without departing from the spirit of the present invention as outlined herein.

It will also be understood that the term "comprises" (or its grammatical
15 variants) as used in this specification is equivalent to the term "includes" and should not be taken as excluding the presence of other elements or features.

Documents cited in this specification are for reference purposes only and their inclusion is not acknowledgment that they form part of the common general knowledge in the relevant art.

CLAIMS

1. A substantially purified or isolated nucleic acid or nucleic acid fragment encoding a flavonoid biosynthetic enzyme selected from the group consisting of chalcone isomerase (CHI), chalcone synthase (CHS), chalcone reductase (CHR), dihydroflavonol 4-reductase (DFR), leucoanthocyanidin reductase (LCR), flavonoid 3', 5' hydrolase (F3'5'H), flavanone 3-hydroxylase (F3H), flavonoid 3'-hydroxylase (F3'H), phenylalanine ammonia-lyase (PAL) and vestitone reductase (VR) from a clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species, or a functionally active fragment or variant thereof.
2. A nucleic acid or nucleic acid fragment according to Claim 1, wherein said clover species is white clover (*Trifolium repens*) and said ryegrass species is perennial ryegrass (*Lolium perenne*).
3. A nucleic acid or nucleic acid fragment according to Claim 1, encoding a CHI or CHI-like protein and including a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 1, 3, 4, 6, 7, 9, 10, 12, 122 and 127 hereto (Sequence ID Nos: 1, 3 to 7, 8, 10 to 12, 13, 15 and 16, 17, 19 to 22, 307, and 309, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).
4. A nucleic acid or nucleic acid fragment according to Claim 1, encoding a CHS or CHS-like protein and including a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 13, 15, 16, 18, 19, 21, 22, 24, 25, 27, 28, 30, 31, 33, 34, 137, 142, 147, 152, 157 and 162 hereto (Sequence ID Nos: 23, 25 to 63, 64, 66 to 68, 69, 71 to 77, 78, 80 to 90, 91, 93 and 94, 95, 97 to 100, 101, 103 to 105, 106, 313, 315, 317, 319, 321, and 323, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

5. A nucleic acid or nucleic acid fragment according to Claim 1, encoding a CHR or CHR-like protein and including nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 36, 38, 40, 41, 43 and 132 hereto (Sequence ID Nos: 108, 110, 112 to 116, 117, 119 to 134, and 311, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

6. A nucleic acid or nucleic acid fragment according to Claim 1, encoding a DFR or DFR-like protein and including a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 44, 46, 47, 49, 50, 52, 54, 55, 57, 59, 61, 62, 64, 101, 103, 104, 106, 117 and 167 hereto (Sequence ID Nos: 135, 137 to 146, 147, 149 to 152, 153, 155, 157 and 158, 159, 161, 163, 165 to 167, 168, 170 to 184, 286, 288 to 292, 293, 295 to 297, 305, and 325, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

7. A nucleic acid or nucleic acid fragment according to Claim 1, encoding an LCR or LCR-like protein and including a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 65 and 67 hereto (Sequence ID Nos: 185 and 187 to 193, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

8. A nucleic acid or nucleic acid fragment according to Claim 1, encoding a F3'5'H or F3'5'H-like protein and including a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 68, 70 and 72 hereto (Sequence ID Nos: 194, 196, and 198 to 201, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

9. A nucleic acid or nucleic acid fragment according to Claim 1, encoding a F3H or F3H-like protein and including a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 73, 75, 76, 78, 107, 109, 111 and 172 hereto (Sequence ID Nos: 202, 204 to 244, 245, 247, 298, 300
5 to 302, 303, and 327, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

10. A nucleic acid or nucleic acid fragment according to Claim 1,
10 encoding a F3'H or F3'H-like protein and including a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 80 and 82 hereto (Sequence ID Nos: 249, and 251 and 252, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences
15 recited in (a), (b) and (c).

11. A nucleic acid or nucleic acid fragment according to Claim 1, encoding a PAL or PAL-like protein and including a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 83, 85, 86, 88, 89, 91, 93, 95, 97, 177, 182 and 187 hereto (Sequence ID Nos: 253, 255 to 257, 258,
20 260 to 267, 268, 270, 272, 274, 276 and 277, 329, 331, and 333, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

12. A nucleic acid or nucleic acid fragment according to Claim 1,
25 encoding a VR or VR-like protein and including a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 98, 100 and 192 hereto (Sequence ID Nos: 278, 280 to 285, and 335, respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants
30 of the sequences recited in (a), (b) and (c).

13. A construct including a nucleic acid or nucleic acid fragment according to Claim 1.
14. A vector including a nucleic acid or nucleic acid fragment according to Claim 1.
- 5 15. A vector according to Claim 14, further including a promoter and a terminator, said promoter, nucleic acid or nucleic acid fragment and terminator being operatively linked.
16. A plant cell, plant, plant seed or other plant part, including a construct according to claim 13 or a vector according to Claim 14.
- 10 17. A plant, plant seed or other plant part derived from a plant cell or plant according to Claim 16.
18. A method of modifying flavonoid biosynthesis in a plant, said method including introducing into said plant an effective amount of a nucleic acid or nucleic acid fragment according to Claim 1, a construct according to claim 13 and/or a
15 vector according to Claim 14.
19. A method of modifying protein binding, metal chelation, anti-oxidation, and/or UV-light absorption in a plant, said method including introducing into said plant an effective amount of a nucleic acid or nucleic acid fragment according to Claim 1, a construct according to claim 13 and/or a vector according to
20 Claim 14.
20. A method of modifying pigment production in a plant, said method including introducing into said plant an effective amount of a nucleic acid or nucleic acid fragment according to Claim 1, a construct according to claim 13 and/or a vector according to Claim 14.
- 25 21. A method of modifying plant defense to a biotic stress, said method including introducing into said plant an effective amount of a nucleic acid or nucleic

acid fragment according to Claim 1, a construct according to claim 13 and/or a vector according to Claim 14.

22. A method according to claim 21 wherein said biotic stress is selected from the group consisting of viruses, microorganisms, insects and fungal
5 pathogens.

23. A method of modifying forage quality of a plant by disrupting protein foam and/or conferring protection from rumen pasture bloat, said method including introducing into said plant an effective amount of a nucleic acid or nucleic acid fragment according to Claim 1, a construct according to claim 13 and/or a vector
10 according to Claim 14.

24. Use of a nucleic acid or nucleic acid fragment according to Claim 1, and/or nucleotide sequence information thereof, and/or single nucleotide polymorphisms thereof as a molecular genetic marker.

25. A substantially purified or isolated polypeptide from a clover
15 (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species, selected from the group consisting of ASR and ASR-like, A22 and A22-like, CYS and CYS-like, LEA and LEA-like, DHN and DHN-like and PKABA and PKABA-like; and functionally active fragments and variants thereof.

26. A polypeptide according to Claim 25, wherein said clover species is
20 white clover (*Trifolium repens*) and said ryegrass species is perennial ryegrass (*Lolium perenne*).

27. A polypeptide according to Claim 25, wherein said polypeptide is CHI or CHI-like and includes an amino acid sequence selected from the group consisting of sequences shown in Figures 2, 5, 8, 11, 123 and 128 hereto
25 (Sequence ID Nos: 2, 9, 14, 18, 308, and 310, respectively); and functionally active fragments and variants thereof.

28. A polypeptide according to Claim 25, wherein said polypeptide is CHS or CHS-like and includes an amino acid sequence selected from the group

consisting of sequences shown in Figures 14, 17, 20, 23, 26, 29, 32, 35, 138, 143, 148, 153, 158 and 163 hereto (Sequence ID Nos: 24, 65, 70, 79, 92, 96, 102, 107, 314, 316, 318, 320, 322, and 324, respectively); and functionally active fragments and variants thereof.

5 29. A polypeptide according to Claim 25, wherein said polypeptide is CHR or CHR-like and includes an amino acid sequence selected from the group consisting of sequences shown in Figures 37, 39, 42 and 133 hereto (Sequence ID Nos: 109, 111, 118, and 312, respectively); and functionally active fragments and variants thereof.

10 30. A polypeptide according to Claim 25, wherein said polypeptide is DFR or DFR-like and includes an amino acid sequence selected from the group consisting of sequences shown in Figures 45, 48, 51, 53, 56, 58, 60, 63, 102, 105, 118 and 168 hereto (Sequence ID Nos: 136, 148, 54, 156, 160, 162, 164, 169, 287, 294, 306, and 326, respectively); and functionally active fragments and
15 variants thereof.

31. A polypeptide according to Claim 25, wherein said polypeptide is LCR or LCR-like and includes an amino acid sequence shown in Figure 66 hereto (Sequence ID No: 186); and functionally active fragments and variants thereof.

32. A polypeptide according to Claim 25, wherein said polypeptide is
20 F3'5'H or F3'5'H-like and includes an amino acid sequence selected from the group consisting of sequences shown in Figures 69 and 71 hereto (Sequence ID Nos: 195 and 197, respectively); and functionally active fragments and variants thereof.

33. A polypeptide according to Claim 25, wherein said polypeptide is
25 F3H or F3H-like and includes an amino acid sequence selected from the group consisting of sequences shown in Figures 74, 77, 79, 108, 112 and 173 hereto (Sequence ID Nos: 203, 246, 248, 299, 304, and 328, respectively); and functionally active fragments and variants thereof.

34. A polypeptide according to Claim 25, wherein said polypeptide is F3'H or F3'H-like and includes an amino acid sequence selected from the group consisting of sequences shown in Figure 81 hereto (Sequence ID No: 250); and functionally active fragments and variants thereof.
- 5 35. A polypeptide according to Claim 25, wherein said polypeptide is PAL or PAL-like and includes an amino acid sequence selected from the group consisting of sequences shown in Figures 84, 87, 90, 92, 94, 96, 178, 183 and 188 hereto (Sequence ID Nos: 254, 259, 269, 271, 273, 275, 330, 332, and 334, respectively); and functionally active fragments and variants thereof.
- 10 36. A polypeptide according to Claim 25, wherein said polypeptide is VR or VR-like and includes an amino acid sequence selected from the group consisting of sequences shown in Figures 99 and 193 hereto (Sequence ID Nos: 279 and 336, respectively); and functionally active fragments and variants thereof.

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TrCH1a : GCATTAAACANTGAAANITGACACAGTCCCAACAAAGATCTGAAACACATAGCTCCCCATT : 60
 * 20 * 40 * 60

TrCH1a : TTTTAACATTAAACTAAAAATATGTCGGCCATCACCGBAATCCAAGTCGAGAACCTTGAA : 120
 * 80 * 100 * 120

TrCH1a : TTTCCGGCTGTGATTACTTCTCCGGCCACCGGTAAAGTCATATTTTCTGGTGGTGCAGGG : 180
 * 140 * 160 * 180

TrCH1a : GAGAGAGGTTTGACTATTGAAGGAACTTCATCAAGTTCAGTCCATAGGAGTATATTTG : 240
 * 200 * 220 * 240

TrCH1a : GAAGATGTAGCAGTGGCTTCACTTGCCACTAAATGGAAGGGCAAATCCTCTGAAGAGTTG : 300
 * 260 * 280 * 300

TrCH1a : CTTGAGACCCTTGACTTCTACAGAGATATCATTTTCAGGACCATTGAGAAGTTGATTCTGA : 360
 * 320 * 340 * 360

TrCH1a : GGATCGAAGATTAGGGAATTGAGTGGTCTCTGAGTACTCAAGGAAGGTTAATGAAAACGTGT : 420
 * 380 * 400 * 420

TrCH1a : GTGGCACACTTAAAATCTGTTGGGACTTATGGAGATGCAGAAGTTGAAGCTATGCAAAAA : 480
 * 440 * 460 * 480

TrCH1a : TTTGTTGAAGCCTTCAAGCCTATTAATTTTCCACCTGGTGCCCTCTGTTTTTTACAGGCAA : 540
 * 500 * 520 * 540

TrCH1a : TCACCTGATGGAATATTAGGGCTTAGTTTCTCTCAAGATGCAAGTATACCAGAAAAGGAA : 600
 * 560 * 580 * 600

TrCH1a : GCTGCAGTAATAGAGAAACAAAGGGAGCTTCATCGGCG : 636
 * 620 *

FIGURE 1

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      *           20           *           40           *           60
TrCH1a : MSAITAIQVENLEPPAVITSPATGKSYFLGGAGERGLTIEGNPIKFTAIQVYLEDVAVAS : 60

      *           80           *           100          *           120
TrCH1a : LATKWKGKSSEELLETLDFYRDIISGPFEKLIRGSKIRELSGPEYSRKVNENCVAHLKSV : 120

      *           140          *           160          *           180
TrCH1a : GTYGDAEVEAMQKFVEAFKPINFPPGASVFYRQSPDGILGLSPSQDASIQEKEAAVIENK : 180

TrCH1a : GASSA : 185

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FIGURE 2

TrChIA1: 20 40 60 80 100 120 140 160 180 200 220 240 260 280 300 320 340 360 380 400 420
TrChIA2: SCATTAACAACTGAAATATGCTGATATGAAGAAGATCTGAAACACATAGCTCCCAAT : 57
TrChIA3: GATTCGCGTCCCAACAAGATCTGAAACACATAGCTCCCAAT : 45
TrChIA4: GATCTGAAACACATAGCTCCCAAT : 23
TrChIA5: GATCTGAAACACATAGCTCCCAAT : 24

TrChIA1: 20 40 60 80 100 120 140 160 180 200 220 240 260 280 300 320 340 360 380 400 420
TrChIA2: TTTTAACATTAACATAAAATATGTCGGCCATCACCAGCAATCCAAGTCGAGAACCCTGAA : 117
TrChIA3: TTTTAACATTAACATAAAATATGTCGGCCATCACCAGCAATCCAAGTCGAGAACCCTGAA : 105
TrChIA4: TTTTAACATTAACATAAAATATGTCGGCCATCACCAGCAATCCAAGTCGAGAACCCTGAA : 81
TrChIA5: TTTTAACATTAACATAAAATATGTCGGCCATCACCAGCAATCCAAGTCGAGAACCCTGAA : 111

TrChIA1: 20 40 60 80 100 120 140 160 180 200 220 240 260 280 300 320 340 360 380 400 420
TrChIA2: TTTCCGCGCTGCTTACTTCTCCGGCCACCGGTAAAGTCATATTTCTTGGTGGTGCAGGG : 177
TrChIA3: TTTCCGCGCTGCTTACTTCTCCGGCCACCGGTAAAGTCATATTTCTTGGTGGTGCAGGG : 165
TrChIA4: TTTCCGCGCTGCTTACTTCTCCGGCCACCGGTAAAGTCATATTTCTTGGTGGTGCAGGG : 143
TrChIA5: TTTCCGCGCTGCTTACTTCTCCGGCCACCGGTAAAGTCATATTTCTTGGTGGTGCAGGG : 144

TrChIA1: 20 40 60 80 100 120 140 160 180 200 220 240 260 280 300 320 340 360 380 400 420
TrChIA2: SAGAGAGGTTGACATATTGAAGGAAATTCATCAAGTTCACCTGCAATAGGAGTATATTTC : 237
TrChIA3: SAGAGAGGTTGACATATTGAAGGAAATTCATCAAGTTCACCTGCAATAGGAGTATATTTC : 225
TrChIA4: SAGAGAGGTTGACATATTGAAGGAAATTCATCAAGTTCACCTGCAATAGGAGTATATTTC : 203
TrChIA5: SAGAGAGGTTGACATATTGAAGGAAATTCATCAAGTTCACCTGCAATAGGAGTATATTTC : 231

TrChIA1: 20 40 60 80 100 120 140 160 180 200 220 240 260 280 300 320 340 360 380 400 420
TrChIA2: GAAGATGTAGCAGTGGCTTCACCTGCCACATAATGGAAGGGCAAAATCCTCTGAAGAGTTG : 284
TrChIA3: GAAGATGTAGCAGTGGCTTCACCTGCCACATAATGGAAGGGCAAAATCCTCTGAAGAGTTG : 283
TrChIA4: GAAGATGTAGCAGTGGCTTCACCTGCCACATAATGGAAGGGCAAAATCCTCTGAAGAGTTG : 268
TrChIA5: GAAGATGTAGCAGTGGCTTCACCTGCCACATAATGGAAGGGCAAAATCCTCTGAAGAGTTG : 291

TrChIA1: 20 40 60 80 100 120 140 160 180 200 220 240 260 280 300 320 340 360 380 400 420
TrChIA2: CTTGAGACCTTTGACTTCTACAGAGATATCATTTTCAGGACCAATTTGAGAAGTTGATTCGG : 345
TrChIA3: CTTGAGACCTTTGACTTCTACAGAGATATCATTTTCAGGACCAATTTGAGAAGTTGATTCGG : 323
TrChIA4: CTTGAGACCTTTGACTTCTACAGAGATATCATTTTCAGGACCAATTTGAGAAGTTGATTCGG : 351
TrChIA5: CTTGAGACCTTTGACTTCTACAGAGATATCATTTTCAGGACCAATTTGAGAAGTTGATTCGG : 351

TrChIA1: 20 40 60 80 100 120 140 160 180 200 220 240 260 280 300 320 340 360 380 400 420
TrChIA2: CGATCGAAGATTAGGGAATTGAGTGGTCTTGAGTACTCAAGGAAGGTTAAATGAAACATGT : 405
TrChIA3: CGATCGAAGATTAGGGAATTGAGTGGTCTTGAGTACTCAAGGAAGGTTAAATGAAACATGT : 383
TrChIA4: CGATCGAAGATTAGGGAATTGAGTGGTCTTGAGTACTCAAGGAAGGTTAAATGAAACATGT : 383
TrChIA5: CGATCGAAGATTAGGGAATTGAGTGGTCTTGAGTACTCAAGGAAGGTTAAATGAAACATGT : 411

FIGURE 3

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	*	440	*	460	*	480	
TrCH1a1:	-----		-----		-----		-
TrCH1a2:	GTGGC	CACCTTAA	AATCTGTTGCC	ACTTACGG	GAGATGCAGA	AGTTGAAG	CTATGCAAAA : 465
TrCH1a3:	GTGGC	CACCTTAA	AATCTGTTGGG	ACTTATGG	GAGATGCTGAAG	CTGAAG	CTATGCAAAA : 443
TrCH1a4:	-----		-----		-----		-
TrCH1a5:	GTGGC	CACCTTAA	AATCTGTTGGG	ACTTATGG	GAGATGCAGA	AGTTGAAG	CTATGCAAAA : 471
	*	500	*	520	*	540	
TrCH1a1:	-----		-----		-----		-
TrCH1a2:	TTTGT	TGAAGCCTTCAAG	CCTATTAA	TTTTCAC	CTGGTG	CTCTGTTT	TTTACAGGC : 525
TrCH1a3:	TTTGT	TGAAGCCTTCAAG	CCTATTAA	TTTTCAC	CTGGTG	CTCTGTTT	TTTACAGGC : 503
TrCH1a4:	-----		-----		-----		-
TrCH1a5:	TTTGT	TGAAGCCTTCAAG	CCTATTAA	TTTTCAC	CTGGTG	CTCTGTTT	TTTACAGGC : 531
	*	560	*	580	*	600	
TrCH1a1:	-----		-----		-----		-
TrCH1a2:	TCACCT	GATGGAATATTAGGG	CTTAGT	TTCTCTCAAG	ATGCAAGTATACC	CAGAAAAGG	AA : 585
TrCH1a3:	TCACCT	GATGGAATATTAGGG	CTTAGT	TTCTCTCAAG	ATGCAAGTATACC	CAGAAAAGG	AG : 563
TrCH1a4:	-----		-----		-----		-
TrCH1a5:	TCACCT	GATGGAATATTAGGG	CTTAGT	TTCTCTCAAG	ATGCAAGTATACC	CAGAAAAGG	AA : 589
	*	620	*				
TrCH1a1:	-----		-----				-
TrCH1a2:	GCTGC	AGTAATAGAGA	CAAA	-----			: 606
TrCH1a3:	GCTGC	AGTAATAGAGA	CAAAAGGG	AGCTTCAT	GGGG		: 599
TrCH1a4:	-----		-----				-
TrCH1a5:	-----		-----				-

FIGURE 3 (cont)

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      *           20           *           40           *           60
TrCH1b : TTAAAAATTGACACAGTCCCAACCTTAAANTTGACCNNGTCCCAACAAAGATCTGAAACA : 60

      *           80           *           100          *           120
TrCH1b : ACATAGCCCCCATTTTAAACATTAAACTAAAAATATGTCTGCCATCACCGCAATCCAA : 120

      *           140          *           160          *           180
TrCH1b : GTCGAGAACCTTGAATTCCCGGGGTGATTACTTCTCCGSTCAACGGTAAGTCATATTTT : 180

      *           200          *           220          *           240
TrCH1b : CTTGGTGGTGCAGGGGAGAGAGGTINGACTATTGAAGGAAACTTCATCAAGTTCACTGCC : 240

      *           260          *           280          *           300
TrCH1b : ATAGGAGTATATTGGAAGATGTAGCAGGGGCTTCACTTGCCACTAAATGGAAGGGCAGA : 300

      *           320           *
TrCH1b : TCCTCTGAAGAGNGCTTGAGACCCCTNGACTNC : 332

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FIGURE 4

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                *           20           *           40           *           60
TrChIb : MSAITAIQVENLEFPVITSPVNGKSYPLGGAGERGXTIEGNFIKFTAIQVYLEDVAGAS : 60

                *
TrChIb : LATKWKGGRSSEEXLRPXT : 78

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```

      *           20           *           40           *           60
TrCH1b1: TTAATAATTGACCNAGTCCNAACCTTAAANTTGACCNNGGTCCCAAACAAAGATCTGAAACA : 60
TrCH1b2: TTAATAATTGACACAGTCCCAACCTTAAANTTGACCNNGGTCCCAAACAAAGATCTGAAACA : 59
TrCH1b3: -----GCGTTAAANTTGACCCAGTCCNAACAAAGATCTGAAAG-- : 38

      *           80           *           100          *           120
TrCH1b1: ACATAGCCCCCATTTTTTAACATTAAACTAAAAATATGTCTGCCATCACCGCAATCCAA : 120
TrCH1b2: ACATAGCCCCCATTTTTTAACATTAAACTAAAAATATGTCTGCCATCACCGCAATCCAA : 119
TrCH1b3: ACATAGCCCCCATTTTTTAACATTAAACTAAAAATATGTCTGCCATCACCGCAATCCAA : 98

      *           140          *           160          *           180
TrCH1b1: GTCGAGAACCTTGAATTCCCGGCGGTGATTACTTCTCCGGTCAACGGTAAGTCATATTT : 180
TrCH1b2: GTCGAGAACCTTGAATTCCCGGCGGTGATTACTTCTCCGGTCAACGGTAAGTCATATTT : 179
TrCH1b3: GTCGAGAACCTTGAATTCCCGGCGGTGATTACTTCTCCGGTCAACGGTAAGTCATATTT : 158

      *           200          *           220          *           240
TrCH1b1: CTGTGTTGGTGCAGGGGACAGAGGTTTACTATTGAAGGAAACTTCATCAAGTTCAGTGGC : 240
TrCH1b2: CTGTGTTGGTGCAGGGGACAGAGGTTTACTATTGAAGGAAACTTCATCAAGTTCAGTGGC : 239
TrCH1b3: CTGTGTTGGTGCAGGGGACAGAGGTTTACTATTGAAGGAAACTTCATCAAGTTCAGTGGC : 186

      *           260          *           280          *           300
TrCH1b1: TTAGGAGTATATTTTGAAGATGTAGCAGGGGCTTCACTTCCCACTAAATGGAAGGCCA : 300
TrCH1b2: TTAGGAGTATATTTTGAAGATGTAGCAGGGGCTTCACTTCCCACTAAATGGAAGGCCA : 299
TrCH1b3: ----- : -

      *           320           *
TrCH1b1: TCCTCTGAATAGNCNTTGAACCTTNGACTNN : 332
TrCH1b2: TCCTCTGAAGAGCGCTTGAGACCTTGACTTC : 331
TrCH1b3: ----- : -

```

FIGURE 6

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      *           20           *           40           *           60
TrCHic : GTTAGNAGNAGNATNTCNGGCACCCCTTTGAAAAGTTGATTGAGGATCGAAGATTAGGGA : 60

      *           80           *           100          *           120
TrCHic : ATTGAGTGGTCTGAGTACTCAAGGAAGGTTAATGAAAAGTGCCTGGGCACACTTAAATC : 120

      *           140          *           160          *           180
TrCHic : TGTGGGACTTATGGAGATGCAGAAGCTGAAGCTATGCAAAAATTTGTTGAAGCCTTCAA : 180

      *           200          *           220          *           240
TrCHic : GCCTATTAAFTTTCCACCTGGTGCCCTCTGTTTTTACAGGCAATCACCTGATGGAATATT : 240

      *           260          *
TrCHic : AGGGGTTAGTATTGCCAATTCATTTTTTTTAACT : 274

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FIGURE 7

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TrCHIC : * 20 * 40 * 60
 : A P F E K L I R G S K I R E L S G P E Y S R K V N E N C V A H L K S V G T Y G D A E A E A M Q K F V E A F K P I N F P P : 60

 * 80 *
TrCHIC : G A S V F Y R Q S P D G I L G V S I A N S F F L T I L I R V R P D C : 94

FIGURE 8

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      *           20           *           40           *           60
TrCHic1: GTTAGNAGNATNNTTTCNGGCACCCTTTGAAAAGTTGATTTCGAGGATCGAAGATTAGGGA : 60
TrCHic2: -----GNATNTTTCGACCCCTTGAAAAGTTGATTTCGAGGATCGAAGATTAGGGA : 50

      *           80           *           100          *           120
TrCHic1: ATTGAGTGGTCCTGAGTACTCAAGGAAGGTTAATGAAAAC TGCGTGGCACACTTAAAAATC : 120
TrCHic2: ATTGAGTGGTCCTGAGTACTCAAGGAAGGTTAATGAAAAC TGCGTGGCACACTTAAAAATC : 110

      *           140          *           160          *           180
TrCHic1: TCTTGGGACTTATGGAGATGCAGAAGCTGAAGCTATGCAAAAAATTTGTGTAAGCCITCAG : 180
TrCHic2: TCTTGGGACTTATGGAGATGCAGAAGCTGAAGCTATGCAAAAAATTTGTGTAAGCCITCAG : 170

      *           200          *           220          *           240
TrCHic1: GCCTATTAAATTTCCACCTGGTGCCCTCTGTTTTTTACAGGCAATCACCTGATGGAATATT : 240
TrCHic2: GCCTATTAAATTTCCACCTGGTGCCCTCTGTTTTTTACAGGCAATCACCTGATGGAATATT : 230

      *           260           *
TrCHic1: AGGGGTTAGTATTGCCAATTCATTTTTTTTAACT : 274
TrCHic2: AGGGGTTAGTATTGCCAATTCATTTTTTTTAACT : 264

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FIGURE 9

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TrCHid : TTNANTNNNNNTNNCGGGCAATTACAACACACCTTCTCCATTACCATCTATCTT : 60

TrCHid : CTACTAAGTTCAACGAGATCAATGGCACTTCCTTCTGTACCGCTTTGAATATCGAGAAC : 120

TrCHid : AATCTATTCCCTCCTACCGTCACACCACGGGATCCACCAACAATTCTTCTCTCGCGGT : 180

TrCHid : GCAGGAGAGCGGGTCTTCAAATTCAAGACAAATTGTCAAATTACCGCTATTGGTGTT : 240

TrCHid : TATCTACAGGACATTGCTGTTCCTTACCTCGCCACTAAATGGAAGGTAAGACTGCTCAA : 300

TrCHid : GAGCTAACGGAACTGTTTCCTTCTTCAGGACATCGTTACAGGTCCATTGAGAAATTT : 360

TrCHid : ATGCAGGTGACAATGATCTTGCCATTGACTGGGCAACAATACTCAGAGAAAGTGTCAGAA : 420

TrCHid : AATTGTGTAGCTATTGGGAAGTCTCTTGGGATTTATACCGACGAAGAAGCCAAAGCAATT : 480

TrCHid : GAGAAGNNTGTTTCTGTCTTCAAAGANGAAACATTCCCACCGGCTCCTCTATCTCTTTC : 540

TrCHid : ACAGNATTACCCAAAGGATTAGGATCACTAACGATAAGNTTCTCTAAAGATGGATCCATT : 600

TrCHid : CCAGAGACCGAGTCTGCAGTTATAGAGAATAAGTACTCTCACAGCTGTGCTNGAGTCG : 660

TrCHid : ATGATAGGGGCACACGGTGTCTCCCTGCGAGCAAAACAGAGTTTGGCCACCAGGNTAHC : 720

TrCHid : CGAGNTATTCAACGAGGNTGGCTGATGCCTAGCAACTTGATNATATCAACAAACGAAAA : 780

TrCHid : TGAAAGNCCTTTCTGCAATAAAGAACAAGCGGAAATTTATTTT : 825

FIGURE 10

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      *           20           *           40           *           60
TrCHid : MALPSVTALNIENNLFPPPTVTPPGSTNNFFLGGAGERGLQIQDKFVKFTAIGVYLQDIAY : 60

      *           80           *           100          *           120
TrCHid : PYLATKWKGKTAQELTETVPFFRDIVTGPFKEFMQVMTMILPLTGQQYSEKVSENCVAIWK : 120

      *           140          *           160          *           180
TrCHid : SLGIYTDEBAKAIEKVSVFKETFPFPGSSILFTLPKGLGSLTIXFSKDGSI PETESAVIEN : 180

      *           200          *           220          *
TrCHid : KLLSQAVXESMIGAHGVSPAAKQSFQGHQXXRXIQRXWLMPSNLI XISTKRK : 230

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FIGURE 11

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      *           20           *           40           *           60
TrCHid1: TTNANTNNNN/PTNNCGGTGTTTNNANAACACACACACCTTCT-TTTCATTTATCTT : 59
TrCHid2: -----GCAATTACAACCTNNCAACACCTTCTCCG-PTA-CTCTATCTT : 41
TrCHid3: -----TTAG-AGT-CACACACCTTCTCCATTACCATCTATCTT : 37
TrCHid4: -----TCACATTTATACAACTACAACCTAAACAT : 28

      *           80           *           100          *           120
TrCHid1: CTACTAAGTTCAACGAGATCAATGGCACCTTCTTCTGTGTCNCCGCTTTGAATATCGAGAAC : 119
TrCHid2: CTACTAAGTTCAACGAGATCAATGGCACCTTCTTCTGTGTCNCCGCTTTGAATATCGAGAAC : 101
TrCHid3: CTACTAAGTTCAACGAGATCAATGGCACCTTCTTCTGTGTCNCCGCTTTGAATATCGAGAAC : 97
TrCHid4: TNACCTGTTAAAGAGATNAAAGGCACCTTCTTCTGTGTCNCCGCTTTGAATATCGAGAAC : 87

      *           140          *           160          *           180
TrCHid1: AATCTATTCCCTCCTACCGTCACACCAACGGGATCCCAACAACATTTCTTCTCGGCGGT : 179
TrCHid2: AATCTATTCCCTCCTACCGTCACACCAACGGGATCCCAACAACATTTCTTCTCGGCGGT : 161
TrCHid3: AATCTATTCCCTCCTACCGTCACACCAACGGGATCCCAACAACATTTCTTCTCGGCGGT : 157
TrCHid4: AATCTATTCCCTCCTACCGTCACACCAACGGGATCCCAACAACATTTCTTCTCGGCGGT : 147

      *           200          *           220          *           240
TrCHid1: GCAGGAGAGCGGGGTCTTCAAAATCAAGACAACATTTGTCAAATTCACCGCTATTGGTGT : 239
TrCHid2: GCAGGAGAGCGGGGTCTTCAAAATCAAGACAACATTTGTCAAATTCACCGCTATTGGTGT : 221
TrCHid3: GCAGGAGAGCGGGGTCTTCAAAATCAAGACAACATTTGTCAAATTCACCGCTATTGGTGT : 217
TrCHid4: GCAGGAGAGCGGGGTCTTCAAAATCAAGACAACATTTGTCAAATTCACCGCTATTGGTGT : 207

      *           260          *           280          *           300
TrCHid1: TATCTACAGGACATTGCTGTTCCTTACCTGCGCATTAATGGAAGGGTTGAGCTGCTCTT : 299
TrCHid2: TATCTACAGGACATTGCTGTTCCTTACCTGCGCATTAATGGAAGGGTTGAGCTGCTCTT : 266
TrCHid3: TATCTACAGGACATTGCTGTTCCTTACCTGCGCATTAATGGAAGGGTTGAGCTGCTCTT : 277
TrCHid4: TATCTACAGGACATTGCTGTTCCTTACCTGCGCATTAATGGAAGGGTTGAGCTGCTCTT : 267

      *           320          *           340          *           360
TrCHid1: GAGCTAACCGAACTGTTCTTCTTTCAGGGACATGTTNNCAGGTCCATTGTGAGAAATTT : 359
TrCHid2: ----- : -
TrCHid3: GAGCTAACCGAACTGTTCTTCTTTCAGGGACATGTTTACAGGTCCATTGTGAGAAATTT : 337
TrCHid4: GAGCTAACCTGTTCTTCTTTCAGGGACATGTTTACAGGTCCATTGTGAGAAATTT : 327

      *           380          *           400          *           420
TrCHid1: ATTGAGGTGACAAATGATCTTGCCATTGACTGGGCAACAATACTCAGAGAAAGTGTGAG : 419
TrCHid2: ----- : -
TrCHid3: ATTGAGGTGACAAATGATCTTGCCATTGACTGGGCAACAATACTCAGAGAAAGTGTGAG : 397
TrCHid4: ATTGAGGTGACAAATGATCTTGCCATTGACTGGGCAACAATACTCAGAGAAAGTGTGAG : 387

      *           440          *           460          *           480
TrCHid1: AATTGTGTAGCTATTTGCTGAAGTCTCTTTCGGATTATATACCGACCAAGAAGCCAAAGCAATT : 479
TrCHid2: ----- : -
TrCHid3: AATTGTGTAGCTATTTGGAAGTCTCTTGGGATTATATACCGACGAAGAAGCCAAAGCAATT : 457
TrCHid4: AATTGTGTAGCTATTTGGAAGTCTCTTGGGATTATATACCGACGAAGAAGCCAAAGCAATT : 447

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FIGURE 12

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      *           500           *           520           *           540
TrCHid1: GAGAAGNNTGTTTCTGTCCTTCAAAGANGAAACATCCCACCAGGCTCCTCTATCCTTTTC : 539
TrCHid2: ----- : -
TrCHid3: GAGAAGTTTGTTCCTGCTTCAAAGATGAAACATCCCACCAGGCTCCCTCATCCTTTTC : 517
TrCHid4: GANAANNNTGNTTCTGNTTNN----- : 468

      *           560           *           580           *           600
TrCHid1: TCAGNATTACCCAAAGGATTANGATCACTAACGATAAGNTTCTCTAAAGATGGATCCAT : 599
TrCHid2: ----- : -
TrCHid3: ACAGTATTACCCAAAGGATTAGGATCACTAACGATAAGNTTCTCTAAAGATGGATCCAT : 577
TrCHid4: ----- : -

      *           620           *           640           *           660
TrCHid1: CCAGAGACCGAGTCTGCAGTTATAGNGAATAAGCTACTCTCACAGCTGTGCTNGAGTCG : 659
TrCHid2: ----- : -
TrCHid3: CCAGAGACCGAGTCTGCAGTTATAGAGAATAAGCTACTCTCACAGCTGTGCTNGAGTCG : 637
TrCHid4: ----- : -

      *           680           *           700           *           720
TrCHid1: ATGATAGGGGCANNCGGTGCTCTNNCNTGCANCAANCAAGCTTTGNNACCAGGNTANC : 719
TrCHid2: ----- : -
TrCHid3: ATGATAGGGGCCTACGGTGTCTCCCCCTGCAGCAAAACAGAGTTTGGCCACCAGGTTATC : 696
TrCHid4: ----- : -

      *           740           *           760           *           780
TrCHid1: CHAGNTATCAACGAGGNTGGCTGATGCCTAGCANCTTGATNNNTNAAACAAAACNAAAA : 779
TrCHid2: ----- : -
TrCHid3: CGAGTTATTCACCGAGGTTGGTGGATGCTAGCAACGGATATATCAACAAAACGAAAA : 753
TrCHid4: ----- : -

      *           800           *           820
TrCHid1: TGNANGNCCTTTTCTGCNTTAAAGAAACA----- : 807
TrCHid2: ----- : -
TrCHid3: TGAAGTCCTTTCTGCAATAAAGATCAAGCGGAAATTTTATTTT : 797
TrCHid4: ----- : -

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FIGURE 12 (cont)

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TrCHSa: TATTNTNNGAAACCACTTTGTGTTGAAGNCGTGAACCTTNGCTACCCCTCCATATNATCATAT : 60

TrCHSa: NACCTCTTCTGAGACCCCTTCATCATAGAAANACAACACACNTCAGCNCTTTGCTTNTTCT : 120

TrCHSa: ACAACAACCTATAACTANACATATTTATTTTATNTATTTAGTATATATTAATGAAATAAAT : 180

TrCHSa: GCTAAAGATANTTTATTAGATATGGTGAAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT : 240

TrCHSa: GAAGGCCCTGCAACCACTTTTGGCCATTGGCACTGCAAAATCCAGCAAAACCGTGTGAGCAG : 300

TrCHSa: AGCACATATCCTGATTTCTACTTCAAAATCACAACAGTGAGCACAAGACTGAGCTCAA : 360

TrCHSa: GAGAAATCCAGCGCATGTGTGACAAATCTATGATCAAGAGCAGATACATGTATCTAACA : 420

TrCHSa: GAAGAGATTTTGAAGAAAAATCCTAGTCTTTTGAATACATGGCACCTTCATTGGATGCT : 480

TrCHSa: AGGCAAGACATGGTGGTGGTTGAGGTACCTAGACTTTGGGAAGGAGGCTGCAGTGAAGGCT : 540

TrCHSa: ATTAAGAATGGGGTCAACCAAAGTCAAAGATTACTCACTTAATCTTTTGCAACCACAAAT : 600

TrCHSa: GGTGTAGACATGCCCTGGTGCCTGATTACCAACTCACAAAATCTTTAGGTCTTCGCCCATAT : 660

TrCHSa: GTGAAGAGGTACATGATGTACCAACAAGGGTGCCTTTCAGGTGGGACGGTCTTCGTTTG : 720

TrCHSa: GCAAAAGATTTGGCCGAGAAACAACAAGGTGCTCGTGTGTGGTTGTTTGTCTGAAGTA : 780

TrCHSa: ACCGCAGTCACATTCGCGGGCCCACTGACACTCACTTGGACAGTCTTGTGGACAAGCA : 840

TrCHSa: CTATTTGGAGATGGAGCTGCTGCACTCATTTGTTGGCTCAGACCCAGTACCAGAAATTGAG : 900

TrCHSa: AAACCAATATTTGAGATGGTATGGACCGCACAGACAATTGCTCCAGACAGTGAAGGTGCC : 960

TrCHSa: ATTGATGGTCACCTTGTGAAGCTGGACTAACATTTTCATCTTCTTAAAGATGTTCTCTGGG : 1020

TrCHSa: ATTGTATCAAAAGACATTAATAAAGCATTGGTGCAGGCTTTCCAAACCATTAGGAATTTCT : 1080

TrCHSa: GATTACAACCTCAATCTTTTGGATTGCACACCCGGTGGACCTGCAATTTCT : 1130

FIGURE 13

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      *           20           *           40           *           60
TrCHSa : MVSVAEIRKAQRABGPATILAIGTANPANRVBQSTYPDFYFKITNSEHKTTELKEKFRMC : 60

      *           80           *           100          *           120
TrCHSa : DKSMIKSRMYLTEEILKENPSLCEYMAPSLDARQDMVVVEVPRLGKEAAVKAKEWGQP : 120

      *           140          *           160          *           180
TrCHSa : KSKITHLIFCTTSGVDMPGADYQLTKLLGLRPYVKRYMMYQQGCFAGGTVLRRLAKDLAEN : 180

      *           200          *           220          *           240
TrCHSa : NKGARVLVVCSEVTAVTFRGPSDTHLDSLVGQALFGDGAAALIVGSDPVPPEIEKPIFEMV : 240

      *           260          *           280          *           300
TrCHSa : WTAQTIAPDSEGAIDGHLREAGLTFHLLKDVPGIVSKNINKALVEAFQPLGISDYNSIFW : 300

TrCHSa : IAHPGGPAI : 309

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FIGURE 14

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	*	20	*	40	*	60	
TrCHSa1 :	<u>PATNTNNGAAACCACTTGTGTTGAAGNCGTGAACCTTNGCTACCCCTCCATATNATACTAT</u>						: 60
TrCHSa2 :	-----						: -
TrCHSa3 :	-----						: -
TrCHSa4 :	-----						: -
TrCHSa5 :	-----						: -
TrCHSa6 :	-----						: -
TrCHSa7 :	-----						: -
TrCHSa8 :	-----						: -
TrCHSa9 :	-----						: -
TrCHSa10 :	-----						: -
TrCHSa11 :	-----						: -
TrCHSa12 :	-----						: -
TrCHSa13 :	-----						: -
TrCHSa14 :	-----						: -
TrCHSa15 :	-----						: -
TrCHSa16 :	-----						: -
TrCHSa17 :	-----						: -
TrCHSa18 :	-----						: -
TrCHSa19 :	-----						: -
TrCHSa20 :	-----						: -
TrCHSa21 :	-----						: -
TrCHSa22 :	-----						: -
TrCHSa23 :	-----						: -
TrCHSa24 :	-----						: -
TrCHSa25 :	-----						: -
TrCHSa26 :	-----						: -
TrCHSa27 :	-----						: -
TrCHSa28 :	-----						: -
TrCHSa29 :	-----						: -
TrCHSa30 :	-----						: -
TrCHSa31 :	-----						: -
TrCHSa32 :	-----						: -
TrCHSa33 :	-----						: -
TrCHSa34 :	-----						: -
TrCHSa35 :	-----						: -
TrCHSa36 :	-----						: -
TrCHSa37 :	-----						: -
TrCHSa38 :	-----						: -
TrCHSa39 :	-----						: -

FIGURE 15

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		*	80	*	100	*	120	
TrCHSa1 :	NACCTCTTCTGAGACCCCTTCATCATATATATATAACNCATCTCACTCATACATATTTC							: 120
TrCHSa2 :	-----GNANNACAACACACCTTCAC-----CTTTGCTCTTTCT							: 32
TrCHSa3 :	-----CACNTTACGNCCTTTGCTCTTTCT							: 23
TrCHSa4 :	-----CACNTTACGCTTTGCTCTTTCT							: 21
TrCHSa5 :	-----GCANACGCT							: 9
TrCHSa6 :	-----ACN							: 3
TrCHSa7 :	-----CC							: 3
TrCHSa8 :	-----CN							: 2
TrCHSa9 :	-----CC							: 2
TrCHSa10 :	-----							: -
TrCHSa11 :	-----							: -
TrCHSa12 :	-----							: -
TrCHSa13 :	-----							: -
TrCHSa14 :	-----							: -
TrCHSa15 :	-----							: -
TrCHSa16 :	-----							: -
TrCHSa17 :	-----							: -
TrCHSa18 :	-----							: -
TrCHSa19 :	-----							: -
TrCHSa20 :	-----							: -
TrCHSa21 :	-----							: -
TrCHSa22 :	-----							: -
TrCHSa23 :	-----							: -
TrCHSa24 :	-----							: -
TrCHSa25 :	-----							: -
TrCHSa26 :	-----							: -
TrCHSa27 :	-----							: -
TrCHSa28 :	-----							: -
TrCHSa29 :	-----							: -
TrCHSa30 :	-----							: -
TrCHSa31 :	-----							: -
TrCHSa32 :	-----							: -
TrCHSa33 :	-----							: -
TrCHSa34 :	-----							: -
TrCHSa35 :	-----							: -
TrCHSa36 :	-----							: -
TrCHSa37 :	-----							: -
TrCHSa38 :	-----							: -
TrCHSa39 :	-----							: -

FIGURE 15 (cont)

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      *           140           *           160           *           180
TrCHSa1 : ACAACAAGCTATAACTTNNCTCTTATCTTAAACCAATTGAGTTTCAAATTACATAATA :180
TrCHSa2 : ACAACAAGCTTATATTAAGACTTTTCTTACTTAA--AACTTATAGCAATGCTATA--TA : 85
TrCHSa3 : ACAACAAGCTTTTGTCTTAAAGCTTTTCTTACTTAAATTGCTATAGATAGAAANKCTANCT : 83
TrCHSa4 : AGACAGTCTCTGCTACTTAAAGCTTTTCTTACTTAAATTGAGTTTAACTTGTATACATAGAAA--GTA--CT : 74
TrCHSa5 : CTATGCGCTTACTTTTCTTAAATTTAAAGCTCTTGTATATAAGCAAGCTGCTTTTCTTCT : 69
TrCHSa6 : AATCAACCTATGCTATATTTATATTTATTA--TATATGCTATATAATGAGTAA--CT : 57
TrCHSa7 : NGGAAGAGCTCTCTCTCAGCATATTTCTTATATATATTTNGTCTATAATTGAAAGAACT : 62
TrCHSa8 : CAAATTAATCTCTCTTAAACATATTTATCTCTCTTCTTATAATTGAAAGAA--CT : 57
TrCHSa9 : CAAATTAATCTCTCTTAAACATATTTATTTATATATTTTATATATAATTGAAAGAACT : 62
TrCHSa10 : TCTACAATCTTAACTTNNCTCTTATTTTAAATTTAGCTTNNAAATTTACATACAAA : 60
TrCHSa11 : AATACAACCTCAACATATTTATATTTATATA--TATNGTCTATAATTGAAAGAA--CT : 52
TrCHSa12 : CAACAACCTTAACTT--CTCTTATTTAAAGCTATTGAGTTTAAATTTAGTACATA : 50
TrCHSa13 : CAACAACCTTAACTTNNCTCTTATTTTAAATTTAGCTTNNAAATTTAGTACATA : 59
TrCHSa14 : GATTAATCTCTCTGCAATATATTTATCTTNTTACTGTATAATTGAAAGAACT : 58
TrCHSa15 : AACAACCTATAACTT--CTCTTATTTAAAGCTATTGAGTTTAAATTTAGTACATA : 50
TrCHSa16 : AATACAACCTCAACATATTTATTTATATTTAGCTTATAATTGAAAGAACT : 58
TrCHSa17 : AATACAACCTATAACTTNNCTCTTATTTTAAATTTAGCTTNNAAATTTAGTACATA : 57
TrCHSa18 : GGTCTTAAACACCTAAAGGCTTCTATTTTCTTAAATTTAGCTTATAATTGAAAGAACT : 56
TrCHSa19 : AATACAACCTCAACATATTTATTTATTTATTTAGCTTATAATTGAAAGAACT : 55
TrCHSa20 : AATACAACCTCAACATATTTATTTATTTATTTAGCTTATAATTGAAAGAACT : 53
TrCHSa21 : AATACAACCTCAACATATTTATTTATTTATTTAGCTTATAATTGAAAGAACT : 52
TrCHSa22 : AATACAACCTCAACATATTTATTTATTTATTTAGCTTATAATTGAAAGAACT : 49
TrCHSa23 : AATACAACCTCAACATATTTATTTATTTATTTAGCTTATAATTGAAAGAACT : 45
TrCHSa24 : AATACAACCTCAACATATTTATTTATTTATTTAGCTTATAATTGAAAGAACT : 47
TrCHSa25 : AATACAACCTCAACATATTTATTTATTTATTTAGCTTATAATTGAAAGAACT : 47
TrCHSa26 : AATACAACCTCAACATATTTATTTATTTATTTAGCTTATAATTGAAAGAACT : 40
TrCHSa27 : AATACAACCTCAACATATTTATTTATTTATTTAGCTTATAATTGAAAGAACT : 37
TrCHSa28 : AATACAACCTCAACATATTTATTTATTTATTTAGCTTATAATTGAAAGAACT : 42
TrCHSa29 : AATACAACCTCAACATATTTATTTATTTATTTAGCTTATAATTGAAAGAACT : 21
TrCHSa30 : AATACAACCTCAACATATTTATTTATTTATTTAGCTTATAATTGAAAGAACT : 2
TrCHSa31 : AATACAACCTCAACATATTTATTTATTTATTTAGCTTATAATTGAAAGAACT : 2
TrCHSa32 : AATACAACCTCAACATATTTATTTATTTATTTAGCTTATAATTGAAAGAACT : -
TrCHSa33 : AATACAACCTCAACATATTTATTTATTTATTTAGCTTATAATTGAAAGAACT : -
TrCHSa34 : AATACAACCTCAACATATTTATTTATTTATTTAGCTTATAATTGAAAGAACT : -
TrCHSa35 : AATACAACCTCAACATATTTATTTATTTATTTAGCTTATAATTGAAAGAACT : 3
TrCHSa36 : AATACAACCTCAACATATTTATTTATTTATTTAGCTTATAATTGAAAGAACT : 1
TrCHSa37 : AATACAACCTCAACATATTTATTTATTTATTTAGCTTATAATTGAAAGAACT : -
TrCHSa38 : AATACAACCTCAACATATTTATTTATTTATTTAGCTTATAATTGAAAGAACT : -
TrCHSa39 : AATACAACCTCAACATATTTATTTATTTATTTAGCTTATAATTGAAAGAACT : -

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FIGURE 15 (cont)

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      *           200           *           220           *           240
TrCHSa1 : GCGGAACATAGTAAATACAGATGGTACTGTTTCTGAAATTCGCAAGGCTCAAGGGGCT :240
TrCHSa2 : G-----TATCAAC-----ATGGTACTGTCTCTGAAATTCGCAAGGCTCAAGGGGCT :137
TrCHSa3 : GCTAAAGATANNATCAAGNATGGTACTGTCTCTGAAATTCGCAAGGCTCAAGGGGCT :143
TrCHSa4 : GCTAAAGA-----TATCAAC-----ATGGTACTGTCTCTGAAATTCGCAAGGCTCAAGGGGCT :128
TrCHSa5 : TTAATACTTACTATTATTAAGATATGGTGAGTGTATCTGAAATTCGTAAGGCTCAAGGGGCT :129
TrCHSa6 : GCTAAAGATA-TTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT :116
TrCHSa7 : TCTAAAGATANTTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT :122
TrCHSa8 : GCTAAAGATA-TTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT :116
TrCHSa9 : TCTAAAGATANTTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT :122
TrCHSa10: GCGGAATATATTAATAAGATATGGTACTGTCTCTGAAATTCGCAAGGCTCAAGGGGCT :120
TrCHSa11: GCTAAAGATA-TTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT :111
TrCHSa12: GCGGAATATATTAATAAGATATGGTACTGTCTCTGAAATTCGCAAGGCTCAGAGGGCT :110
TrCHSa13: GCGGAATATATTAATAAGATATGGTACTGTCTCTGAAATTCGCAAGGCTCAGAGGGCT :119
TrCHSa14: GCTAAAGATA-TTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT :117
TrCHSa15: GCGGAATATATTAATAAGATATGGTACTGTCTCTGAAATTCGCAAGGCTCAGAGGGCT :110
TrCHSa16: TCTAAAGATANTTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT :118
TrCHSa17: GCGGAATATATTAATAAGATATGGTACTGTCTCTGAAATTCGCAAGGCTCAGAGGGCT :117
TrCHSa18: GCGGAATATAGTATTAAGATATGGTACTGTCTCTGAAATTCGCAAGGCTCAGAGGGCT :116
TrCHSa19: GCTAAAGATANTTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT :115
TrCHSa20: TCTAAAGATANTTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT :113
TrCHSa21: TCTAAAGATANTTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT :112
TrCHSa22: TCTAAAGATANTTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT :109
TrCHSa23: G-----TATCAAC-----ATGGTACTGTCTCTGAAATTCGCAAGGCTCAAGGGGCT :103
TrCHSa24: GCGGAATATAGTATTAAGATATGGTACTGTCTCTGAAATTCGCAAGGCTCAGAGGGCT :107
TrCHSa25: GCTAAAGATANTTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT :107
TrCHSa26: GCGGAATATATTAATAAGATATGGTACTGTCTCTGAAATTCGCAAGGCTCAGAGGGCT :98
TrCHSa27: GCGGAATATAGTATTAAGATATGGTACTGTCTCTGAAATTCGCAAGGCTCAGAGGGCT :95
TrCHSa28: GCGGAATATAGTATTAAGATATGGTACTGTCTCTGAAATTCGCAAGGCTCAGAGGGCT :102
TrCHSa29: GCGGAATATAGTATTAAGATATGGTACTGTCTCTGAAATTCGCAAGGCTCAGAGGGCT :77
TrCHSa30: GCTAAAGATA-TTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT :61
TrCHSa31: TCTAAAGATANTTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT :58
TrCHSa32: TCTAAAGATA-TTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT :58
TrCHSa33: TCTAAAGATANTTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT :58
TrCHSa34: GCGGAATATAGTATTAAGATATGGTACTGTCTCTGAAATTCGCAAGGCTCAGAGGGCT :13
TrCHSa35: GCGGAATATAGTATTAAGATATGGTACTGTCTCTGAAATTCGCAAGGCTCAGAGGGCT :11
TrCHSa36: GCGGAATATAGTATTAAGATATGGTACTGTCTCTGAAATTCGCAAGGCTCAGAGGGCT :9
TrCHSa37: TCTAAAGATANTTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT :5
TrCHSa38: TCTAAAGATANTTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT :4
TrCHSa39: TCTAAAGATANTTATTAAGATATGGTGAGTGTAGCTGAAATTCGCAAGGCTCAGAGGGCT :4

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FIGURE 15 (cont)

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                *           260           *           280           *           300
TrCHSa1 : GAAGGCCCTGCAACATTTTGGCCATTGGCACTGCAAAATCCAGCAAAACCGTGTGAGCAG :300
TrCHSa2 : GAAGGCCCTGCAACATTTTGGCCATTGGCACTGCAAAATCCAGCAAAACCGTGTGAGCAG :197
TrCHSa3 : GAAGGCCCTGCAACATTTTGGCCATTGGCACTGCAAAATCCAGCAAAACCGTGTGAGCAG :203
TrCHSa4 : GAAGGCCCTGCAACATTTTGGCCATTGGCACTGCAAAATCCAGCAAAACCGTGTGAGCAG :188
TrCHSa5 : GAAGGCCCTGCAACATTTTGGCCATTGGCACTGCAAAATCCAGCAAAACCGTGTGAGCAG :189
TrCHSa6 : GAAGGCCCTGCAACATTTTGGCCATTGGCACTGCAAAATCCAGCAAAACCGTGTGAGCAG :176
TrCHSa7 : GAAGGCCCTGCAACATTTTGGCCATTGGCACTGCAAAATCCAGCAAAACCGTGTGAGCAG :182
TrCHSa8 : GAAGGCCCTGCAACATTTTGGCCATTGGCACTGCAAAATCCAGCAAAACCGTGTGAGCAG :176
TrCHSa9 : GAAGGCCCTGCAACATTTTGGCCATTGGCACTGCAAAATCCAGCAAAACCGTGTGAGCAG :182
TrCHSa10 : GAAGGCCCTGCAACATTTTGGCCATTGGCACTGCAAAATCCAGCAAAACCGTGTGAGCAG :180
TrCHSa11 : GAAGGCCCTGCAACATTTTGGCCATTGGCACTGCAAAATCCAGCAAAACCGTGTGAGCAG :171
TrCHSa12 : GAAGGCCCTGCAACATTTTGGCCATTGGCACTGCAAAATCCAGCAAAACCGTGTGAGCAG :170
TrCHSa13 : GAAGGCCCTGCAACATTTTGGCCATTGGCACTGCAAAATCCAGCAAAACCGTGTGAGCAG :179
TrCHSa14 : GAAGGCCCTGCAACATTTTGGCCATTGGCACTGCAAAATCCAGCAAAACCGTGTGAGCAG :177
TrCHSa15 : GAAGGCCCTGCAACATTTTGGCCATTGGCACTGCAAAATCCAGCAAAACCGTGTGAGCAG :170
TrCHSa16 : GAAGGCCCTGCAACATTTTGGCCATTGGCACTGCAAAATCCAGCAAAACCGTGTGAGCAG :178
TrCHSa17 : GAAGGCCCTGCAACATTTTGGCCATTGGCACTGCAAAATCCAGCAAAACCGTGTGAGCAG :177
TrCHSa18 : GAAGGCCCTGCAACATTTTGGCCATTGGCACTGCAAAATCCAGCAAAACCGTGTGAGCAG :176
TrCHSa19 : GAAGGCCCTGCAACATTTTGGCCATTGGCACTGCAAAATCCAGCAAAACCGTGTGAGCAG :175
TrCHSa20 : GAAGGCCCTGCAACATTTTGGCCATTGGCACTGCAAAATCCAGCAAAACCGTGTGAGCAG :173
TrCHSa21 : GAAGGCCCTGCAACATTTTGGCCATTGGCACTGCAAAATCCAGCAAAACCGTGTGAGCAG :172
TrCHSa22 : GAAGGCCCTGCAACATTTTGGCCATTGGCACTGCAAAATCCAGCAAAACCGTGTGAGCAG :169
TrCHSa23 : GAAGGCCCTGCAACATTTTGGCCATTGGCACTGCAAAATCCAGCAAAACCGTGTGAGCAG :163
TrCHSa24 : GAAGGCCCTGCAACATTTTGGCCATTGGCACTGCAAAATCCAGCAAAACCGTGTGAGCAG :167
TrCHSa25 : GAAGGCCCTGCAACATTTTGGCCATTGGCACTGCAAAATCCAGCAAAACCGTGTGAGCAG :167
TrCHSa26 : GAAGGCCCTGCAACATTTTGGCCATTGGCACTGCAAAATCCAGCAAAACCGTGTGAGCAG :158
TrCHSa27 : GAAGGCCCTGCAACATTTTGGCCATTGGCACTGCAAAATCCAGCAAAACCGTGTGAGCAG :155
TrCHSa28 : GAAGGCCCTGCAACATTTTGGCCATTGGCACTGCAAAATCCAGCAAAACCGTGTGAGCAG :162
TrCHSa29 : GAAGGCCCTGCAACATTTTGGCCATTGGCACTGCAAAATCCAGCAAAACCGTGTGAGCAG :137
TrCHSa30 : GAAGGCCCTGCAACATTTTGGCCATTGGCACTGCAAAATCCAGCAAAACCGTGTGAGCAG :121
TrCHSa31 : GAAGGCCCTGCAACATTTTGGCCATTGGCACTGCAAAATCCAGCAAAACCGTGTGAGCAG :118
TrCHSa32 : GAAGGCCCTGCAACATTTTGGCCATTGGCACTGCAAAATCCAGCAAAACCGTGTGAGCAG :118
TrCHSa33 : GAAGGCCCTGCAACATTTTGGCCATTGGCACTGCAAAATCCAGCAAAACCGTGTGAGCAG :118
TrCHSa34 : GAAGGCCCTGCAACATTTTGGCCATTGGCACTGCAAAATCCAGCAAAACCGTGTGAGCAG : 71
TrCHSa35 : -----ACTTTTCTCTTGGCACTGCAAAATCCAGCAAAACCGTGTGAGCAG : 59
TrCHSa36 : -----TCCATTGTCCTTGGCACTGCAAAATCCAGCAAAACCGTGTGAGCAG : 57
TrCHSa37 : -----
TrCHSa38 : -----
TrCHSa39 : -----

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FIGURE 15 (cont)

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      *           320           *           340           *           360
TrCHSa1 : AGACATATCCTGATTTCCTACTTCAAAATCACTAACAGTGAGCCTAACGGTTGAGCTC :360
TrCHSa2 : AGACATATCCTGATTTCCTACTTCAAAATCACTAACAGTGAGCCTAACGGTTGAGCTC :367
TrCHSa3 : AGACATATCCTGATTTCCTACTTCAAAATCACTAACAGTGAGCCTAACGGTTGAGCTC :368
TrCHSa4 : AGACATATCCTGATTTCCTACTTCAAAATCACTAACAGTGAGCCTAACGGTTGAGCTC :368
TrCHSa5 : AGACATATCCTGATTTCCTACTTCAAAATCACTAACAGTGAGCCTAACGGTTGAGCTC :369
TrCHSa6 : AGACATATCCTGATTTCCTACTTCAAAATCACTAACAGTGAGCCTAACGGTTGAGCTC :369
TrCHSa7 : AGACATATCCTGATTTCCTACTTCAAAATCACTAACAGTGAGCCTAACGGTTGAGCTC :369
TrCHSa8 : AGACATATCCTGATTTCCTACTTCAAAATCACTAACAGTGAGCCTAACGGTTGAGCTC :369
TrCHSa9 : AGACATATCCTGATTTCCTACTTCAAAATCACTAACAGTGAGCCTAACGGTTGAGCTC :369
TrCHSa10 : AGACATATCCTGATTTCCTACTTCAAAATCACTAACAGTGAGCCTAACGGTTGAGCTC :369
TrCHSa11 : AGACATATCCTGATTTCCTACTTCAAAATCACTAACAGTGAGCCTAACGGTTGAGCTC :369
TrCHSa12 : AGACATATCCTGATTTCCTACTTCAAAATCACTAACAGTGAGCCTAACGGTTGAGCTC :369
TrCHSa13 : AGACATATCCTGATTTCCTACTTCAAAATCACTAACAGTGAGCCTAACGGTTGAGCTC :369
TrCHSa14 : AGACATATCCTGATTTCCTACTTCAAAATCACTAACAGTGAGCCTAACGGTTGAGCTC :369
TrCHSa15 : AGACATATCCTGATTTCCTACTTCAAAATCACTAACAGTGAGCCTAACGGTTGAGCTC :369
TrCHSa16 : AGACATATCCTGATTTCCTACTTCAAAATCACTAACAGTGAGCCTAACGGTTGAGCTC :369
TrCHSa17 : AGACATATCCTGATTTCCTACTTCAAAATCACTAACAGTGAGCCTAACGGTTGAGCTC :369
TrCHSa18 : AGACATATCCTGATTTCCTACTTCAAAATCACTAACAGTGAGCCTAACGGTTGAGCTC :369
TrCHSa19 : AGACATATCCTGATTTCCTACTTCAAAATCACTAACAGTGAGCCTAACGGTTGAGCTC :369
TrCHSa20 : AGACATATCCTGATTTCCTACTTCAAAATCACTAACAGTGAGCCTAACGGTTGAGCTC :369
TrCHSa21 : AGACATATCCTGATTTCCTACTTCAAAATCACTAACAGTGAGCCTAACGGTTGAGCTC :369
TrCHSa22 : AGACATATCCTGATTTCCTACTTCAAAATCACTAACAGTGAGCCTAACGGTTGAGCTC :369
TrCHSa23 : AGACATATCCTGATTTCCTACTTCAAAATCACTAACAGTGAGCCTAACGGTTGAGCTC :369
TrCHSa24 : AGACATATCCTGATTTCCTACTTCAAAATCACTAACAGTGAGCCTAACGGTTGAGCTC :369
TrCHSa25 : AGACATATCCTGATTTCCTACTTCAAAATCACTAACAGTGAGCCTAACGGTTGAGCTC :369
TrCHSa26 : AGACATATCCTGATTTCCTACTTCAAAATCACTAACAGTGAGCCTAACGGTTGAGCTC :369
TrCHSa27 : AGACATATCCTGATTTCCTACTTCAAAATCACTAACAGTGAGCCTAACGGTTGAGCTC :369
TrCHSa28 : AGACATATCCTGATTTCCTACTTCAAAATCACTAACAGTGAGCCTAACGGTTGAGCTC :369
TrCHSa29 : AGACATATCCTGATTTCCTACTTCAAAATCACTAACAGTGAGCCTAACGGTTGAGCTC :369
TrCHSa30 : AGACATATCCTGATTTCCTACTTCAAAATCACTAACAGTGAGCCTAACGGTTGAGCTC :369
TrCHSa31 : AGACATATCCTGATTTCCTACTTCAAAATCACTAACAGTGAGCCTAACGGTTGAGCTC :369
TrCHSa32 : AGACATATCCTGATTTCCTACTTCAAAATCACTAACAGTGAGCCTAACGGTTGAGCTC :369
TrCHSa33 : AGACATATCCTGATTTCCTACTTCAAAATCACTAACAGTGAGCCTAACGGTTGAGCTC :369
TrCHSa34 : AGACATATCCTGATTTCCTACTTCAAAATCACTAACAGTGAGCCTAACGGTTGAGCTC :369
TrCHSa35 : AGACATATCCTGATTTCCTACTTCAAAATCACTAACAGTGAGCCTAACGGTTGAGCTC :369
TrCHSa36 : AGACATATCCTGATTTCCTACTTCAAAATCACTAACAGTGAGCCTAACGGTTGAGCTC :369
TrCHSa37 : -----CTGAGCTC : 17
TrCHSa38 : ----- : -
TrCHSa39 : ----- : -

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FIGURE 15 (cont)

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      *           390           *           400           *           420
TrCHSa1 : GAGAAATTCCAGCGCATGTGTGACAAATCTATGATCAAGAGCAGATACATGTTATCTAAAC :420
TrCHSa2 : GAGAAATTCAGCGCATGTGTGACAAATCTATGATCAAGAGCAGATACATGTTATCTAAAC :317
TrCHSa3 : GAGAAATTCAGCGCATGTGTGACAAATCTATGATCAAGAGCAGATACATGTTATCTAAAC :323
TrCHSa4 : GAGAAATTCAGCGCATGTGTGACAAATCTATGATCAAGAGCAGATACATGTTATCTAAAC :308
TrCHSa5 : GAGAAATTCAGCGCATGTGTGACAAATCTATGATCAAGAGCAGATACATGTTATCTAAAC :309
TrCHSa6 : GAGAAATTCAGCGCATGTGTGACAAATCTATGATCAAGAGCAGATACATGTTATCTAAAC :296
TrCHSa7 : GAGAAATTCAGCGCATGTGTGACAAATCTATGATCAAGAGCAGATACATGTTATCTAAAC :302
TrCHSa8 : GAGAAATTCAGCGCATGTGTGACAAATCTATGATCAAGAGCAGATACATGTTATCTAAAC :296
TrCHSa9 : GAGAAATTCAGCGCATGTGTGACAAATCTATGATCAAGAGCAGATACATGTTATCTAAAC :302
TrCHSa10 : GAGAAATTCAGCGCATGTGTGACAAATCTATGATCAAGAGCAGATACATGTTATCTAAAC :300
TrCHSa11 : GAGAAATTCAGCGCATGTGTGACAAATCTATGATCAAGAGCAGATACATGTTATCTAAAC :291
TrCHSa12 : GAGAAATTCAGCGCATGTGTGACAAATCTATGATCAAGAGCAGATACATGTTATCTAAAC :290
TrCHSa13 : GAGAAATTCAGCGCATGTGTGACAAATCTATGATCAAGAGCAGATACATGTTATCTAAAC :299
TrCHSa14 : GAGAAATTCAGCGCATGTGTGACAAATCTATGATCAAGAGCAGATACATGTTATCTAAAC :297
TrCHSa15 : GAGAAATTCAGCGCATGTGTGACAAATCTATGATCAAGAGCAGATACATGTTATCTAAAC :290
TrCHSa16 : GAGAAATTCAGCGCATGTGTGACAAATCTATGATCAAGAGCAGATACATGTTATCTAAAC :298
TrCHSa17 : GAGAAATTCAGCGCATGTGTGACAAATCTATGATCAAGAGCAGATACATGTTATCTAAAC :297
TrCHSa18 : GAGAAATTCAGCGCATGTGTGACAAATCTATGATCAAGAGCAGATACATGTTATCTAAAC :296
TrCHSa19 : GAGAAATTCAGCGCATGTGTGACAAATCTATGATCAAGAGCAGATACATGTTATCTAAAC :295
TrCHSa20 : GAGAAATTCAGCGCATGTGTGACAAATCTATGATCAAGAGCAGATACATGTTATCTAAAC :293
TrCHSa21 : GAGAAATTCAGCGCATGTGTGACAAATCTATGATCAAGAGCAGATACATGTTATCTAAAC :292
TrCHSa22 : GAGAAATTCAGCGCATGTGTGACAAATCTATGATCAAGAGCAGATACATGTTATCTAAAC :289
TrCHSa23 : GAGAAATTCAGCGCATGTGTGACAAATCTATGATCAAGAGCAGATACATGTTATCTAAAC :283
TrCHSa24 : GAGAAATTCAGCGCATGTGTGACAAATCTATGATCAAGAGCAGATACATGTTATCTAAAC :287
TrCHSa25 : GAGAAATTCAGCGCATGTGTGACAAATCTATGATCAAGAGCAGATACATGTTATCTAAAC :287
TrCHSa26 : GAGAAATTCAGCGCATGTGTGACAAATCTATGATCAAGAGCAGATACATGTTATCTAAAC :278
TrCHSa27 : GAGAAATTCAGCGCATGTGTGACAAATCTATGATCAAGAGCAGATACATGTTATCTAAAC :275
TrCHSa28 : GAGAAATTCAGCGCATGTGTGACAAATCTATGATCAAGAGCAGATACATGTTATCTAAAC :282
TrCHSa29 : GAGAAATTCAGCGCATGTGTGACAAATCTATGATCAAGAGCAGATACATGTTATCTAAAC :257
TrCHSa30 : GAGAAATTCAGCGCATGTGTGACAAATCTATGATCAAGAGCAGATACATGTTATCTAAAC :241
TrCHSa31 : GAGAAATTCAGCGCATGTGTGACAAATCTATGATCAAGAGCAGATACATGTTATCTAAAC :238
TrCHSa32 : GAGAAATTCAGCGCATGTGTGACAAATCTATGATCAAGAGCAGATACATGTTATCTAAAC :238
TrCHSa33 : GAGAAATTCAGCGCATGTGTGACAAATCTATGATCAAGAGCAGATACATGTTATCTAAAC :238
TrCHSa34 : GAGAAATTCAGCGCATGTGTGACAAATCTATGATCAAGAGCAGATACATGTTATCTAAAC :191
TrCHSa35 : GAGAAATTCAGCGCATGTGTGACAAATCTATGATCAAGAGCAGATACATGTTATCTAAAC :177
TrCHSa36 : GAGAAATTCAGCGCATGTGTGACAAATCTATGATCAAGAGCAGATACATGTTATCTAAAC :179
TrCHSa37 : GAGAAATTCAGCGCATGTGTGACAAATCTATGATCAAGAGCAGATACATGTTATCTAAAC :77
TrCHSa38 : GAGAAATTCAGCGCATGTGTGACAAATCTATGATCAAGAGCAGATACATGTTATCTAAAC :27
TrCHSa39 : -----

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FIGURE 15 (cont)

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      *           440           *           460           *           480
TrCHSa1 :  GAAGAGATTTTGAAGAGAAAATCCTAGTCTTTGTGGAATACATGGCACCTTCATTGGATGCT 480
TrCHSa2 :  GAAGAGATTTTGAAGAGAAAATCCTAGTCTTTGTGGAATACATGGCACCTTCATTGGATGCT 377
TrCHSa3 :  GAAGAGATTTTGAAGAGAAAATCCTAGTCTTTGTGGAATACATGGCACCTTCATTGGATGCT 383
TrCHSa4 :  GAAGAGATTTTGAAGAGAAAATCCTAGTCTTTGTGGAATACATGGCACCTTCATTGGATGCT 368
TrCHSa5 :  GAAGAGATTTTGAAGAGAAAATCCTAGTCTTTGTGGAATACATGGCACCTTCATTGGATGCT 369
TrCHSa6 :  GAAGAGATTTTGAAGAGAAAATCCTAGTCTTTGTGGAATACATGGCACCTTCATTGGATGCT 356
TrCHSa7 :  GAAGAGATTTTGAAGAGAAAATCCTAGTCTTTGTGGAATACATGGCACCTTCATTGGATGCT 362
TrCHSa8 :  GAAGAGATTTTGAAGAGAAAATCCTAGTCTTTGTGGAATACATGGCACCTTCATTGGATGCT 356
TrCHSa9 :  GAAGAGATTTTGAAGAGAAAATCCTAGTCTTTGTGGAATACATGGCACCTTCATTGGATGCT 362
TrCHSa10 : GAAGAGATTTTGAAGAGAAAATCCTAGTCTTTGTGGAATACATGGCACCTTCATTGGATGCT 360
TrCHSa11 : GAAGAGATTTTGAAGAGAAAATCCTAGTCTTTGTGGAATACATGGCACCTTCATTGGATGCT 351
TrCHSa12 : GAAGAGATTTTGAAGAGAAAATCCTAGTCTTTGTGGAATACATGGCACCTTCATTGGATGCT 350
TrCHSa13 : GAAGAGATTTTGAAGAGAAAATCCTAGTCTTTGTGGAATACATGGCACCTTCATTGGATGCT 359
TrCHSa14 : GAAGAGATTTTGAAGAGAAAATCCTAGTCTTTGTGGAATACATGGCACCTTCATTGGATGCT 357
TrCHSa15 : GAAGAGATTTTGAAGAGAAAATCCTAGTCTTTGTGGAATACATGGCACCTTCATTGGATGCT 350
TrCHSa16 : GAAGAGATTTTGAAGAGAAAATCCTAGTCTTTGTGGAATACATGGCACCTTCATTGGATGCT 358
TrCHSa17 : GAAGAGATTTTGAAGAGAAAATCCTAGTCTTTGTGGAATACATGGCACCTTCATTGGATGCT 357
TrCHSa18 : GAAGAGATTTTGAAGAGAAAATCCTAGTCTTTGTGGAATACATGGCACCTTCATTGGATGCT 356
TrCHSa19 : GAAGAGATTTTGAAGAGAAAATCCTAGTCTTTGTGGAATACATGGCACCTTCATTGGATGCT 355
TrCHSa20 : GAAGAGATTTTGAAGAGAAAATCCTAGTCTTTGTGGAATACATGGCACCTTCATTGGATGCT 353
TrCHSa21 : GAAGAGATTTTGAAGAGAAAATCCTAGTCTTTGTGGAATACATGGCACCTTCATTGGATGCT 352
TrCHSa22 : GAAGAGATTTTGAAGAGAAAATCCTAGTCTTTGTGGAATACATGGCACCTTCATTGGATGCT 349
TrCHSa23 : GAAGAGATTTTGAAGAGAAAATCCTAGTCTTTGTGGAATACATGGCACCTTCATTGGATGCT 343
TrCHSa24 : GAAGAGATTTTGAAGAGAAAATCCTAGTCTTTGTGGAATACATGGCACCTTCATTGGATGCT 347
TrCHSa25 : GAAGAGATTTTGAAGAGAAAATCCTAGTCTTTGTGGAATACATGGCACCTTCATTGGATGCT 347
TrCHSa26 : GAAGAGATTTTGAAGAGAAAATCCTAGTCTTTGTGGAATACATGGCACCTTCATTGGATGCT 338
TrCHSa27 : GAAGAGATTTTGAAGAGAAAATCCTAGTCTTTGTGGAATACATGGCACCTTCATTGGATGCT 335
TrCHSa28 : GAAGAGATTTTGAAGAGAAAATCCTAGTCTTTGTGGAATACATGGCACCTTCATTGGATGCT 342
TrCHSa29 : GAAGAGATTTTGAAGAGAAAATCCTAGTCTTTGTGGAATACATGGCACCTTCATTGGATGCT 317
TrCHSa30 : GAAGAGATTTTGAAGAGAAAATCCTAGTCTTTGTGGAATACATGGCACCTTCATTGGATGCT 301
TrCHSa31 : GAAGAGATTTTGAAGAGAAAATCCTAGTCTTTGTGGAATACATGGCACCTTCATTGGATGCT 298
TrCHSa32 : GAAGAGATTTTGAAGAGAAAATCCTAGTCTTTGTGGAATACATGGCACCTTCATTGGATGCT 298
TrCHSa33 : GAAGAGATTTTGAAGAGAAAATCCTAGTCTTTGTGGAATACATGGCACCTTCATTGGATGCT 298
TrCHSa34 : GAAGAGATTTTGAAGAGAAAATCCTAGTCTTTGTGGAATACATGGCACCTTCATTGGATGCT 251
TrCHSa35 : GAAGAGATTTTGAAGAGAAAATCCTAGTCTTTGTGGAATACATGGCACCTTCATTGGATGCT 239
TrCHSa36 : GAAGAGATTTTGAAGAGAAAATCCTAGTCTTTGTGGAATACATGGCACCTTCATTGGATGCT 237
TrCHSa37 : GAAGAGATTTTGAAGAGAAAATCCTAGTCTTTGTGGAATACATGGCACCTTCATTGGATGCT 137
TrCHSa38 : GAAGAGATTTTGAAGAGAAAATCCTAGTCTTTGTGGAATACATGGCACCTTCATTGGATGCT 87
TrCHSa39 : -----

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FIGURE 15 (cont)

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      *           500           *           520           *           540
TrChSa1 : AGGCAAGACATCGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCGTGCAGTGAAGGCT : 540
TrChSa2 : AGGCAAGACATCGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCGTGCAGTGAAGGCT : 543
TrChSa3 : AGGCAAGACATCGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCGTGCAGTGAAGGCT : 437
TrChSa4 : AGGCAAGACATCGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCGTGCAGTGAAGGCT : 428
TrChSa5 : AGGCAAGACATCGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCGTGCAGTGAAGGCT : 429
TrChSa6 : AGGCAAGACATCGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCGTGCAGTGAAGGCT : 416
TrChSa7 : GC CAAGACATCGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCGTGCAGTGAAGGCT : 407
TrChSa8 : AGGCAAGACATCGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCGTGCAGTGAAGGCT : 416
TrChSa9 : GC CAAGACATCGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCGTGCAGTGAAGGCT : 422
TrChSa10 : AGGCAAGACATCGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCGTGCAGTGAAGGCT : 420
TrChSa11 : AGGCAAGACATCGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCGTGCAGTGAAGGCT : 411
TrChSa12 : AGGCAAGACATCGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCGTGCAGTGAAGGCT : 410
TrChSa13 : AGGCAAGACATCGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCGTGCAGTGAAGGCT : 419
TrChSa14 : AGGCAAGACATCGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCGTGCAGTGAAGGCT : 417
TrChSa15 : GC CAAGACATCGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCGTGCAGTGAAGGCT : 390
TrChSa16 : AGGCAAGACATCGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCGTGCAGTGAAGGCT : 418
TrChSa17 : AGGCAAGACATCGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCGTGCAGTGAAGGCT : 417
TrChSa18 : AGGCAAGACATCGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCGTGCAGTGAAGGCT : 416
TrChSa19 : AGGCAAGACATCGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCGTGCAGTGAAGGCT : 415
TrChSa20 : AGGCAAGACATCGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCGTGCAGTGAAGGCT : 413
TrChSa21 : AGGCAAGACATCGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCGTGCAGTGAAGGCT : 412
TrChSa22 : AGGCAAGACATCGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCGTGCAGTGAAGGCT : 409
TrChSa23 : AGGCAAGACATCGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCGTGCAGTGAAGGCT : 403
TrChSa24 : AGGCAAGACATCGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCGTGCAGTGAAGGCT : 407
TrChSa25 : AGGCAAGACATCGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCGTGCAGTGAAGGCT : 407
TrChSa26 : AGGCAAGACATCGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCGTGCAGTGAAGGCT : 398
TrChSa27 : GC CAAGACATCGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCGTGCAGTGAAGGCT : 395
TrChSa28 : AGGCAAGACATCGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCGTGCAGTGAAGGCT : 402
TrChSa29 : AGGCAAGACATCGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCGTGCAGTGAAGGCT : 377
TrChSa30 : AGGCAAGACATCGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCGTGCAGTGAAGGCT : 361
TrChSa31 : AGGCAAGACATCGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCGTGCAGTGAAGGCT : 358
TrChSa32 : AGGCAAGACATCGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCGTGCAGTGAAGGCT : 358
TrChSa33 : AGGCAAGACATCGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCGTGCAGTGAAGGCT : 358
TrChSa34 : AGGCAAGACATCGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCGTGCAGTGAAGGCT : 311
TrChSa35 : AGGCAAGACATCGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCGTGCAGTGAAGGCT : 299
TrChSa36 : AGGCAAGACATCGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCGTGCAGTGAAGGCT : 297
TrChSa37 : AGGCAAGACATCGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCGTGCAGTGAAGGCT : 197
TrChSa38 : AGGCAAGACATCGTGGTGGTTGAGGTACCTAGACTTGGGAAGGAGGCGTGCAGTGAAGGCT : 147
TrChSa39 : -----

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FIGURE 15 (cont)

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      *           560           *           580           *           600
TrCHSa1 : ATTTAAAGAAATGGGGTCAACCAAAGTCAAAGATTACTCAGTTAATCTTTTGACCCACAAGT : 600
TrCHSa2 : ATTTAAAGAAATGGGGTCAACCAAAGTCAAAGATTACTCAGTTAATCTTTTGACCCACAAGT : 497
TrCHSa3 : ATTTAAAGAAATGGGGTCAACCAAAGTCAAAGATTACTCAGTTAATCTTTTGACCCACAAGT : 503
TrCHSa4 : ATTTAAAGAAATGGGGTCAACCAAAGTCAAAGATTACTCAGTTAATCTTTTGACCCACAAGT : 488
TrCHSa5 : ATTTAAAGAAATGGGGTCAACCAAAGTCAAAGATTACTCAGTTAATCTTTTGACCCACAAGT : 489
TrCHSa6 : ATTTAAAGAAATGGGGTCAACCAAAGTCAAAGATTACTCAGTTAATCTTTTGACCCACAAGT : 476
TrCHSa7 : ----- : 476
TrCHSa8 : ATTTAAAGAAATGGGGTCAACCAAAGTCAAAGATTACTCAGTTAATCTTTTGACCCACAAGT : 476
TrCHSa9 : ATTTAAAGAAATGGGGTCAACCAAAGTCAAAGATTACTCAGTTAATCTTTTGACCCACAAGT : 482
TrCHSa10 : ATTTAAAGAAATGGGGTCAACCAAAGTCAAAGATTACTCAGTTAATCTTTTGACCCACAAGT : 480
TrCHSa11 : ATTTAAAGAAATGGGGTCAACCAAAGTCAAAGATTACTCAGTTAATCTTTTGACCCACAAGT : 471
TrCHSa12 : ATTTAAAGAAATGGGGTCAACCAAAGTCAAAGATTACTCAGTTAATCTTTTGACCCACAAGT : 470
TrCHSa13 : ATTTAAAGAAATGGGGTCAACCAAAGTCAAAGATTACTCAGTTAATCTTTTGACCCACAAGT : 479
TrCHSa14 : ATTTAAAGAAATGGGGTCAACCAAAGTCAAAGATTACTCAGTTAATCTTTTGACCCACAAGT : 477
TrCHSa15 : ----- : -
TrCHSa16 : ATTTAAAGAAATGGGGTCAACCAAAGTCAAAGATTACTCAGTTAATCTTTTGACCCACAAGT : 478
TrCHSa17 : ATTTAAAGAAATGGGGTCAACCAAAGTCAAAGATTACTCAGTTAATCTTTTGACCCACAAGT : 477
TrCHSa18 : ATTTAAAGAAATGGGGTCAACCAAAGTCAAAGATTACTCAGTTAATCTTTTGACCCACAAGT : 437
TrCHSa19 : ATTTAAAGAAATGGGGTCAACCAAAGTCAAAGATTACTCAGTTAATCTTTTGACCCACAAGT : 475
TrCHSa20 : ATTTAAAGAAATGGGGTCAACCAAAGTCAAAGATTACTCAGTTAATCTTTTGACCCACAAGT : 473
TrCHSa21 : ATTTAAAGAAATGGGGTCAACCAAAGTCAAAGATTACTCAGTTAATCTTTTGACCCACAAGT : 472
TrCHSa22 : ATTTAAAGAAATGGGGTCAACCAAAGTCAAAGATTACTCAGTTAATCTTTTGACCCACAAGT : 469
TrCHSa23 : ATTTAAAGAAATGGGGTCAACCAAAGTCAAAGATTACTCAGTTAATCTTTTGACCCACAAGT : 463
TrCHSa24 : ATTTAAAGAAATGGGGTCAACCAAAGTCAAAGATTACTCAGTTAATCTTTTGACCCACAAGT : 467
TrCHSa25 : ATTTAAAGAAATGGGGTCAACCAAAGTCAAAGATTACTCAGTTAATCTTTTGACCCACAAGT : 467
TrCHSa26 : ATTTAAAGAAATGGGGTCAACCAAAGTCAAAGATTACTCAGTTAATCTTTTGACCCACAAGT : 458
TrCHSa27 : ATTTAAAGAAATGGGGTCAACCAAAGTCAAAGATTACTCAGTTAATCTTTTGACCCACAAGT : 455
TrCHSa28 : ATTTAAAGAAATGGGGTCAACCAAAGTCAAAGATTACTCAGTTAATCTTTTGACCCACAAGT : 462
TrCHSa29 : ATTTAAAGAAATGGGGTCAACCAAAGTCAAAGATTACTCAGTTAATCTTTTGACCCACAAGT : 437
TrCHSa30 : ATTTAAAGAAATGGGGTCAACCAAAGTCAAAGATTACTCAGTTAATCTTTTGACCCACAAGT : 421
TrCHSa31 : ATTTAAAGAAATGGGGTCAACCAAAGTCAAAGATTACTCAGTTAATCTTTTGACCCACAAGT : 418
TrCHSa32 : ATTTAAAGAAATGGGGTCAACCAAAGTCAAAGATTACTCAGTTAATCTTTTGACCCACAAGT : 418
TrCHSa33 : ATTTAAAGAAATGGGGTCAACCAAAGTCAAAGATTACTCAGTTAATCTTTTGACCCACAAGT : 418
TrCHSa34 : ATTTAAAGAAATGGGGTCAACCAAAGTCAAAGATTACTCAGTTAATCTTTTGACCCACAAGT : 371
TrCHSa35 : ATTTAAAGAAATGGGGTCAACCAAAGTCAAAGATTACTCAGTTAATCTTTTGACCCACAAGT : 359
TrCHSa36 : ATTTAAAGAAATGGGGTCAACCAAAGTCAAAGATTACTCAGTTAATCTTTTGACCCACAAGT : 357
TrCHSa37 : ATTTAAAGAAATGGGGTCAACCAAAGTCAAAGATTACTCAGTTAATCTTTTGACCCACAAGT : 257
TrCHSa38 : ATTTAAAGAAATGGGGTCAACCAAAGTCAAAGATTACTCAGTTAATCTTTTGACCCACAAGT : 207
TrCHSa39 : ----- : 61

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FIGURE 15 (cont)

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      *           620           *           640           *           660
TrCHSa1 : GGTGTTGACATGCCCTGGTGCCTGATTACCAACTCACA AAAACTCTTAGGCTCTTCGCCCATAT :660
TrCHSa2 : GGTGTAGACATGCCCTGGTGCCTGATTACCAAGCCACAAAACCTTTAGGACTCTTCGCCCATAT :557
TrCHSa3 : GGTGTGACATGCCCTGGTGCCTGATTACCAACTCACA AAAACTCTTAGGCTCTTCGCCCATAT :563
TrCHSa4 : GGTGTGACATGCCCTGGTGCCTGATTACCAACTCACA AAAACTCTTAGGCTCTTCGCCCATAT :548
TrCHSa5 : GGTGTAGACATGCCCTGGTGCCTGATTACCAACTCACA AAAACTCTTAGGCTCTTCGCCCATAT :549
TrCHSa6 : GGTGTGACATGCCCTGGTGCCTGATTACCAACTCACA AAAACTCTTAGGCTCTTCGCCCATAT :536
TrCHSa7 : ----- : -
TrCHSa8 : GGGCCCT : 483
TrCHSa9 : GGTGTAGACATGCCCTGGTGCCTGATTACCAACTCACA AAAACTCTTAGGACTTCGCCCATAT :542
TrCHSa10 : GGTGTAGACATGCCCTGGAGCTGATTACCAACTCACA AAAACTCTTAGGCTCTTCGCCCATAT :540
TrCHSa11 : GGTGTAGACATGCCCTGGAGCTGATTACCAACTCACA AAAACTCTTAGGCTCTTCGCCCATAT :531
TrCHSa12 : GGTGTGACATGCCCTGGTGCCTGATTACCAACTCACA AAAACTCTTAGGCTCTTCGCCCATAT :530
TrCHSa13 : GGTGTAGACATGCCCTGGAGCTGATTACCAACTCACA AAAACTCTTAGGCTCTTCGCCCATAT :539
TrCHSa14 : GGTGTGACATGCCCTGGTGCCTGATTACCAACTCACA AAAACTCTTAGGCTCTTCGCCCATAT :537
TrCHSa15 : ----- : -
TrCHSa16 : GGTGTAGACATGCCCTGGTGCCTGATTACCAACTCACA AAAACTCTTAGGCTCTTCGCCCATAT :538
TrCHSa17 : GGTGTGACATGCCCTGGTGCCTGATTACCAACTCACA AAAACTCTTAGGCTCTTCGCCCATAT :537
TrCHSa18 : ----- : -
TrCHSa19 : GGTGTAGACATGCCCTGGAGCTGATTACCAACTCACA AAAACTCTTAGGCTCTTCGCCCATAT :535
TrCHSa20 : GGTGTAGACATGCCCTGGTGCCTGATTACCAACTCACA AAAACTCTTAGGCTCTTCGCCCATAT :533
TrCHSa21 : GGTGTAGACATGCCCTGGTGCCTGATTACCAACTCACA AAAACTCTTAGGCTCTTCGCCCATAT :532
TrCHSa22 : GGTGTAGACATGCCCTGGAGCTGATTACCAACTCACA AAAACTCTTAGGCTCTTCGCCCATAT :529
TrCHSa23 : GGTGTAGACATGCCCTGGTGCCTGATTACCAACTCACA AAAACTCTTAGGCTCTTCGCCCATAT :523
TrCHSa24 : GGTGTAGACATGCCCTGGTGCCTGATTACCAACTCACA AAAACTCTTAGGCTCTTCGCCCATAT :527
TrCHSa25 : GGTGTAGACATGCCCTGGTGCCTGATTACCAACTCACA AAAACTCTTAGGCTCTTCGCCCATAT :527
TrCHSa26 : GGTGTAGACATGCCCTGGTGCCTGATTACCAACTCACA AAAACTCTTAGGCTCTTCGCCCATAT :518
TrCHSa27 : GGTGTAGACATGCCCTGGTGCCTGATTACCAACTCACA AAAACTCTTAGGCTCTTCGCCCATAT :515
TrCHSa28 : GGTGTAGACATGCCCTGGTGCCTGATTACCAACTCACA AAAACTCTTAGGCTCTTCGCCCATAT :522
TrCHSa29 : GGTGTAGACATGCCCTGGTGCCTGATTACCAACTCACA AAAACTCTTAGGCTCTTCGCCCATAT :497
TrCHSa30 : GGTGTGACATGCCCTGGTGCCTGATTACCAACTCACA AAAACTCTTAGGCTCTTCGCCCATAT :481
TrCHSa31 : GGTGTGACATGCCCTGGTGCCTGATTACCAACTCACA AAAACTCTTAGGCTCTTCGCCCATAT :478
TrCHSa32 : GGTGTAGACATGCCCTGGTGCCTGATTACCAACTCACA AAAACTCTTAGGCTCTTCGCCCATAT :478
TrCHSa33 : GGTGTAGACATGCCCTGGTGCCTGATTACCAACTCACA AAAACTCTTAGGCTCTTCGCCCATAT :478
TrCHSa34 : GGTGTGACATGCCCTGGTGCCTGATTACCAACTCACA AAAACTCTTAGGCTCTTCGCCCATAT :431
TrCHSa35 : GGTGTGACATGCCCTGGTGCCTGATTACCAACTCACA AAAACTCTTAGGCTCTTCGCCCATAT :419
TrCHSa36 : GGTGTGACATGCCCTGGTGCCTGATTACCAACTCACA AAAACTCTTAGGCTCTTCGCCCATAT :417
TrCHSa37 : GGTGTAGACATGCCCTGGTGCCTGATTACCAACTCACA AAAACTCTTAGGCTCTTCGCCCATAT :317
TrCHSa38 : GGTGTAGACATGCCCTGGTGCCTGATTACCAACTCACA AAAACTCTTAGGCTCTTCGCCCATAT :267
TrCHSa39 : GGTGTAGACATGCCCTGGTGCCTGATTACCAACTCACA AAAACTCTTAGGCTCTTCGCCCATAT :121

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FIGURE 15 (cont)

	680	*	700	*	720
TrChSA1:	CTC				:663
TrChSA2:	GTGAAGAGGTACATGATGTACCAACAAAGGGTGC	TTTGCAGGTG			:675
TrChSA3:	GTGAAGAGGTACATGATGTACCAACAAAGGGTGC	TTTGCAGGTG			:575
TrChSA4:	GTGAAGAGGTACATGATGTACCAACAAAGGGTGC	TTTGCAGGTG			:606
TrChSA5:	GTGAAGAGGTACATGATGTACCAACAAAGGGTGC	TTTGCAGGTG			:594
TrChSA6:	GTGAAGAGGTACATGATGTACCAACAAAGGGTGC	TTTGCAGGTG			:596
TrChSA7:					
TrChSA8:					
TrChSA9:	GTGAAGAGGTACATGATGTACCAACAAAGGGTGC	TTTGCAGGTG			:586
TrChSA10:	GTGAAGAGGTACATGATGTACCAACAAAGGGTGC				:574
TrChSA11:	GTGAAGAGGTACATGATGTACCAACAAAGGGTGC	TTTGCAGGTG			:591
TrChSA12:	GTGAAGAGGTACATGATGTACCAACAAAGGGTGC	TTTGCAGGTG			:570
TrChSA13:	GTGAAGAGGTACATGATGTACCAACAAAGGGTGC	TTTGCAGGTG			:598
TrChSA14:	GTGAAGAGGTACATGATGTACCAACAAAGGGTGC	TTTGCAGGTG			:597
TrChSA15:					
TrChSA16:	GTGAAGAGGTACATGATGTACCAACAAAGGGTGC	TTTGCAGGTG			:561
TrChSA17:	GTGAAG				:543
TrChSA18:					
TrChSA19:	GTGAAGAGGTACATGATGTACCAACAAAGGGTGC	TTTGCAGGTG			:595
TrChSA20:	GTGAAGAGGTACATGATGTACCAACAAAGGGTGC	TTTGCAGGTG			:581
TrChSA21:	GTGAAGAGGTACATGATGTACCAACAAAGGGTGC	TTTGCAGGTG			:588
TrChSA22:	GTGAAGAGGTACATGATGTACCAACAAAGGGTGC	TTTGCAGGTG			:589
TrChSA23:	GTGAAGAGGTACATGATGTACCAACAAAGGGTGC	TTTGCAGGTG			:544
TrChSA24:	GTGAAGAGGTACATGATGTACCAACAAAGGGTGC	TTTGCAGGTG			:555
TrChSA25:	GTGAAGAGGTACATGATGTACCAACAAAGGGTGC	TTTGCAGGTG			:570
TrChSA26:	GTGAAGAGGTACATGATGTACCAACAAAGGGTGC	TTTGCAGGTG			:546
TrChSA27:	GTGAAGAGGTACATGATGTACCAACAAAGGGTGC	TTTGCAGGTG			:575
TrChSA28:	GTGAAGAGGTACATGATGTACCAACAAAGGGTGC	TTTGCAGGTG			:582
TrChSA29:	GTGAAGAGGTACATGATGTACCAACAAAGGGTGC	TTTGCAGGTG			:521
TrChSA30:	GTGAAGAGGTACATGATGTACCAACAAAGGGTGC	TTTGCAGGTG			:506
TrChSA31:	GTGAAGAGGTACATGATGTACCAACAAAGGGTGC	TTTGCAGGTG			:504
TrChSA32:	GTGAAGAGGTACATGATGTACCAACAAAGGGTGC	TTTGCAGGTG			:538
TrChSA33:	GTGAAGAGGTACATGATGTACCAACAAAGGGTGC	TTTGCAGGTG			:491
TrChSA34:	GTGAAGAGGTACATGATGTACCAACAAAGGGTGC	TTTGCAGGTG			:479
TrChSA35:	GTGAAGAGGTACATGATGTACCAACAAAGGGTGC	TTTGCAGGTG			:477
TrChSA36:	GTGAAGAGGTACATGATGTACCAACAAAGGGTGC	TTTGCAGGTG			:327
TrChSA37:	GTGAAGAGGTACATGATGTACCAACAAAGGGTGC	TTTGCAGGTG			:181

FIGURE 15 (cont)

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	*	740	*	760	*	780	
TrCHSa1 :	-----						:
TrCHSa2 :	-----						:
TrCHSa3 :	-----						:
TrCHSa4 :	-----						:
TrCHSa5 :	-----						:
TrCHSa6 :	GC AAAAGATT TGGCCGAGAACAACAAGGTGCTCGTGTGCTAGTGTGTTGTCTGAAGTC						: 656
TrCHSa7 :	-----						:
TrCHSa8 :	-----						:
TrCHSa9 :	-----						:
TrCHSa10 :	-----						:
TrCHSa11 :	GC AAAAGATT TGC						: 604
TrCHSa12 :	-----						:
TrCHSa13 :	-----						:
TrCHSa14 :	GC AAAAGATT TGC						: 609
TrCHSa15 :	-----						:
TrCHSa16 :	-----						:
TrCHSa17 :	-----						:
TrCHSa18 :	-----						:
TrCHSa19 :	GC AAAAGATT TGC						: 607
TrCHSa20 :	-----						:
TrCHSa21 :	-----						:
TrCHSa22 :	GC AAAAGATT TGGCCGAGAACAAC						: 613
TrCHSa23 :	-----						:
TrCHSa24 :	-----						:
TrCHSa25 :	-----						:
TrCHSa26 :	-----						:
TrCHSa27 :	GC AAAAG						: 582
TrCHSa28 :	GC AAAAGATT TGGCCGAGAACAACAACAAATGNGTCTCGNGNGSTTGGNTGGTTGCTCTNAATG						: 642
TrCHSa29 :	-----						:
TrCHSa30 :	-----						:
TrCHSa31 :	-----						:
TrCHSa32 :	GC AAAAGATT TGGCCGAGAACAACAAGGTCTCTGTGTGTGTGTGTGTGTCTGAAGTC						: 598
TrCHSa33 :	GC AAAAGATT TGGCCGAGAACAACAAGGTCTCTGTGTGTGTGTGTGTGTCTGAAGTC						: 597
TrCHSa34 :	GC AAAAGATT TGGCCGAGAACAACAAGGTCTCTGTGTGTGTGTGTGTGTCTGAAGTC						: 551
TrCHSa35 :	GC AAAAGATT TGGCCGAGAACAACAAGGTCTCTGTGTGTGTGTGTGTGTCTGAAGTC						: 539
TrCHSa36 :	GC AAAAGATT TGGCCGAGAACAACAAGGTCTCTGTGTGTGTGTGTGTGTCTGAAGTC						: 537
TrCHSa37 :	GC AAAAGATT TGGCCGAGAACAACAAGGTCTCTGTGTGTGTGTGTGTGTCTGAAGTC						: 437
TrCHSa38 :	GC AAAAGATT TGGCCGAGAACAACAAGGTCTCTGTGTGTGTGTGTGTGTCTGAAGTC						: 387
TrCHSa39 :	GC AAAAGATT TGGCCGAGAACAACAAGGTCTCTGTGTGTGTGTGTGTGTCTGAAGTC						: 241

FIGURE 15 (cont)

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		*	800	*	820	*	840	
TrCHSa1 :	-----							:-
TrCHSa2 :	-----							:-
TrCHSa3 :	-----							:-
TrCHSa4 :	-----							:-
TrCHSa5 :	-----							:-
TrCHSa6 :	ACCGCAGTCACATTTCGCGGGCCCCAGTGATAC							708
TrCHSa7 :	-----							:-
TrCHSa8 :	-----							:-
TrCHSa9 :	-----							:-
TrCHSa10 :	-----							:-
TrCHSa11 :	-----							:-
TrCHSa12 :	-----							:-
TrCHSa13 :	-----							:-
TrCHSa14 :	-----							:-
TrCHSa15 :	-----							:-
TrCHSa16 :	-----							:-
TrCHSa17 :	-----							:-
TrCHSa18 :	-----							:-
TrCHSa19 :	-----							:-
TrCHSa20 :	-----							:-
TrCHSa21 :	-----							:-
TrCHSa22 :	-----							:-
TrCHSa23 :	-----							:-
TrCHSa24 :	-----							:-
TrCHSa25 :	-----							:-
TrCHSa26 :	-----							:-
TrCHSa27 :	-----							:-
TrCHSa28 :	ACCGCAT							649
TrCHSa29 :	-----							:-
TrCHSa30 :	-----							:-
TrCHSa31 :	-----							:-
TrCHSa32 :	ACCGCAGTCACATTTCGCGGGCCCCAGTGACACTCACATTGGACAGCTTTGTTGGACAAGCA							658
TrCHSa33 :	-----							:-
TrCHSa34 :	ACCGCAGTCACATTTCGCGGGCCCCAGTGACACTCACATTGGACAGCTTTGTTGGACAAGCA							590
TrCHSa35 :	ACCGCAGTCACATTTCGCGGGCCCCAGTGACACTCACATTGGACAGCTTTGTTGGACAAGCA							599
TrCHSa36 :	ACCGCAGTCACATTTCGCGGGCCCCAGTGACACTCACATTGGACAGCTTTGTTGGACAAGCA							597
TrCHSa37 :	ACCGCAGTCACATTTCGCGGGCCCCAGTGACACTCACATTGGACAGCTTTGTTGGACAAGCA							497
TrCHSa38 :	ACCGCAGTCACATTTCGCGGGCCCCAGTGACACTCACATTGGACAGCTTTGTTGGACAAGCA							447
TrCHSa39 :	ACCGCAGTCACATTTCGCGGGCCCCAGTGACACTCACATTGGACAGCTTTGTTGGACAAGCA							301

FIGURE 15 (cont)

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	*	860	*	880	*	900	
TrCHSa1 :	-----		-----		-----		:
TrCHSa2 :	-----		-----		-----		:
TrCHSa3 :	-----		-----		-----		:
TrCHSa4 :	-----		-----		-----		:
TrCHSa5 :	-----		-----		-----		:
TrCHSa6 :	-----		-----		-----		:
TrCHSa7 :	-----		-----		-----		:
TrCHSa8 :	-----		-----		-----		:
TrCHSa9 :	-----		-----		-----		:
TrCHSa10 :	-----		-----		-----		:
TrCHSa11 :	-----		-----		-----		:
TrCHSa12 :	-----		-----		-----		:
TrCHSa13 :	-----		-----		-----		:
TrCHSa14 :	-----		-----		-----		:
TrCHSa15 :	-----		-----		-----		:
TrCHSa16 :	-----		-----		-----		:
TrCHSa17 :	-----		-----		-----		:
TrCHSa18 :	-----		-----		-----		:
TrCHSa19 :	-----		-----		-----		:
TrCHSa20 :	-----		-----		-----		:
TrCHSa21 :	-----		-----		-----		:
TrCHSa22 :	-----		-----		-----		:
TrCHSa23 :	-----		-----		-----		:
TrCHSa24 :	-----		-----		-----		:
TrCHSa25 :	-----		-----		-----		:
TrCHSa26 :	-----		-----		-----		:
TrCHSa27 :	-----		-----		-----		:
TrCHSa28 :	-----		-----		-----		:
TrCHSa29 :	-----		-----		-----		:
TrCHSa30 :	-----		-----		-----		:
TrCHSa31 :	-----		-----		-----		:
TrCHSa32 :	CTATTGGAGATGGAGCTGCTGCACCTCATCTGTGGCTTCCTGATCCAGTCCAGAAATTGAG						: 718
TrCHSa33 :	-----		-----		-----		:
TrCHSa34 :	-----		-----		-----		:
TrCHSa35 :	CTATTGGAGATGGAGCTGCTG						: 618
TrCHSa36 :	CTATTGGAGATGGAGCTGCTG						: 619
TrCHSa37 :	CTATTGGAGATGGAGCTGCTGCACCTCATCTGTGGCTCAGACCCAGTACCAGAAATTGAG						: 557
TrCHSa38 :	CTATTGGAGATGGAGCTGCTGCCTCATCTGTGGCTTCCTGATCCAGTACCAGAAATTGAG						: 507
TrCHSa39 :	CTATTGGAGATGGAGCTGCTGCCTCATCTGTGGCTCAGACCCCTACCCAGAAATTGAG						: 361

FIGURE 15 (cont)

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	*	920	*	940	*	960	
TrCHSa1 :	-----		-----		-----		:
TrCHSa2 :	-----		-----		-----		:
TrCHSa3 :	-----		-----		-----		:
TrCHSa4 :	-----		-----		-----		:
TrCHSa5 :	-----		-----		-----		:
TrCHSa6 :	-----		-----		-----		:
TrCHSa7 :	-----		-----		-----		:
TrCHSa8 :	-----		-----		-----		:
TrCHSa9 :	-----		-----		-----		:
TrCHSa10 :	-----		-----		-----		:
TrCHSa11 :	-----		-----		-----		:
TrCHSa12 :	-----		-----		-----		:
TrCHSa13 :	-----		-----		-----		:
TrCHSa14 :	-----		-----		-----		:
TrCHSa15 :	-----		-----		-----		:
TrCHSa16 :	-----		-----		-----		:
TrCHSa17 :	-----		-----		-----		:
TrCHSa18 :	-----		-----		-----		:
TrCHSa19 :	-----		-----		-----		:
TrCHSa20 :	-----		-----		-----		:
TrCHSa21 :	-----		-----		-----		:
TrCHSa22 :	-----		-----		-----		:
TrCHSa23 :	-----		-----		-----		:
TrCHSa24 :	-----		-----		-----		:
TrCHSa25 :	-----		-----		-----		:
TrCHSa26 :	-----		-----		-----		:
TrCHSa27 :	-----		-----		-----		:
TrCHSa28 :	-----		-----		-----		:
TrCHSa29 :	-----		-----		-----		:
TrCHSa30 :	-----		-----		-----		:
TrCHSa31 :	-----		-----		-----		:
TrCHSa32 :	AAACCAATATTGAGATGGT	TTGGAC	TGCACAAACAAT	TGCTCCAGACAGTGAAGGTGCC			: 778
TrCHSa33 :	-----		-----		-----		:
TrCHSa34 :	-----		-----		-----		:
TrCHSa35 :	-----		-----		-----		:
TrCHSa36 :	-----		-----		-----		:
TrCHSa37 :	AN		-----		-----		: 559
TrCHSa38 :	AAACCAATATTGAGATGGTATGGACCGCACAGACAAT	TGCTCCAG					: 553
TrCHSa39 :	AAACCAATATTGAGATGGTATGGACCGCACAGACAAT	TGCTCCAGACAGTGAAGGTGCC					: 421

FIGURE 15 (cont)

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	*	980	*	1000	*	1020	
TrCHSa1 :	----		----		----		:
TrCHSa2 :	----		----		----		:
TrCHSa3 :	----		----		----		:
TrCHSa4 :	----		----		----		:
TrCHSa5 :	----		----		----		:
TrCHSa6 :	----		----		----		:
TrCHSa7 :	----		----		----		:
TrCHSa8 :	----		----		----		:
TrCHSa9 :	----		----		----		:
TrCHSa10 :	----		----		----		:
TrCHSa11 :	----		----		----		:
TrCHSa12 :	----		----		----		:
TrCHSa13 :	----		----		----		:
TrCHSa14 :	----		----		----		:
TrCHSa15 :	----		----		----		:
TrCHSa16 :	----		----		----		:
TrCHSa17 :	----		----		----		:
TrCHSa18 :	----		----		----		:
TrCHSa19 :	----		----		----		:
TrCHSa20 :	----		----		----		:
TrCHSa21 :	----		----		----		:
TrCHSa22 :	----		----		----		:
TrCHSa23 :	----		----		----		:
TrCHSa24 :	----		----		----		:
TrCHSa25 :	----		----		----		:
TrCHSa26 :	----		----		----		:
TrCHSa27 :	----		----		----		:
TrCHSa28 :	----		----		----		:
TrCHSa29 :	----		----		----		:
TrCHSa30 :	----		----		----		:
TrCHSa31 :	----		----		----		:
TrCHSa32 :	ATTG		----		----		: 782
TrCHSa33 :	----		----		----		:
TrCHSa34 :	----		----		----		:
TrCHSa35 :	----		----		----		:
TrCHSa36 :	----		----		----		:
TrCHSa37 :	----		----		----		:
TrCHSa38 :	----		----		----		:
TrCHSa39 :	ATTGATGGTCACCTTCGCGAAGCTGGACTAACATTTCATCTTCTTAAAGAATGTCCTGGG		----		----		: 481

FIGURE 15 (cont)

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	*	1040	*	1060	*	1080	
TrCHSa1 :	-----		-----		-----		:
TrCHSa2 :	-----		-----		-----		:
TrCHSa3 :	-----		-----		-----		:
TrCHSa4 :	-----		-----		-----		:
TrCHSa5 :	-----		-----		-----		:
TrCHSa6 :	-----		-----		-----		:
TrCHSa7 :	-----		-----		-----		:
TrCHSa8 :	-----		-----		-----		:
TrCHSa9 :	-----		-----		-----		:
TrCHSa10 :	-----		-----		-----		:
TrCHSa11 :	-----		-----		-----		:
TrCHSa12 :	-----		-----		-----		:
TrCHSa13 :	-----		-----		-----		:
TrCHSa14 :	-----		-----		-----		:
TrCHSa15 :	-----		-----		-----		:
TrCHSa16 :	-----		-----		-----		:
TrCHSa17 :	-----		-----		-----		:
TrCHSa18 :	-----		-----		-----		:
TrCHSa19 :	-----		-----		-----		:
TrCHSa20 :	-----		-----		-----		:
TrCHSa21 :	-----		-----		-----		:
TrCHSa22 :	-----		-----		-----		:
TrCHSa23 :	-----		-----		-----		:
TrCHSa24 :	-----		-----		-----		:
TrCHSa25 :	-----		-----		-----		:
TrCHSa26 :	-----		-----		-----		:
TrCHSa27 :	-----		-----		-----		:
TrCHSa28 :	-----		-----		-----		:
TrCHSa29 :	-----		-----		-----		:
TrCHSa30 :	-----		-----		-----		:
TrCHSa31 :	-----		-----		-----		:
TrCHSa32 :	-----		-----		-----		:
TrCHSa33 :	-----		-----		-----		:
TrCHSa34 :	-----		-----		-----		:
TrCHSa35 :	-----		-----		-----		:
TrCHSa36 :	-----		-----		-----		:
TrCHSa37 :	-----		-----		-----		:
TrCHSa38 :	-----		-----		-----		:
TrCHSa39 :	-----		-----		-----		:
	ATTGTTATCAAAGAACATTAAATAAAGCATTTGGTCGAGGCTTTCCAACCATPAGGAATTTTC						: 541

FIGURE 15 (cont)

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	*	1100	*	1120	*	
TrCHSa1	:	-----	-----	-----	-----	:
TrCHSa2	:	-----	-----	-----	-----	:
TrCHSa3	:	-----	-----	-----	-----	:
TrCHSa4	:	-----	-----	-----	-----	:
TrCHSa5	:	-----	-----	-----	-----	:
TrCHSa6	:	-----	-----	-----	-----	:
TrCHSa7	:	-----	-----	-----	-----	:
TrCHSa8	:	-----	-----	-----	-----	:
TrCHSa9	:	-----	-----	-----	-----	:
TrCHSa10	:	-----	-----	-----	-----	:
TrCHSa11	:	-----	-----	-----	-----	:
TrCHSa12	:	-----	-----	-----	-----	:
TrCHSa13	:	-----	-----	-----	-----	:
TrCHSa14	:	-----	-----	-----	-----	:
TrCHSa15	:	-----	-----	-----	-----	:
TrCHSa16	:	-----	-----	-----	-----	:
TrCHSa17	:	-----	-----	-----	-----	:
TrCHSa18	:	-----	-----	-----	-----	:
TrCHSa19	:	-----	-----	-----	-----	:
TrCHSa20	:	-----	-----	-----	-----	:
TrCHSa21	:	-----	-----	-----	-----	:
TrCHSa22	:	-----	-----	-----	-----	:
TrCHSa23	:	-----	-----	-----	-----	:
TrCHSa24	:	-----	-----	-----	-----	:
TrCHSa25	:	-----	-----	-----	-----	:
TrCHSa26	:	-----	-----	-----	-----	:
TrCHSa27	:	-----	-----	-----	-----	:
TrCHSa28	:	-----	-----	-----	-----	:
TrCHSa29	:	-----	-----	-----	-----	:
TrCHSa30	:	-----	-----	-----	-----	:
TrCHSa31	:	-----	-----	-----	-----	:
TrCHSa32	:	-----	-----	-----	-----	:
TrCHSa33	:	-----	-----	-----	-----	:
TrCHSa34	:	-----	-----	-----	-----	:
TrCHSa35	:	-----	-----	-----	-----	:
TrCHSa36	:	-----	-----	-----	-----	:
TrCHSa37	:	-----	-----	-----	-----	:
TrCHSa38	:	-----	-----	-----	-----	:
TrCHSa39	:	SATTCACAACTCAATCTTTTGGATTGCACACCCGGGTGGACCTGCAATTCT				:

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FIGURE 15 (cont)

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TrCHSb : TCTTCGNCNAGCTGGACNAACATTNTTGCTTCTTAAAGATGTTCTCTGAGATTGTCTCAAA : 60

TrCHSb : GAACATTGATAAGGCATTGGTTGAGGCATTCCAACCATTAACATCTCTGATTACAATTC : 120

TrCHSb : AATCTTTTGGATTGCTCATCCAGGTGGTCTGCAATCTAGACCAAGTTGAGATAAAGTT : 180

TrCHSb : GGGCTTAAACCTGAAAAATGAAGGCCACCAGAGATGTACTTAGTGAATATGGTAACAT : 240

TrCHSb : GTC AAGTGCATGTGTATTGTTTCATCTTAGATGAGATGCAAAAGAAATCGGCTGAAAATGG : 300

TrCHSb : ACTGAAAACCAAGGAGAGGACTTGACTGGGGTGTGTTGTTGGATTGGAACAGGACT : 360

TrCHSb : TACCATTGAAACTGTGTTCTACATAGTGTGGCTATATGAGAAATGCGAGACTTGATTGTT : 420

TrCHSb : TTGTATTGTATTGTATTGTATTGATTACTTTTAACTCTTGCTTGAATTTCCATTAAACAA : 480

TrCHSb : TAAATATGGAGTTCAATAAGTACCATCAGTGTAAATTAATATATCGTTAATAGCTATTA : 540

TrCHSb : TTTTAGTGTCTGTTCTTTTCTAAACTATATTTTATTTTAGTATTTGCTATTGATTG : 600

TrCHSb : AAATAAATATTGTCTCTTAACTGAAAAAAAA : 634

FIGURE 16

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TrCHSb : LRXAGXTFXLLKDVPEIVSKNIDKALVEAFQPLNISDYNISIPWIAHPGGPAILDQVEIKL : 60

TrCHSb : GLKPEKMKATRDVLS EYGNMSSACVLFILDEMQKSAENGLKTTGEGLDWGVLFGFGPGL : 120

TrCHSb : TIETVVLHSAI : 132

FIGURE 17

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TrCHSb1:	TCTTCGNCNAGCTGGACNAACATTINTGCTTCCTTAAAGA*GTTCTCTGAGATTGTCACAA	: 60
TrCHSb2:	-----	: -
TrCHSb3:	-----	: -
TrCHSb1:	GAACATTGATAAGGCATTGGTTGAGGCATTCACACCATTAACATCTCTGAT*TAACAATTC	: 120
TrCHSb2:	-----	: -
TrCHSb3:	-----	: -
TrCHSb1:	ATCTTTTGGATTGCTCATCCAGGTGGTCTCTGCAATTC*TAGACCAAGTTGAGATAAAGTT	: 180
TrCHSb2:	-----	: -
TrCHSb3:	-----	: -
TrCHSb1:	GGGCTTAAACCTGAAAAATGAAGGCCACAGAGATGTACTTAGTGAATATGGTAACAT	: 240
TrCHSb2:	-----	: -
TrCHSb3:	-----	: -
TrCHSb1:	GTCAGTGCATGTGATTGTTCATCTT*GAGATGAGATGCAATGAAATCGGCTGAAAAATGG	: 300
TrCHSb2:	-----GAGATGCCATGAAATCGGCTGAAAAATGG	: 29
TrCHSb3:	-----GAGATGCCATGAAATCGGCTGAAAAATGG	: 29
TrCHSb1:	ACTGAAACCCACAGGAGAAGGACTTGACTGGGGTGTGTGTTTGGATT*TTGGCCCGGAGACT	: 360
TrCHSb2:	ACTGAAACCCACAGGAGAAGGACTTGACTGGGGTGTGTGTTTGGATT*TTGGACCAAGGACT	: 89
TrCHSb3:	ACTGAAACCCACAGGAGAAGGACTTGACTGGGGTGTGTGTTTGGATT*TTGGACCAAGGACT	: 89
TrCHSb1:	TACCATTGAAACTGTGTTCTACATAGTGTGGCTATATGAGAATCGAGACTTGATTTGT	: 420
TrCHSb2:	TACCATTGAAACTGTGTTCTACATAGTGTGGCTATATGAGAATCGAGACTTGATTTGT	: 149
TrCHSb3:	TACCATTGAAACTGTGTTCTACATAGTGTGGCTATATGAGAATCGAGACTTGATTTGT	: 149
TrCHSb1:	ATTGATTTGATTTACTTTTAACTCTGCTGAAATTC*CCATTTAACAT	: 470
TrCHSb2:	TTGTATTGTATTGTATTGTATTGATTACTTTAACTCTGCTGAAATTC*CCATTTAACAT	: 209
TrCHSb3:	TTGTATTGTATTGTATTGTATTGATTACTTTAACTCTGCTGAAATTC*CCATTTAACAT	: 209
TrCHSb1:	TAAATATGGAGTTCAATCAATTC	: 500
TrCHSb2:	TAAATATGGAGTTCAATCAATTC	: 491
TrCHSb3:	TAAATATGGAGTTCAATCAATTC	: 269
TrCHSb1:	TTTATGATGCTGTTCTTTTTTACTAAACTATATTTTATTTAGTATT*TTGCTATGATTTG	: 560
TrCHSb2:	TTTATGATGCTGTTCTTTTTTACTAAACTATATTTTATTTAGTATT*TTGCTATGATTTG	: 329
TrCHSb3:	TTTATGATGCTGTTCTTTTTTACTAAACTATATTTTATTTAGTATT*TTGCTATGATTTG	: 329
TrCHSb1:	AAATAAATATTTGCTCTTTAACTGAAAAA	: 620
TrCHSb2:	AAATAAATATTTGCTCTTTAACTGAAAAA	: 363
TrCHSb3:	AAATAAATATTTGCTCTTTAACTGAAAAA	: 363

FIGURE 18

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TrCHSc : GNTTCAATCTGTTGTGCATAAAATTNCTTTGCNATAGAAAAACCATACACATTTGATCTTG : 60
          *           20           *           40           *           60
TrCHSc : CAAAGAGAGAAATATGGGAGACGAAGGTATAGTGAGAGGTGTCACAAAGCAGACACCCCT : 120
          *           80           *           100          *           120
TrCHSc : GGGAAGGCTACTATATTGGCTCTTGGCAAGGCATTCCCTCACCAACTTGTGTATGCAAGAG : 180
          *           140          *           160          *           180
TrCHSc : TATTTAGTTGATGGTTATTTTAGGGACACTAATTGTGACAATCCTGAACTTAAGCAGAAA : 240
          *           200          *           220          *           240
TrCHSc : CTTGCTAGACTTTGTAAGACAACCACGGTAAAAACAAGGTATGTTGTTATGAATGAGGAG : 300
          *           260          *           280          *           300
TrCHSc : ATACTAAAGAAATATCCAGAACTTGTGTGCGAAGGCGCTCAACTGTAAAACACACGTTTA : 360
          *           320          *           340          *           360
TrCHSc : GAGATATGTAATGAGGCAGTAACACAAATGGCAATTGAAGCTTCCCAAGTTTGCCTAAAG : 420
          *           380          *           400          *           420
TrCHSc : AATTGGGGTAGATCCTTATCGGACATAACTCATGTGGTTTATGTTTCATCTAGTGAAGCT : 480
          *           440          *           460          *           480
TrCHSc : AGATTACCGGTGGTGACCTATACTTGTCAAAGGACTAGGACTAAACCCTAAAAATTCAA : 540
          *           500          *           520          *           540
TrCHSc : AGAACCATGCTCTATTTCTCTGGATGCTCGGGAGGCGTAGCCGCTTCGCGTTGCGAAA : 600
          *           560          *           580          *           600
TrCHSc : GACATAGCTGAGAAACCCCTGGAAGTAGAGTTTGTCTTGCTACTTCTGAAACTACAAAT : 660
          *           620          *           640          *           660
TrCHSc : AITGGATTCAAGCCACCAAGTGTGATAGACCTTATGATCTTGTGGTGTGGCACTCTTT : 720
          *           680          *           700          *           720
TrCHSc : GGAGATGGTGCTGGTGCTATGATAATTGGCTCAGACCCAATCTTGAAACTGAGACTCCA : 780
          *           740          *           760          *           780
TrCHSc : TTGPTTAGCTTTCATACCTCAGCTCAGGAGTTTATACCAGACACAGAGAAGAAAATAGAT : 840
          *           800          *           820          *           840
TrCHSc : GGGGCGCTGACGGAGGAGGGCATAAGTTTACGCTACGAGGGGAAC TGCCGCAGATA : 897
          *           860          *           880          *

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FIGURE 19

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      *           20           *           40           *           60
TrCHSc : MGDEGIVRGVTKQTTPGKATILALGKAFPHQLVMQEYLVDPGYFRDNCNPELKQKLARL : 60

      *           80           *           100          *           120
TrCHSc : CKTTTVKTRYVVMNEEILKKYPELVVEGASTVKQRLEICNEAVTQMAIEASQVCLKNMGR : 120

      *           140          *           160          *           180
TrCHSc : SLSDITHVVVYSSSEARLPGGDLVLSKGLGLNPKIQRMTLYFSGCSGGVAGLRVAKDIAE : 180

      *           200          *           220          *           240
TrCHSc : NNPGSRVLLATSETTIIGFKPPSVDRPYDLVGVALFGDGAGAMIIGSDPILETETPLFEL : 240

      *           260           *
TrCHSc : HTSAQEFIPDTEKKIDGRLTEEGISFTLARELPQI : 275

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FIGURE 20

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		20	*	40	*	60	
TrChSc1:	-----	NTTCAATCTGTTGGCATAAATTC	TTTGCNATAGAAAAC	NTACACATTTGATCTTG	-----	60	
TrChSc2:	-----	TCATATCTGCTTGGCATTTT	TTCNCTTTGCNATAGAAAAC	CATACACATTTTGATCTTG	-----	60	
TrChSc3:	-----	ACTGTTTGCNNTAACTTTC	TTTGCNNTAGAAAAC	CATACACATTTTGATCTTG	-----	53	
TrChSc4:	-----	ACTGTTTGCNNTAACTTTC	TTTGCNNTAGAAAAC	CATACACATTTTGATCTTG	-----	53	
TrChSc5:	-----	TTTAACTTTTTCATTTG	ATGATTTAGAAAAC	CTTACATTTTGATCTTG	-----	50	
TrChSc6:	-----	-----	CTTTCATAGAAAAC	CTTACACATTTTGATCTTG	-----	30	
TrChSc7:	-----	-----	-----	-----	-----	-----	
		80	*	100	*	120	
TrChSc1:	-----	CAAGAAGAAATATGGGAGACGAAGT	TATAGTGAGAGGTGTCACAAAGCAGACACCCCT	-----	120		
TrChSc2:	-----	CTTTAGAAGAAATATGGGAGACGAAGT	TATAGTGAGAGGTGTCACAAAGCAGACACCCCT	-----	117		
TrChSc3:	-----	CAAGAAGAAATATGGGAGACGAAGT	TATAGTGAGAGGTGTCACAAAGCAGACACCCCT	-----	113		
TrChSc4:	-----	CAAGAAGAAATATGGGAGACGAAGT	TATAGTGAGAGGTGTCACAAAGCAGACACCCCT	-----	113		
TrChSc5:	-----	CAAGAAGAAATATGGGAGACGAAGT	TATAGTGAGAGGTGTCACAAAGCAGACACCCCT	-----	100		
TrChSc6:	-----	CAAGAAGAAATATGGGAGACGAAGT	TATAGTGAGAGGTGTCACAAAGCAGACACCCCT	-----	90		
TrChSc7:	-----	-----	-----	-----	-----	-----	
		140	*	160	*	180	
TrChSc1:	-----	GGGAAGGCTACTATATTGGCTCTGGC	CAAGGCATTCCTCACCAACTTGTGATGC	CAAGAG	-----	180	
TrChSc2:	-----	GGGAAGGCTACTATATTGGCTCTGGC	CAAGGCATTCCTCACCAACTTGTGATGC	CAAGAG	-----	177	
TrChSc3:	-----	GGGAAGGCTACTATATTGGCTCTGGC	CAAGGCATTCCTCACCAACTTGTGATGC	CAAGAG	-----	173	
TrChSc4:	-----	GGGAAGGCTACTATATTGGCTCTGGC	CAAGGCATTCCTCACCAACTTGTGATGC	CAAGAG	-----	173	
TrChSc5:	-----	GGGAAGGCTACTATATTGGCTCTGGC	CAAGGCATTCCTCACCAACTTGTGATGC	CAAGAG	-----	160	
TrChSc6:	-----	GGGAAGGCTACTATATTGGCTCTGGC	CAAGGCATTCCTCACCAACTTGTGATGC	CAAGAG	-----	150	
TrChSc7:	-----	-----	-----	-----	-----	-----	
		200	*	220	*	240	
TrChSc1:	-----	TATTAGTGTGATGGTTATT	TATAGGACACTAATGTGACATTC	TGAACCTTAAGCAGAA	-----	240	
TrChSc2:	-----	TATTAGTGTGATGGTTATT	TATAGGACACTAATGTGACATTC	TGAACCTTAAGCAGAA	-----	237	
TrChSc3:	-----	TATTAGTGTGATGGTTATT	TATAGGACACTAATGTGACATTC	TGAACCTTAAGCAGAA	-----	233	
TrChSc4:	-----	TATTAGTGTGATGGTTATT	TATAGGACACTAATGTGACATTC	TGAACCTTAAGCAGAA	-----	230	
TrChSc5:	-----	TATTAGTGTGATGGTTATT	TATAGGACACTAATGTGACATTC	TGAACCTTAAGCAGAA	-----	223	
TrChSc6:	-----	TATTAGTGTGATGGTTATT	TATAGGACACTAATGTGACATTC	TGAACCTTAAGCAGAA	-----	210	
TrChSc7:	-----	-----	-----	-----	-----	-----	
		260	*	280	*	300	
TrChSc1:	-----	CTTGC	TAGACTTTGTAAGACAACCA	CGGTAAAAACAAGGTATGTTGTTATGAATGAGGAG	-----	300	
TrChSc2:	-----	CTTGC	TAGACTTTGTAAGACAACCA	CGGTAAAAACAAGGTATGTTGTTATGAATGAGGAG	-----	297	
TrChSc3:	-----	CTTGC	TAGACTTTGTAAGACAACCA	CGGTAAAAACAAGGTATGTTGTTATGAATGAGGAG	-----	293	
TrChSc4:	-----	CTTGC	TAGACTTTGTAAGACAACCA	CGGTAAAAACAAGGTATGTTGTTATGAATGAGGAG	-----	293	
TrChSc5:	-----	CTTGC	TAGACTTTGTAAGACAACCA	CGGTAAAAACAAGGTATGTTGTTATGAATGAGGAG	-----	280	
TrChSc6:	-----	CTTGC	TAGACTTTGTAAGACAACCA	CGGTAAAAACAAGGTATGTTGTTATGAATGAGGAG	-----	270	
TrChSc7:	-----	-----	-----	-----	-----	-----	
		320	*	340	*	360	
TrChSc1:	-----	TACTAAAGAAATATCCAGAAC	TGTTGTCTGAAGGCCCTTCACCTGTA	TAAACACGCTTTT	-----	360	
TrChSc2:	-----	TACTAAAGAAATATCCAGAAC	TGTTGTCTGAAGGCCCTTCACCTGTA	TAAACACGCTTTT	-----	357	
TrChSc3:	-----	TACTAAAGAAATATCCAGAAC	TGTTGTCTGAAGGCCCTTCACCTGTA	TAAACACGCTTTT	-----	353	
TrChSc4:	-----	TACTAAAGAAATATCCAGAAC	TGTTGTCTGAAGGCCCTTCACCTGTA	TAAACACGCTTTT	-----	353	
TrChSc5:	-----	TACTAAAGAAATATCCAGAAC	TGTTGTCTGAAGGCCCTTCACCTGTA	TAAACACGCTTTT	-----	340	
TrChSc6:	-----	TACTAAAGAAATATCCAGAAC	TGTTGTCTGAAGGCCCTTCACCTGTA	TAAACACGCTTTT	-----	330	
TrChSc7:	-----	-----	-----	-----	-----	-----	

FIGURE 21

FIGURE 21 (cont)

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          *       740       *       760       *       780
TrCHSc1:  ----- : -
TrCHSc2:  ----- : -
TrCHSc3:  ----- : -
TrCHSc4:  ----- : -
TrCHSc5:  ----- : -
TrCHSc6:  ----- : -
TrCHSc7:  GGAGATGGTGCTGGTGCTATGATAATTGGCTCAGACCCCAATACTTGAAACTGAGACTCC : 467

          *       800       *       820       *       840
TrCHSc1:  ----- : -
TrCHSc2:  ----- : -
TrCHSc3:  ----- : -
TrCHSc4:  ----- : -
TrCHSc5:  ----- : -
TrCHSc6:  ----- : -
TrCHSc7:  TTGTTTGAGCTTCACTACTCAGCTCAGGAGTTTATACCAGACACAGAGAGAGAAATAGAT : 527

          *       860       *       880       *
TrCHSc1:  ----- : -
TrCHSc2:  ----- : -
TrCHSc3:  ----- : -
TrCHSc4:  ----- : -
TrCHSc5:  ----- : -
TrCHSc6:  ----- : -
TrCHSc7:  GGGCGGCTGACGGAGGAGGGCATAAGTTTTCACGCTAGCGAGGGAAC TGCCGCAGATM : 584

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FIGURE 21 (cont)

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TrCHSd : GTAGCAACACACACTTTGATTTCCTTTTGGAGTCCTTGCTACGTGGCNTTACCAAAAAACG : 60

TrCHSd : TTGCTAAGTCATCAACCATTCCAATTCTTAATATAACCTATCAGTACTCACCATCTTTT : 120

TrCHSd : CTTCCTCCCTGCTAACTTTATACCTTAGAGAAGATGGTGAAAGTTAATGAGATCCGCCAGG : 180

TrCHSd : CACAGAGAGCTGAAGGCCCTGCCACTGTGTGGCAATCGGCACTGCAACTCCTCCAAACT : 240

TrCHSd : GTGTTGATCAGAGTACATACCCCGACTACTACTCCGCATCACAAACAGTGAGCACAAGA : 300

TrCHSd : CAGAGCTCAAAGAAAAATCCAGCGCATGTGTGACAAATCTATGATTAGAAGAGATACA : 360

TrCHSd : TGCATTTGACAGAAGAGATTTTGAAGGAGAATCCAAGTTTATGTGAGTACATGGCACCTT : 420

TrCHSd : CATTGGATGCAAGACAAGACATGGTGGTTGTGGAAGTACCAAGGCTAGGAAAAAGGGCAG : 480

TrCHSd : CAACAAAGGCAATCAAGGAATGGGGTCAACCTAAGTCCAAGATTACCCACCTCATCTTTT : 540

TrCHSd : GCACCACAAGTGGTGTGGACATGCCCGGTGCCGACTATCAGCTTACAAGCTTTTAGGCC : 600

TrCHSd : TTCGTCGCATGTGAAGCGTTACATGATGTACCAACAAGGTGTGTTTGTGGTGGCACGG : 660

TrCHSd : TGCTTCGTTTGGCTAAGACTTGGCTGAAACAACAAGGTGCCCGTGTATGTGGTGGTTT : 720

TrCHSd : GTTCAGAGATAACTG : 735

FIGURE 22

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TrCHSd : * 20 * 40 * 60
 : M V K V N E I R Q A R A B G P A T V L A I G T A T P P N C V D Q S T Y P D Y I F R I T N S E H K T E L K E X F Q R M C : 60

 * 80 * 100 * 120
TrCHSd : D K S M I K K R Y M H L T E E I L K E N P S L C E Y M A P S L D A R Q D M V V V E V P R L G K E A A T K A I K E W G Q P : 120

 * 140 * 160 * 180
TrCHSd : K S K I T H L I F C T T S G V D M P G A D Y Q L T K L L G L R P H V K R Y M M Y Q Q G C F A G G T V L R L A K D L A E N : 180

 *
TrCHSd : N K G A R V L V V C S E I T : 194

FIGURE 23

FIGURE 24

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      *           260           *           280           *           300
TrCHSd1 : G*GTGATCAGAGTACATACCCGACTACTACTTCCGCATCACAACAGTGAGCACAAG :300
TrCHSd2 : GTGTGATCAGAGTACATACCCGACTACTACTTCCGCATCACAACAGTGAGCACAAG :300
TrCHSd3 : G*GTGATCAGAGTACATACCCGACTACTACTTCCGCATCACAACAGTGAGCACAAG :300
TrCHSd4 : GTGTGATCAGAGTACATACCCGACTACTACTTCCGCATCACAACAGTGAGCACAAG :300
TrCHSd5 : GTGTGATCAGAGTACTTACCCGACTACTACTTCCGCATCACAACAGGGAACACAAG :190
TrCHSd6 : GTGTGATCAGAGTACTTACCCGACTACTACTTCCGCATCACAACAGGGAACACAAG :190
TrCHSd7 : GTGTGATCAGAGTACTTACCCGACTACTACTTCCGCATCACAACAGGGAACACAAG :186
TrCHSd8 : GTGTGATCAGAGTACATACCCGACTACTACTTCCGCATCACAACAGTGAGCACAAG :173
TrCHSd9 : GTGTGATCAGAGTACATACCCGACTACTACTTCCGCATCACAACAGTGAGCACAAG :168
TrCHSd10 : GTGTGATCAGAGTACTTACCCGACTACTACTTCCGCATCACAACAGGGAACACAAG :165
TrCHSd11 : GTGTGATCAGAGTACTTACCCGACTACTACTTCCGCATCACAACAGGGAACACAAG : 67

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      *           320           *           340           *           360
TrCHSd1 : CAGAGCTCAAAGAAAAATCCAGCGCATGTGTGACAAATCTATGATTAAAGAGAGATAC :360
TrCHSd2 : CAGAGCTCAAAGAAAAATCCAGCGCATGTGTGACAAATCTATGATTAAAGAGAGATAC :360
TrCHSd3 : CAGAGCTCAAAGAAAAATCCAGCGCATGTGTGACAAATCTATGATTAAAGAGAGATAC :360
TrCHSd4 : CAGAGCTCAAAGAAAAATCCAGCGCATGTGTGACAAATCTATGATTAAAGAGAGATAC :350
TrCHSd5 : CAGAGCTCAAAGAAAAATCCAGCGCATGTGTGACAAATCTATGATTAAAGAGAGATAC :250
TrCHSd6 : CAGAGCTCAAAGAAAAATCCAGCGCATGTGTGACAAATCTATGATTAAAGAGAGATAC :250
TrCHSd7 : CAGAGCTCAAAGAAAAATCCAGCGCATGTGTGACAAATCTATGATTAAAGAGAGATAC :246
TrCHSd8 : CAGAGCTCAAAGAAAAATCCAGCGCATGTGTGACAAATCTATGATTAAAGAGAGATAC :233
TrCHSd9 : CAGAGCTCAAAGAAAAATCCAGCGCATGTGTGACAAATCTATGATTAAAGAGAGATAC :228
TrCHSd10 : CAGAGCTCAAAGAAAAATCCAGCGCATGTGTGACAAATCTATGATTAAAGAGAGATAC :225
TrCHSd11 : CAGAGCTCAAAGAAAAATCCAGCGCATGTGTGACAAATCTATGATTAAAGAGAGATAC :127

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      *           380           *           400           *           420
TrCHSd1 : TGCATTTGACAGAAGAGATTTTGAAGGAGAATCCAAAGTTTATGTGAGTACATGGCACCT :420
TrCHSd2 : TGCATTTGACAGAAGAGATTTTGAAGGAGAATCCAAAGTTTATGTGAGTACATGGCACCT :420
TrCHSd3 : TGCATTTGACAGAAGAGATTTTGAAGGAGAATCCAAAGTTTATGTGAGTACATGGCACCT :420
TrCHSd4 : TGCATTTGACAGAAGAGATTTTGAAGGAGAATCCAAAGTTTATGTGAGTACATGGCACCT :410
TrCHSd5 : TGCATTTGACAGAAGAGATTTTGAAGGAGAATCCAAAGTTTATGTGAGTACATGGCACCT :310
TrCHSd6 : TGCATTTGACAGAAGAGATTTTGAAGGAGAATCCAAAGTTTATGTGAGTACATGGCACCT :310
TrCHSd7 : TGCATTTGACAGAAGAGATTTTGAAGGAGAATCCAAAGTTTATGTGAGTACATGGCACCT :306
TrCHSd8 : TGCATTTGACAGAAGAGATTTTGAAGGAGAATCCAAAGTTTATGTGAGTACATGGCACCT :293
TrCHSd9 : TGCATTTGACAGAAGAGATTTTGAAGGAGAATCCAAAGTTTATGTGAGTACATGGCACCT :288
TrCHSd10 : TGCATTTGACAGAAGAGATTTTGAAGGAGAATCCAAAGTTTATGTGAGTACATGGCACCT :285
TrCHSd11 : TGCATTTGACAGAAGAGATTTTGAAGGAGAATCCAAAGTTTATGTGAGTACATGGCACCT :187

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      *           440           *           460           *           480
TrCHSd1 : CATTTGGATGCAAGACAAGACATGGTGGTTGTGGAAGTACCAAGGCTAGGAAAAGAGGCG :480
TrCHSd2 : CATTTGGATGCAAGACAAGACATGGTGGTTGTGGAAGTACCAAGGCTAGGAAAAGAGGCG :480
TrCHSd3 : CATTTGGATGCAAGACAAGACATGGTGGTTGTGGAAGTACCAAGGCTAGGAAAAGAGGCG :480
TrCHSd4 : CATTTGGATGCAAGACAAGACATGGTGGTTGTGGAAGTACCAAGGCTAGGAAAAGAGGCG :470
TrCHSd5 : CATTTGGATGCAAGACAAGACATGGTGGTTGTGGAAGTACCAAGGCTAGGAAAAGAGGCG :370
TrCHSd6 : CATTTGGATGCAAGACAAGACATGGTGGTTGTGGAAGTACCAAGGCTAGGAAAAGAGGCG :370
TrCHSd7 : CATTTGGATGCAAGACAAGACATGGTGGTTGTGGAAGTACCAAGGCTAGGAAAAGAGGCG :366
TrCHSd8 : CATTTGGATGCAAGACAAGACATGGTGGTTGTGGAAGTACCAAGGCTAGGAAAAGAGGCG :353
TrCHSd9 : CATTTGGATGCAAGACAAGACATGGTGGTTGTGGAAGTACCAAGGCTAGGAAAAGAGGCG :348
TrCHSd10 : CATTTGGATGCAAGACAAGACATGGTGGTTGTGGAAGTACCAAGGCTAGGAAAAGAGGCG :345
TrCHSd11 : CATTTGGATGCAAGACAAGACATGGTGGTTGTGGAAGTACCAAGGCTAGGAAAAGAGGCG :247

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FIGURE 24 (cont)

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		500	*	520	*	540	
TrChsD1:	CAACAAAGGCAATTAAAGGAATGGGGTCAACCTAAGTCCAAAGATTACCACCTCATCTTTT						: 540
TrChsD2:	CAACAAAGGCAATTCAAGGAATGGGGTCAACCTAAGTCCAAAGATTACCACCTCATCTTTT						: 540
TrChsD3:	CAACAAAGGCAATTCAAGGAATGGGGTCAACCTAAGTCCAAAGATTACCACCTCATCTTTT						: 540
TrChsD4:	CAACAAAGGCAATTAAAGGAATGGGGTCAACCTAAGTCCAAAGATTACCACCTCATCTTTT						: 530
TrChsD5:	CAACAAAGGCAATTCAAGGAATGGGGTCAACCTAAGTCCAAAGATTACCACCTCATCTTTT						: 530
TrChsD6:	CAACAAAGGCAATTCAAGGAATGGGGTCAACCTAAGTCCAAAGATTACCACCTCATCTTTT						: 430
TrChsD7:	CAACAAAGGCAATTCAAGGAATGGGGTCAACCTAAGTCCAAAGATTACCACCTCATCTTTT						: 426
TrChsD8:	CAACAAAGGCAATTAAAGGAATGGGGTCAACCTAAGTCCAAAGATTACCACCTCATCTTTT						: 413
TrChsD9:	CAACAAAGGCAATTAAAGGAATGGGGTCAACCTAAGTCCAAAGATTACCACCTCATCTTTT						: 408
TrChsD10:	CAACAAAGGCAATTAAAGGAATGGGGTCAACCTAAGTCCAAAGATTACCACCTCATCTTTT						: 405
TrChsD11:	CGT						: 250
		*	560	*	580	*	600
TrChsD1:	GCACCACAGTGGTGTGACATGCCCGGTGGCCG						: 574
TrChsD2:	GCACCACAGTGGTGTGGACATGCCCGGTGGCCGACTATCAGCTTACAAAGCTTTTGG						: 597
TrChsD3:	GCACCACAGTGGTGTGGACATGCCCGGTGGCCGACTATCAGCTTACAAAGCTTTTGGCC						: 600
TrChsD4:	GCACCACAGTGGTGTGGACATGCCCGGTGGCCGACTATCAGCTTACAAAGCTTTTGGCC						: 585
TrChsD5:	GCACCACAGTGGTGTGGACATGCCCGGTGGCCGACTATCAGCTTACAAAGCTTTTGGCC						: 490
TrChsD6:	GCACCACAGTGGTGTGGACATGCCCGGTGGCCGACTATCAGCTTACAAAGCTTTTGGCC						: 490
TrChsD7:	GCACCACAGTGGTGTGGACATGCCCGGTGGCCGACTATCAGCTTACAAAGCTTTTGGCC						: 486
TrChsD8:	GCACCACAGTGGTGTGACATGCCCGGTGGCCGACTATCAGCTTACAAAGCTTTTGGCC						: 473
TrChsD9:	GCACCACAGTGGTGTGACATGCCCGGTGGCCGACTATCAGCTTACAAAGCTTTTGGCC						: 465
TrChsD10:	GCACCACAGTGGTGTGGACATGCCCGGTGGCCGACTATCAGCTTACAAAGCTTTTGGCC						: 465
TrChsD11:							: -
		*	620	*	640	*	660
TrChsD1:							: -
TrChsD2:							: -
TrChsD3:	TTGGTCCGCGATGCG						: 616
TrChsD4:							: -
TrChsD5:	TTGCTCCGCGATGTGAAGCGTTATGATGTACCAACAAGGTGTGTTTGCCTGGTGGCAACGG						: 550
TrChsD6:	TTGCTCCGCGATGTGAAGCGTTATGATGTACCAACAAGGTGTGTTTGCCTGGTGGCAACGG						: 550
TrChsD7:	TTGCTCCGCGATGTGAAGCGTTATGATGTACCAACAAGGTGTGTTTGCCTGGTGGCAACGG						: 546
TrChsD8:	TTGCTCCGCGATGTGAAGCGTTATGATGTACCAACAAGGTGTGTTTGCCTGGTGGCAACGG						: 533
TrChsD9:	TTGCTCCGCGATGTGAAGCGTTATGATGTACCAACAAGGTGTGTTTGCCTGGTGGCAACGG						: 528
TrChsD10:	TTGCTCCGCGATGTGAAGCGTTATGATGTACCAACAAGGTGTGTTTGCCTGGTGGCAACGG						: 525
TrChsD11:							: -
		*	680	*	700	*	720
TrChsD1:							: -
TrChsD2:							: -
TrChsD3:							: -
TrChsD4:							: -
TrChsD5:	TGCTTCGTTTGGCTAAAGACTTGGCTGAAAACAACAAGGTGCGCC						: 596
TrChsD6:	TGCTTCGTTTGGCTAAAGACTTGGCTGAAAACAACAAGGTGCGCCGTGATTGGTGGTTT						: 610
TrChsD7:	TGCTTCGTTTGGCTAAAGACTTGGCTGAAAACAACAAGGTGCGCCGTGATTGGTGGTTT						: 606
TrChsD8:	TGCTTCGTTTGGCTAAAGACTTGGCTGAAAACAACAAGGTGCGCCGTGATTGGTGGTTT						: 577
TrChsD9:	TGCTTCGTTTGGCTAAAGACTTGGCTGAAAACAACAAGGTGCGCCGTGATTGGTGGTTT						: 588
TrChsD10:	TGCTTCGTTTGGCTAAAGACTTGGCTGAAAACAACAAGGTGCGCCGTGATTGGTGGTTT						: 585
TrChsD11:	TGCTTCGTTTGGCTAAAGACTTGGCTGAAAACAACAAGGTGCGCCGTGATTGGTGGTTT						: 585

FIGURE 24 (cont)

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                                *
TrCHSd1  : ----- : -
TrCHSd2  : ----- : -
TrCHSd3  : ----- : -
TrCHSd4  : ----- : -
TrCHSd5  : ----- : -
TrCHSd6  : GTTCAGAG----- : 618
TrCHSd7  : GTT----- : 609
TrCHSd8  : ----- : -
TrCHSd9  : GTTCAGAGATAACTG : 603
TrCHSd10 : GTT----- : 588
TrCHSd11 : ----- : -

```

FIGURE 24 (cont)

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      *           20           *           40           *           60
TrCHSe : GNAGCAACACACACTTTGATTTCCTTTTGAATCCCTGCTACGTGGCNCACCAAAAAAGT : 60

      *           80           *           100          *           120
TrCHSe : TGCTAAGTCATCAACCATTCCAATTCCCTTAATATAACCTATCAGTACTCACCATCTTTTC : 120

      *           140          *           160          *           180
TrCHSe : TTCCTCCCTGCTAACTTTAGACTCAGTAGAAGATGGTGAATGTTAATGAGATCCGCCAGG : 180

      *           200          *           220          *           240
TrCHSe : CACAGAGAGCTGAAGGCCCTGCCACCGTGTGGCAATCGGCACTGCAACTCCTCCAAACT : 240

      *           260          *           280          *           300
TrCHSe : GTGTTGATCAGAGTACATACCCGGACTACTACTCCGCATCACAAACAGTGAGCAACAAG : 300

      *           320          *           340          *           360
TrCHSe : CAGAGCTCAAAGAAAAATCCAGCGCACGTGTAAGATATTTATCTTATACTCCATGCATG : 360

      *           380          *           400          *           420
TrCHSe : TCTTTTCTGCTGACTGCCGTGTTTATATATTGTTTTGTTTGTTCCTTAATTTGTAT : 420

      *           440          *           460          *           480
TrCHSe : GTCACCTCTCATGTACAAAACACTTAAGACTAAACTGCATATCATTTTTTTCAGGACA : 480

      *           500          *           520          *           540
TrCHSe : AATCTATGATTAAAGAAGAGATACATGCATTTGACAGAAGAGATTTTGAAGGAGAATCCAA : 540

      *           560          *           580
TrCHSe : GTTTATGTGAGNACATGGCACCTTCTTGGGATGCAAGACAAGT : 583

```

FIGURE 25

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TrCHSe : M V N V N E I R Q A R A E G P A T V L A I G T A T P P N C V D Q S T Y P D Y Y F R I T N S E H K T E L K E K F Q R T R : 60

TrCHSe : D K S M I K K R Y M H L T E E I L K E N P S L C E X M A P S W D A R Q : 95

FIGURE 26

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      *           20           *           40           *           60
TrCHSe1: GNAGCAACACACACTTTGATTTCCTTTTGAATCCCTGCTACGTTGGCTTACCAAAAAACGTT : 60
TrCHSe2: -----TACCCAGCTGCGTGGCNCACC-AAAAACGT : 29

      *           80           *           100          *           120
TrCHSe1: TCGTAGTCATCAACCATTCGAATTCCTTAATATAACCTATCAGTACTACCATTTTTC : 120
TrCHSe2: TCGTNAGT-ATGAACC-TTCC-ATTCCCTTAATATAACCTATCAGTACTACCATCTTTTC : 86

      *           140          *           160          *           180
TrCHSe1: TTCTTCCCTGCTAACCTTTAGACTCAG-AGAAGATGGTGAATGTTAATGAGATCCGCCAG : 179
TrCHSe2: TTCTTCCCCTGCTAACCTTTAGACTCAGTAGAAGATGGTGAATGTTAATGAGATCCGCCAG : 146

      *           200          *           220          *           240
TrCHSe1: CACAGAGAGCTGAAGGCCCTGCCACCGTGTGGCAATCGGCACCTGCAACTCCTCCAAACT : 239
TrCHSe2: CACAGAGAGCTGAAGGCCCTG----- : 167

      *           260          *           280          *           300
TrCHSe1: GTGTTGATCAGAGTACATACCCGGACTACTACTCCGCATCACAAACAGTGAGCACAAAG : 299
TrCHSe2: ----- : -

      *           320          *           340          *           360
TrCHSe1: CAGAGCTCAAAGAAAAATTCAGCGCAGGTGAAGATATTATCTTATATCCATGCGATG : 359
TrCHSe2: ----- : -

      *           380          *           400          *           420
TrCHSe1: TCTTTTTCGCTGACTGCCCTGTTTATATATTGTTTGTGTTTGTTCCTTAAATTTGTTAT : 419
TrCHSe2: ----- : -

      *           440          *           460          *           480
TrCHSe1: GTCACCTCACATGTACAAAACACTTAAGACTAAACTGCATATCATTTTTTTCAGGGACT : 479
TrCHSe2: ----- : -

      *           500          *           520          *           540
TrCHSe1: TCTCTATGATTAAAGAGAGATACATGCATTTGACAGAGAGAGATTTTGAAGGAGAAATCC : 539
TrCHSe2: ----- : -

      *           560          *           580
TrCHSe1: GTTATGAGAGACATGGCACCTTCTTGGGATGCAAGACAAGT : 582
TrCHSe2: ----- : -

```

FIGURE 27

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```

      *           20           *           40           *           60
TrCHSf : GCNTAAGCCTTGATTNTTGTGTTTCTTCTAACACAAGAAGTCTAGTGTTTCTTGAATCTTA : 60

      *           80           *           100          *           120
TrCHSf : AGAAAAAATGCCTCAAGGTGATTGTAATGGAAGTTCCTCGGTGAATGGAGCACGCTGCTAG : 120

      *           140          *           160          *           180
TrCHSf : ACGTGCTCCTACTCAGGGAAGGCAACGATACCTTGCATTAGGAAAGGCTTTCCCCGCCCA : 180

      *           200          *           220          *           240
TrCHSf : AGTCCTCCCTCAAGAGTGCCTTGGTGAAGGATTCATTGCGGACACTAAGTGTGACGATAC : 240

      *           260          *           280          *           300
TrCHSf : TTATATTAAAGGAGAAATTGGAGCGTCTTTGCAAAAACACAAGTGTAAAACAAAGATACAC : 300

      *           320          *           340          *           360
TrCHSf : AGTAATGTCAAAGGAGATCTTAGACAACTATCCAGAGCTAGCCATAGATGGAACACCAAC : 360

      *           380          *           400          *           420
TrCHSf : AATAAGGCAAAAGCTTGAAATAGCAAAATCCAGCAGTAGTTGAAATGGCAACAAAGAGCAAG : 420

      *   *           440           *           460           *           480
TrCHSf : CAAAAGATTGCATCAAAGAAATGGGGAAGGTCACTCAAGATATCACACACATAGTCTATGT : 480

      *           500          *           520          *           540
TrCHSf : TTCTCGAGCGAAATTCGCTCTACCCGGTGGTGACCTTTATCTTGCAAAATGAACTCGGCTT : 540

      *           560          *           580          *           600
TrCHSf : AAACAGCGATGTTAATCGCGTAATGCTCTATTTCTCCTCGGTTGCTACGGCGGTGCTACTGG : 600

      *
TrCHSf : CTTACGTGTCGCC : 613

```

FIGURE 28

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```

      *           20           *           40           *           60
TrCHSf : MPQGDNLGSSSVNGARARRAFTQGKATILALGKAPPAQVLPQECLEVEGFIRDTKCDDTYI : 60

      *           80           *           100          *           120
TrCHSf : KEKLERLCKNTTVKTRYTVMSKEILDNYPELAIDGTPPTIRQKLEIANPAVVEMATRSKD : 120

      *           140          *           160          *           180
TrCHSf : CIKEWGRSPQDITHIVYVSSSEIRLPGGDLYLANELGLNSDVNRVMLYFLGCGYGGVTGLR : 180

TrCHSf : VA : 182

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FIGURE 29

FIGURE 30

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      *           500           *           520           *           540
TrCHSf1: TTCTCGAGCGAAATTCGTCTACCCGGTGGTGAACCTTTAACTTGCAATGAACTCGGCTT : 540
TrCHSf2: TTCTCGAGCGAAATTCGTCTACCCGGTGGTGAACCTTTAACTTGCAATGAACTCGGCTT : 537
TrCHSf3: TTCTCGAGCGAAATTCGTCTACCCGGTGGTGAACCTTTAACTTGCAATGAACTCGGCTT : 531
TrCHSf4: TTCTCGAGCGAAATTCGTCTACCCGGTGGTGAACCTTTAACTTGCAATGAACTCGGCTT : 522

      *           560           *           580           *           600
TrCHSf1: AAACAGCGATGTTAATCGCGTAATGCTCTATTTCCCTCGGTTCGTACGGCGGTGTCACCTGC : 600
TrCHSf2: AAACAGCGATGTTAATCGCGTAATGCTCTATTT----- : 570
TrCHSf3: AAACAGCGATGTTAATCGCGTAATGCTCTATTTCCCTCGGTTCGT----- : 575
TrCHSf4: AAACAGCGATGTTAATCGCGTAATGCTCTATTTCCCTCGGTTCGTACGGCGG----- : 573

      *
TrCHSf1 : CTTACGTGTCGCC : 613
TrCHSf2 : ----- : -
TrCHSf3 : ----- : -
TrCHSf4 : ----- : -

```

FIGURE 30 (cont)

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TrCHSg : GTATACCAAGGT*²⁰TGCTGGTGGCACGGTACTTCGTT*⁴⁰TGGCTAAAGACTTGGCTGAA : 60

TrCHSg : AACAAACAAGGT*⁸⁰GCCCCGTGTGTGGTGGTTTGTTCAGAGATAA*¹⁰⁰CTGCAGTTACTTTCCTG : 120

TrCHSg : GGACCCAGTGACACTCACCTTGATAGCCTTGTGGGGCAAGCATTGT*¹⁴⁰TGGAGATGGTGCA : 180

TrCHSg : GCAGCTGTGATTGT*²⁰⁰TGGTTCAGACCCCTTGCCAGAAGTTGAGAAGCCTT*²²⁰GTGTTGAATTG : 240

TrCHSg : GTATGGACCGCACAAACAATCGCTCCAGATAGTGAAGGAGCCATTGATGGTCACCTTCGC : 300

TrCHSg : GAAGCAGGGGTGACATTCCATCTCCTCAAGGATGTTCTAGCCTTGTCTCAAATAACATT : 360

TrCHSg : GAGAAAGCGCTTGT*³⁸⁰TGATGCCTTTCAACCTTTGAATATTTCTGACTACAA*⁴⁰⁰TCCATCTTT : 420

TrCHSg : TGGATTGCACACCCAGGCGGACCAGCAATTCTTGACCAAGTTGAAGCTAAGTTAGGCTTA : 480

TrCHSg : AAGCCAGAGAAAAATGCAAGCCACTCGACATGTACTT*⁵⁰⁰AGCGAATATGGTAACATGTCAAGT : 540

TrCHSg : GCGTGTGTGTTATTATCT*⁵⁶⁰TGGATGAGATGAGGAGGAAGTCAAAAGAA*⁵⁸⁰GACGGACTTGCC : 600

TrCHSg : ACAACAG : 607

FIGURE 31

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TrCHSg : * 20 * 40 * 60
 : VYQGCFAGGTVLRLAKDLAENNKGARVLVCSEITAVTFRGPSDTHLDSLVGQALFGDGA : 60

TrCHSg : * 80 * 100 * 120
 : AAVIVGSDPLPEVEKPLFELVWTAQTIAPDSEGAIDGHLREAGLTFHLLKDVP SLVSNNI : 120

TrCHSg : * 140 * 160 * 180
 : EKALVDAFQPLNISDYNSIFWIAHPGGPAILDQVEAKLGLKPEKMQATRHVLS EYGNMSS : 180

TrCHSg : * 200
 : ACVLFIIDEMRRKSKEDGLATT : 202

FIGURE 32

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```

      *           20           *           40           *           60
TrCHSg1:  GTATACCAAGGTTGTTTGTCTGGTGGCACGGTACTTCGTTTGGCTTAAGACTTGGCTGAA : 60
TrCHSg2:  -----CCAAGGTGTGTTTGTCTGGTGGCACGGTACTTCGTTTGGCTTAAAGACTTGGCTGAA : 55
TrCHSg3:  -----GGTGTGTTTGTCTGGTGGCACGGTACTTCGTTTGGCTTAAAGACTTGGCTGAA : 51

      *           80           *           100          *           120
TrCHSg1:  TTCAACAAAGGTGCCCGTGTGTGTGTTGGTTTGTTCAGAGAATACTGCAGTTACTTTCCGT : 120
TrCHSg2:  TTCAACAAAGGTGCCCGTGTGTGTGTTGGTTTGTTCAGAGAATACTGCAGTTACTTTCCGT : 115
TrCHSg3:  TTCAACAAAGGTGCCCGTGTGTGTGTTGGTTTGTTCAGAGAATACTGCAGTTACTTTCCGT : 111

      *           140          *           160          *           180
TrCHSg1:  GGACCCAGTGACACTCTACTTGATAGCCTTTGTGGGGCAAGCATTGTTTGGAGATGGTGG : 180
TrCHSg2:  GGACCCAGTGACACTCACCTTGATAGCCTTTGTGGGGCAAGCATTGTTTGGAGATGGTGG : 175
TrCHSg3:  GGACCCAGTGACACTCACCTTGATAGCCTTTGTGGGGCAAGCATTGTTTGGAGATGGTGG : 171

      *           200          *           220          *           240
TrCHSg1:  GCAGCTGTGATGTGTGGTTTCAGACCCTTTGCCAGAAGTTGAGAAGCCTTTGTTTGAATTG : 240
TrCHSg2:  GCAGCTGTGATGTGTGGTTTCAGACCCTTTGCCAGAAGTTGAGAAGCCTTTGTTTGAATTG : 235
TrCHSg3:  GCAGCTGTGATGTGTGGTTTCAGACCCTTTGCCAGAAGTTGAGAAGCCTTTGTTTGAATTG : 231

      *           260          *           280          *           300
TrCHSg1:  GATATGGACCCGACAAACAATCGCTCCAGATAGTGAAGGAGCCATTGATGGTCACCTTCGC : 300
TrCHSg2:  GATATGGACCCGACAAACAATCGCTCCAGATAGTGAAGGAGCCATTGATGGTCACCTTCGC : 295
TrCHSg3:  GATATGGACCCGACAAACAATCGCTCCAGATAGTGAAGGAGCCATTGATGGTCACCTTCGC : 291

      *           320          *           340          *           360
TrCHSg1:  GAAGCAGGGCTGACATTCCATCTCCTCAAGGATGTCTTAGCCTTGCTCAAATAACATT : 360
TrCHSg2:  GAAGCAGGGCTGACATTCCATCTCCTCAAGGATGTCTTAGCCTTGCTCAAATAACATT : 355
TrCHSg3:  GAAGCAGGGCTGACATTCCATCTCCTCAAGGATGTCTTAGCCTTGCTCAAATAACATT : 351

      *           380          *           400          *           420
TrCHSg1:  GAGAAGCGCTTGTTGATGCCTTTCAACCTTTGAATATGTCGAAATACAAATTCACATCTT : 420
TrCHSg2:  GAGAAGCGCTTGTTGATGCCTTTCAACCTTTGAATATTTCTGACTACAATTCACATCTT : 415
TrCHSg3:  GAGAAGCGCTTGTTGATGCCTTTCAACCTTTGAATATTTCTGACTACAATTCACATCTT : 411

      *           440          *           460          *           480
TrCHSg1:  TGGATTGCACACCCAGGCGGACCAAGCAATCTTCACCAAGTTGAAGCTTAAGTTAGCGTT : 480
TrCHSg2:  TGGATTGCACACCCAGGCGGACCAAGCAATCTTCACCAAGTTGAAGCTTAAGTTAGCGTT : 475
TrCHSg3:  TGGATTGCACACCCAGGCGGACCAAGCAATCTTCACCAAGTTGAAGCTTAAGTTAGCGTT : 471

      *           500          *           520          *           540
TrCHSg1:  TAAGCCAGAGAAATGCAAAACCACTCGACATGTACTTTAGCGAATATGGTAACATGTCAAGT : 540
TrCHSg2:  TAAGCCAGAGAAATGCAAGCCACTCGACATGTACTTTAGCGAATATGGTAACATGTCAAGT : 535
TrCHSg3:  TAAGCCAGAGAAATGCAAGCCACTCGACATGTACTTTAGCGAATATGGTAACATGTCAAGT : 531

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FIGURE 33

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          *           560           *           580           *           600
TrCHSg1 : GCGTGTGTGTTATTTATCTTGGATGAGATGAGGAGGAAGTCAAAAAGACACGGACTTGCC : 600
TrCHSg2 : GCGTGTGTGTTATTTATCTTGGATGAGATGAGGAGGAAGTCAAAAAGACACGCT--- : 591
TrCHSg3 : GCGTGTGTGTTATTTATCTTGGATGAGATGAGGAGGAAGTCAAAAAGACACGGACTTGC- : 590

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TrCHSg1 : ACAACAG : 607
TrCHSg2 : ----- : -
TrCHSg3 : ----- : -

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FIGURE 33 (cont)

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TrCHSh : AATNACACCNINANACCTTCCAATTCTCGTACCTCACCAATCTCATTTTATTATATATC : 60

TrCHSh : TTGGTACATCTTTTGTACCTCCAACAAAAAATGGTGACCGTAGAAGAGATTCGTAACG : 120

TrCHSh : CCCAACGTTCAAATGGCCCTGCCACTATCTTAGCTTTTGGCACAGCCACTCCTTCTAACT : 180

TrCHSh : GTGTCACTCAAGCTGATTATCCTGATTACTTTTCGTATCACCAACAGCGAACATATGA : 240

TrCHSh : CTGATCTTAAGGAAAAATTCAAGCGGATGTGTGATAGATCAATGATAAAGAAACGTTACA : 300

TrCHSh : TGCACCTAACAGAAAGACTTTCTGAAGGAGAAATCCAAATATGTGTGAATACATGGCACCAT : 360

TrCHSh : CACTAGATGTAAGACGAGACATAGTGGTTGTTGAAGNACCAAAGCTAGGTAAAGAANCAC : 420

TrCHSh : CAAAAAAGCCATATGNGAATGGGGACAACCAAAATCNAAAATCACACATGCTTGCTTTC : 480

TrCHSh : TGACCACTTCGGGTGNTGACATGCCCGGGG : 510

FIGURE 34

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```

      *           20           *           40           *           60
TrCHSh : MVTVEEIRNAQRSNGPATILAFGTATPSNCVTQADYDPDYFPRITNSEHMTDLKEKFRRMC : 60

      *           80           *           100          *           120
TrCHSh : DRSMIKKRYMHLTEDPLKENPNMCEYMAPSLDVRRDIVVVEXPKLKGEPKKAIXEWGQPK : 120

      *
TrCHSh : XKITHAWPLTTSGDMPG : 137

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FIGURE 35

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TrChrA : GACAAATGCGTGTGGTTGGAAATGGGATCCGACCTGATTTTACATGTAAGAAAGACACAA : 60

TrChrA : AAGATGCAATCGTTGAAGCCATCAAAACAGGTTATAGACACTTTGATACTGCTGCTGCTT : 120

TrChrA : ATGGCTCANAAACAGCTCTTGGTGAAGGTTGAAAGAAGCANTTGAACCTTGGTCTTGTGCA : 180

TrChrA : CTANAGAAAGAGCTNTTGTGTACTTCTAAACTTTGGGNNACTGAAAATCACTNCTAACCTTG : 240

FIGURE 36

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TrCHRa : QMXVVGNGSAPDFTCKKDTFKDAIVEAIKQGYRHFDTAAYGSXQALGEGLEKEXELGLVT : 60

TrCHRa : XEEXFVTSKLMXTENHXNL : 79

FIGURE 37

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TrCHRB : GTGTAGCAGAGT* 20 * 40 * 60 : 60
 TrCHRB : TGTATTGAATT* 80 * 100 * 120 : 120
 TrCHRB : GTCCATCAAA* 140 * 160 * 180 : 180
 TrCHRB : ATTCGATTCT* 200 * 220 * 240 : 240
 TrCHRB : CTTTAGAAAA* 260 * 280 * 300 : 300
 TrCHRB : ATACTGATGC* 320 * 340 * 360 : 360
 TrCHRB : GGACGGAGTAT* 380 * 400 * 420 : 420
 TrCHRB : AAAACCCCTG* 440 * 460 * 480 : 480
 TrCHRB : AAGCTATGGA* 500 * 520 * 540 : 540
 TrCHRB : GTACCAAAAA* 560 * 580 * 600 : 600
 TrCHRB : TGGA : 604

FIGURE 38

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```

      *           20           *           40           *           60
TrChRb : MAGKKIPEVLLNSGHKMPVIGMGTSDVNRPSNDVLA SIFVDAIEVGYRHFD S ASVVGTEE : 60

      *           80           *           100          *           120
TrChRb : AIGIALAKALEKGLIKSRDEVFITSKPWN TDADYELIVPALKTTLKKLGTEYVDLYLIHW : 120

      *           140          *           160          *           180
TrChRb : PVRLRHDL ENFVVFTKEDLLPF D IEGTWKAMEECYKLG LAKSIGICNYGT KKLTKLLETA : 180

TrChRb : TITPAVNQV : 189

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FIGURE 39

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TrChRb1:  *      20      *      40      *      60
TrChRb1:  CTGTAGCAGTTTGAAGAAATTTTAAAAAAAACATGCCAGGAAGAAAATCCGAGAG : 60
TrChRb2:  STAGCAGCTTACGTAAGAGTGCACAAAAAACAATGCCAGGAAGAAAATCCGAGAG : 58
TrChRb3:  CTNNCAAAAAGAGAGCAAAAAAACAATGCCAGGAAGAAAATCCGAGAG : 51
TrChRb4:  GCTNCGAAAAAGAGAGCAAAAAAACAATGCCAGGAAGAAAATCCGAGAG : 51
TrChRb5:  -----ACATGCCAGGAAGAAAATCCGAGAG : 27

TrChRb1:  *      80      *      100     *      120
TrChRb1:  TGTATTGAATTTCAGGACACAAAATGCCAGTCATAGGAATGGGAACATCAGTAGACAAT : 120
TrChRb2:  TGTATTGAATTTCAGGACACAAAATGCCAGTCATAGGAATGGGAACATCAGTAGACAAT : 118
TrChRb3:  TGTATTGAATTTCAGGACACAAAATGCCAGTCATAGGAATGGGAACATCAGTAGACAAT : 111
TrChRb4:  TGTATTGAATTTCAGGACACAAAATGCCAGTCATAGGAATGGGAACATCAGTAGACAAT : 111
TrChRb5:  TGTATTGAATTTCAGGACACAAAATGCCAGTCATAGGAATGGGAACATCAGTAGACAAT : 87

TrChRb1:  *      140     *      160     *      180
TrChRb1:  GTCCATCAAAATGATGTTCTTGCCTTCAATCTTTGTGATGCAATTGAAGTTGGTTATCGCC : 180
TrChRb2:  GTCCATCAAAATGATGTTCTTGCCTTCAATCTTTGTGATGCAATTGAAGTTGGTTATCGCC : 178
TrChRb3:  GTCCATCAAAATGATGTTCTTGCCTTCAATCTTTGTGATGCAATTGAAGTTGGTTATCGCC : 171
TrChRb4:  GTCCATCAAAATGATGTTCTTGCCTTCAATCTTTGTGATGCAATTGAAGTTGGTTATCGCC : 171
TrChRb5:  GTCCATCAAAATGATGTTCTTGCCTTCAATCTTTGTGATGCAATTGAAGTTGGTTATCGCC : 147

TrChRb1:  *      200     *      220     *      240
TrChRb1:  ATTTCGATTTCGCTTCTGTGTATGGAACAGAGGAAGCCATAGGAATTGCCTTTAGCAAAAG : 240
TrChRb2:  ATTTCGATTTCGCTTCTGTGTATGGAACAGAGGAAGCCATAGGAATTGCCTTTAGCAAAAG : 238
TrChRb3:  ATTTCGATTTCGCTTCTGTGTATGGAACAGAGGAAGCCATAGGAATTGCCTTTAGCAAAAG : 231
TrChRb4:  ATTTCGATTTCGCTTCTGTGTATGGAACAGAGGAAGCCATAGGAATTGCCTTTAGCAAAAG : 231
TrChRb5:  ATTTCGATTTCGCTTCTGTGTATGGAACAGAGGAAGCCATAGGAATTGCCTTTAGCAAAAG : 207

TrChRb1:  *      260     *      280     *      300
TrChRb1:  CTTTAAAAAGGCTTATTAAAGAGTTTATGTAAGTTTATCACTTTGAAGCATGGT : 300
TrChRb2:  CTTTAAAAAGGCTTATTAAAGAGTAGAGATGAAGTTTATCACTTTGAAGCATGGT : 298
TrChRb3:  CTTTAAAAAGGCTTATTAAAGAGTAGAGATGAAGTTTATCACTTTGAAGCATGGT : 291
TrChRb4:  CTTTAAAAAGGCTTATTAAAGAGTAGAGATGAAGTTTATCACTTTGAAGCATGGT : 291
TrChRb5:  CTTTAAAAAGGCTTATTAAAGAGTAGAGATGAAGTTTATCACTTTGAAGCATGGT : 267

TrChRb1:  *      320     *      340     *      360
TrChRb1:  ATACTGATGCAGATTATGAACCTTATTGTTCCAGCTCTCAAGACCACATTGAAAAAGCTGG : 334
TrChRb2:  ATACTGATGCAGATTATGAACCTTATTGTTCCAGCTCTCAAGACCACATTGAAAAAGCTGG : 358
TrChRb3:  ATACTGATGCAGATTATGAACCTTATTGTTCCAGCTCTCAAGACCACATTGAAAAAGCTGG : 351
TrChRb4:  ATACTGATGCAGATTATGAACCTTATTGTTCCAGCTCTCAAGACCACATTGAAAAAGCTGG : 351
TrChRb5:  ATACTGATGCAGATTATGAACCTTATTGTTCCAGCTCTCAAGACCACATTGAAAAAGCTGG : 327

TrChRb1:  *      380     *      400     *      420
TrChRb1:  ----- : -
TrChRb2:  GGACGGAGTATGCGGATCTTTATCTGATCCATTGGCCAGTGAGACTTAGACATGATCTTTG : 418
TrChRb3:  GGACGGAGTATGCGGATCTTTATCTGATCCATTGGCCAGTGAGACTTAGACATGATCTTTG : 411
TrChRb4:  GGACGGAGTATGCGGATCTTTATCTGATCCATTGGCCAGTGAGACTTAGACATGATCTTTG : 411
TrChRb5:  GGACGCA : 334

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FIGURE 40

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      *           440           *           460           *           480
TrChRb1: ----- : -
TrChRb2: AAAACCCCTGTGTTTTACCAAGAAGATTACTTCCCTTTGATATAGAAGGGACATGG : 478
TrChRb3: AAAACCCCTGTGTTTTACCAAGAAGATTACTTCCCTTTGATATAGAAGGGACATGG : 471
TrChRb4: AAAACCCCTGTGTTTTACCAAGAAGATTACTTCCCTTTGATATAGAAGGGACATGG : 471
TrChRb5: ----- : -

      *           500           *           520           *           540
TrChRb1: ----- : -
TrChRb2: AAGCTATGGAAGAATGTTATAAGTLAGGCTTAGCAAAGCTATTGGTATATGCAATTATG : 538
TrChRb3: AAGCTATGGAAGAATGTTATAAGTLAGGCTTAGCAAAGCTATTGGTATATGCAATTATG : 531
TrChRb4: AAGCTATGGAAGAATGTTATAAGTLAGGCTTAGCAAAGCTATTGGTATATGCAATTATG : 531
TrChRb5: ----- : -

      *           560           *           580           *           600
TrChRb1: ----- : -
TrChRb2: GTACCAAAAACTCACCAAACTCTTGGAACAGCCACCATTACCCCTGCAGTCAATCAGC : 598
TrChRb3: GTACCAAAAACTCACCAAACTCTTGGAACAGCCACCATTACCCCTGCAGTC : 584
TrChRb4: GTACCAAAAACTCAGC : 547
TrChRb5: ----- : -

TrChRb1 : ---- : -
TrChRb2 : TCGA : 502
TrChRb3 : ---- : -
TrChRb4 : ---- : -
TrChRb5 : ---- : -

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FIGURE 40 (cont)

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TrCHRC : TAAAGATGAANCAATTTTATCTNANAAAAGGNNCANGCAAGTNAGTTNNATTCAAACATA : 60

TrCHRC : GNCTTAAAGTGTGTAAACATATCTTAACTTAAANNNTTTNACCCNACAAAAAACA : 120

TrCHRC : AGACAATAACATCGGTAGTGTGAAATTCACAAAGGTTCTTACTAACACTTCTAGTCA : 180

TrCHRC : AGTGAAAATGCCTGTGTTGGAATGGGATCAGCTCCTGATTTTACATGTAAGAAAGATAC : 240

TrCHRC : AAAAGATGCAATCATTGAAGCCATCAAACAAGGTATAGACACTTTGATACTGTGCTGCTGC : 300

TrCHRC : TTATGGCTCAGAACAAAGCTCTTGGTGAAGGTTTGAAAGAAGCAATTGAACTTGGCCTTGT : 360

TrCHRC : CACTAGAGAAGAGCTTTTGTACTTCTAAACTTTGGGTCAGTAAATCATCCTCACCT : 420

TrCHRC : TGTGTTCCTGCTCTTCAAAAATCTCTCAAGACTCTTCATTGGAGTACTTGGACTTGTA : 480

TrCHRC : TTTGATCCATTGGCCACTTAGTTCTCAGCCTGGAAAGTTTTCATTTCCAATTGATGTGGC : 540

TrCHRC : AGATCTCTTGCCATTGTGATGTGAAGGGTGTTGGGAATCCATGGAAGAAGGCTTGAAACT : 600

TrCHRC : TGGACTCACTAAAGCTATTGGTGTAGTAACTTCTCTGTCAAGAAACTTCAAAATCTTGT : 660

TrCHRC : CTCAGTTGCCACCGTTCTTCTCGCGTCAATCAG : 694

FIGURE 41

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      *           20           *           40           *           60
TrCHRC : MGSVEIPTKVLNTNTSSQVKMPVVGMGSAPDFTCKKDKDAIIEAIKQGYRHFPDTAAAYGS : 60

      *           80           *           100          *           120
TrCHRC : EQALGEGGLKEAIEIGLVTR EELFVTSKLVVTENHPHLVVPALQKSLKTLQLEYLDLYLIH : 120

      *           140          *           160          *           180
TrCHRC : WPLSSQPGKFSFFIDVADLLFPDVKGWESMEBGLKLGLTKAIGVSNFSVKKLQNLVSV A : 180

TrCHRC : TVLPAVNQ : 188

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FIGURE 42

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      *           20           *           40           *           60
TrCHrc1 : TAAGAATGAANCAATTTCATCTAAATAAAAGGTCANGCAGATTAAGTTNCTATTAAACATA : 60
TrCHrc2 : TCTNNNAAGGNNCANGCAGATTAAGTTNCTATTAAACATA : 41
TrCHrc3 : GNAATTCAAACATA : 13
TrCHrc4 : ATTCAACATA : 11
TrCHrc5 : TTCAACATA : 10
TrCHrc6 : TTTCAACATA : 10
TrCHrc7 : AACATA : 6
TrCHrc8 : AGA : 3
TrCHrc9 : GA : 2
TrCHrc10 : GA : 2
TrCHrc11 : GA : 2
TrCHrc12 : GA : 2
TrCHrc13 : : -
TrCHrc14 : : -
TrCHrc15 : : -
TrCHrc16 : : -

      *           80           *           100          *           120
TrCHrc1 : GNCCTAAAGTGTCTAACATATTCCTTAACCTTAACCTTTTTCACCAAAAAAACCA : 120
TrCHrc2 : GNCCTAAAGTGTCTAACATATTCCTTAACCTTAACCTTTTTCACCAAAAAAACCA : 101
TrCHrc3 : GNCCTAAAGTGTCTAACATATTCCTTAACCTTAACCTTTTTCACCAAAAAAACCA : 73
TrCHrc4 : GNCCTAAAGTGTCTAACCTTAACCTTAACCTTTTTCACCAAAAAAACCA : 71
TrCHrc5 : GNCCTAAAGTGTCTAACATATTCCTTAACCTTAACCTTTTTCACCAAAAAAACCA : 70
TrCHrc6 : GNCCTAAAGTGTCTAACATATTCCTTAACCTTAACCTTTTTCACCAAAAAAACCA : 70
TrCHrc7 : GNCCTAAAGTGTCTAACCTTAACCTTAACCTTTTTCACCAAAAAAACCA : 66
TrCHrc8 : GNCCTAAAGTGTCTAACCTTAACCTTAACCTTTTTCACCAAAAAAACCA : 63
TrCHrc9 : GNCCTAAAGTGTCTAACCTTAACCTTAACCTTTTTCACCAAAAAAACCA : 62
TrCHrc10 : GNCCTAAAGTGTCTAACCTTAACCTTAACCTTTTTCACCAAAAAAACCA : 62
TrCHrc11 : GNCCTAAAGTGTCTAACCTTAACCTTAACCTTTTTCACCAAAAAAACCA : 62
TrCHrc12 : GNCCTAAAGTGTCTAACCTTAACCTTAACCTTTTTCACCAAAAAAACCA : 62
TrCHrc13 : GNCCTAAAGTGTCTAACCTTAACCTTAACCTTTTTCACCAAAAAAACCA : 52
TrCHrc14 : GNCCTAAAGTGTCTAACCTTAACCTTAACCTTTTTCACCAAAAAAACCA : 52
TrCHrc15 : GNCCTAAAGTGTCTAACCTTAACCTTAACCTTTTTCACCAAAAAAACCA : 52
TrCHrc16 : GNCCTAAAGTGTCTAACCTTAACCTTAACCTTTTTCACCAAAAAAACCA : 38

      *           140          *           160          *           180
TrCHrc1 : AGACAATAACATGGGTAGTGTGAAATTCACAACAAAGGTTCTTACTAACACTTCTAGTC : 180
TrCHrc2 : AGACAATAACATGGGTAGTGTGAAATTCACAACAAAGGTTCTTACTAACACTTCTAGTC : 161
TrCHrc3 : AGACAATAACATGGGTAGTGTGAAATTCACAACAAAGGTTCTTACTAACACTTCTAGTC : 133
TrCHrc4 : AGACAATAACATGGGTAGTGTGAAATTCACAACAAAGGTTCTTACTAACACTTCTAGTC : 131
TrCHrc5 : AGACAATAACATGGGTAGTGTGAAATTCACAACAAAGGTTCTTACTAACACTTCTAGTC : 130
TrCHrc6 : AGACAATAACATGGGTAGTGTGAAATTCACAACAAAGGTTCTTACTAACACTTCTAGTC : 130
TrCHrc7 : AGACAATAACATGGGTAGTGTGAAATTCACAACAAAGGTTCTTACTAACACTTCTAGTC : 126
TrCHrc8 : AGACAATAACATGGGTAGTGTGAAATTCACAACAAAGGTTCTTACTAACACTTCTAGTC : 123
TrCHrc9 : AGACAATAACATGGGTAGTGTGAAATTCACAACAAAGGTTCTTACTAACACTTCTAGTC : 122
TrCHrc10 : AGACAATAACATGGGTAGTGTGAAATTCACAACAAAGGTTCTTACTAACACTTCTAGTC : 122
TrCHrc11 : AGACAATAACATGGGTAGTGTGAAATTCACAACAAAGGTTCTTACTAACACTTCTAGTC : 122
TrCHrc12 : AGACAATAACATGGGTAGTGTGAAATTCACAACAAAGGTTCTTACTAACACTTCTAGTC : 112
TrCHrc13 : AGACAATAACATGGGTAGTGTGAAATTCACAACAAAGGTTCTTACTAACACTTCTAGTC : 112
TrCHrc14 : AGACAATAACATGGGTAGTGTGAAATTCACAACAAAGGTTCTTACTAACACTTCTAGTC : 112
TrCHrc15 : AGACAATAACATGGGTAGTGTGAAATTCACAACAAAGGTTCTTACTAACACTTCTAGTC : 112
TrCHrc16 : AGACAATAACATGGGTAGTGTGAAATTCACAACAAAGGTTCTTACTAACACTTCTAGTC : 98

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FIGURE 43

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	200	*	220	*	240	
TrChrC1:	AGTGAAATGCGCTGGTGTGGAATGGGATCAGCTCTGATTTACATGTGAGAAAGATAC					:240
TrChrC2:	AGTGAAATGCGCTGGTGTGGAATGGGATCAGCTCTGATTTACATGTGAGAAAGATAC					:221
TrChrC3:	AGTGAAATGCGCTGGTGTGGAATGGGATCAGCTCTGATTTACATGTGAGAAAGATAC					:191
TrChrC4:	AGTGAAATGCGCTGGTGTGGAATGGGATCAGCTCTGATTTACATGTGAGAAAGATAC					:191
TrChrC5:	AGTGAAATGCGCTGGTGTGGAATGGGATCAGCTCTGATTTACATGTGAGAAAGATAC					:190
TrChrC6:	AGTGAAATGCGCTGGTGTGGAATGGGATCAGCTCTGATTTACATGTGAGAAAGATAC					:190
TrChrC7:	AGTGAAATGCGCTGGTGTGGAATGGGATCAGCTCTGATTTACATGTGAGAAAGATAC					:186
TrChrC8:	AGTGAAATGCGCTGGTGTGGAATGGGATCAGCTCTGATTTACATGTGAGAAAGATAC					:183
TrChrC9:	AGTGAAATGCGCTGGTGTGGAATGGGATCAGCTCTGATTTACATGTGAGAAAGATAC					:182
TrChrC10:	AGTGAAATGCGCTGGTGTGGAATGGGATCAGCTCTGATTTACATGTGAGAAAGATAC					:182
TrChrC11:	AGTGAAATGCGCTGGTGTGGAATGGGATCAGCTCTGATTTACATGTGAGAAAGATAC					:182
TrChrC12:	AGTGAAATGCGCTGGTGTGGAATGGGATCAGCTCTGATTTACATGTGAGAAAGATAC					:182
TrChrC13:	AGTGAAATGCGCTGGTGTGGAATGGGATCAGCTCTGATTTACATGTGAGAAAGATAC					:172
TrChrC14:	AGTGAAATGCGCTGGTGTGGAATGGGATCAGCTCTGATTTACATGTGAGAAAGATAC					:172
TrChrC15:	AGTGAAATGCGCTGGTGTGGAATGGGATCAGCTCTGATTTACATGTGAGAAAGATAC					:172
TrChrC16:	AGTGAAATGCGCTGGTGTGGAATGGGATCAGCTCTGATTTACATGTGAGAAAGATAC					:158

	260	*	280	*	300
TrCHRc1:	AAAGATGCAATCATTTGAAGCCATCAAAACAGGTTATAGACACTTTGATAC	TCGTGCTG			300
TrCHRc2:	AAAGATGCAATCATTTGAAGCCATCAAAACAGGTTATAGACACTTTGATAC	TCGTGCTG			281
TrCHRc3:	AAAGATGCAATCATTTGAAGCCATCAAAACAGGTTATAGACACTTTGATAC	TCGTGCTG			281
TrCHRc4:	AAAGATGCAATCATTTGAAGCCATCAAAACAGGTTATAGACACTTTGATAC	TCGTGCTG			251
TrCHRc5:	AAAGATGCAATCATTTGAAGCCATCAAAACAGGTTATAGACACTTTGATAC	TCGTGCTG			250
TrCHRc6:	AAAGATGCAATCATTTGAAGCCATCAAAACAGGTTATAGACACTTTGATAC	TCGTGCTG			250
TrCHRc7:	AAAGATGCAATCATTTGAAGCCATCAAAACAGGTTATAGACACTTTGATAC	TCGTGCTG			246
TrCHRc8:	AAAGATGCAATCATTTGAAGCCATCAAAACAGGTTATAGACACTTTGATAC	TCGTGCTG			246
TrCHRc9:	AAAGATGCAATCATTTGAAGCCATCAAAACAGGTTATAGACACTTTGATAC	TCGTGCTG			242
TrCHRc10:	AAAGATGCAATCATTTGAAGCCATCAAAACAGGTTATAGACACTTTGATAC	TCGTGCTG			242
TrCHRc11:	AAAGATGCAATCATTTGAAGCCATCAAAACAGGTTATAGACACTTTGATAC	TCGTGCTG			242
TrCHRc12:	AAAGATGCAATCATTTGAAGCCATCAAAACAGGTTATAGACACTTTGATAC	TCGTGCTG			242
TrCHRc13:	AAAGATGCAATCATTTGAAGCCATCAAAACAGGTTATAGACACTTTGATAC	TCGTGCTG			232
TrCHRc14:	AAAGATGCAATCATTTGAAGCCATCAAAACAGGTTATAGACACTTTGATAC	TCGTGCTG			232
TrCHRc15:	AAAGATGCAATCATTTGAAGCCATCAAAACAGGTTATAGACACTTTGATAC	TCGTGCTG			232
TrCHRc16:	AAAGATGCAATCATTTGAAGCCATCAAAACAGGTTATAGACACTTTGATAC	TCGTGCTG			218

	320	*	340	*	360
TrChrCrc1:	TTATGGCTCAGAACAGCTCTTGGTGAAGGTTTGAAGAAGCAATTGAACCTGGCTCTCT				:360
TrChrCrc2:	TTATGGCTCAGAACAGCTCTTGGTGAAGGTTTGAAGAAGCAATTGAACCTGGCTCTCT				:341
TrChrCrc3:	TTATGGCTCAGAACAGCTCTTGGTGAAGGTTTGAAGAAGCAATTGAACCTGGCTCTCT				:341
TrChrCrc4:	TTATGGCTCAGAACAGCTCTTGGTGAAGGTTTGAAGAAGCAATTGAACCTGGCTCTCT				:311
TrChrCrc5:	TTATGGCTCAGAACAGCTCTTGGTGAAGGTTTGAAGAAGCAATTGAACCTGGCTCTCT				:293
TrChrCrc6:	TTATGGCTCAGAACAGCTCTTGGTGAAGGTTTGAAGAAGCAATTGAACCTGGCTCTCT				:310
TrChrCrc7:	TTATGGCTCAGAACAGCTCTTGGTGAAGGTTTGAAGAAGCAATTGAACCTGGCTCTCT				:303
TrChrCrc8:	TTATGGCTCAGAACAGCTCTTGGTGAAGGTTTGAAGAAGCAATTGAACCTGGCTCTCT				:303
TrChrCrc9:	TTATGGCTCAGAACAGCTCTTGGTGAAGGTTTGAAGAAGCAATTGAACCTGGCTCTCT				:302
TrChrCrc10:	TTATGGCTCAGAACAGCTCTTGGTGAAGGTTTGAAGAAGCAATTGAACCTGGCTCTCT				:302
TrChrCrc11:	TTATGGCTCAGAACAGCTCTTGGTGAAGGTTTGAAGAAGCAATTGAACCTGGCTCTCT				:302
TrChrCrc12:	TTATGGCTCAGAACAGCTCTTGGTGAAGGTTTGAAGAAGCAATTGAACCTGGCTCTCT				:302
TrChrCrc13:	TTATGGCTCAGAACAGCTCTTGGTGAAGGTTTGAAGAAGCAATTGAACCTGGCTCTCT				:292
TrChrCrc14:	TTATGGCTCAGAACAGCTCTTGGTGAAGGTTTGAAGAAGCAATTGAACCTGGCTCTCT				:292
TrChrCrc15:	TTATGGCTCAGAACAGCTCTTGGTGAAGGTTTGAAGAAGCAATTGAACCTGGCTCTCT				:292
TrChrCrc16:	TTATGGCTCAGAACAGCTCTTGGTGAAGGTTTGAAGAAGCAATTGAACCTGGCTCTCT				:278

FIGURE 43 (cont)

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	380	400	*	420
TrCHRc1:	CACCTAGAGAAGAGCCTTTTGTGTTACTCTAAACTTTGGGCACACTGAAAATCATCTCCATCT			:420
TrCHRc2:	CACCTAGAGAAGAGCCTTTTGTGTTACTCTAAACTTTGGGCACACTGAAAATCATCTCCATCT			:401
TrCHRc3:	CACCTAGAGAAGAGCCTTTTGTGTTACTCTAAACTTTGGGCACACTGAAAATCATCTCCATCT			:373
TrCHRc4:	CACCTAGAGAAGAGCCTTTTGTGTTACTCTAAACTTTGGGCACACTGAAAATCATCTCCATCT			:371
TrCHRc5:	-			:
TrCHRc6:	CACCTAGAGAAGAGCCTTTTGTGTTACTCTAAACTTTGGGCACACTGAAAATCATCTCCATCT			:370
TrCHRc7:	CACCTAGAGAAGAGCCTTTTGTGTTACTCTAAACTTTGGGCACACTGAAAATCATCTCCATCT			:366
TrCHRc8:	CACCTAGAGAAGAGCCTTTTGTGTTACTCTAAACTTTGGGCACACTGAAAATCATCTCCATCT			:363
TrCHRc9:	CACCTAGAGAAGAGCCTTTTGTGTTACTCTAAACTTTGGGCACACTGAAAATCATCTCCATCT			:362
TrCHRc10:	CACCTAGAGAAGAGCCTTTTGTGTTACTCTAAACTTTGGGCACACTGAAAATCATCTCCATCT			:362
TrCHRc11:	CACCTAGAGAAGAGCCTTTTGTGTTACTCTAAACTTTGGGCACACTGAAAATCATCTCCATCT			:362
TrCHRc12:	CACCTAGAGAAGAGCCTTTTGTGTTACTCTAAACTTTGGGCACACTGAAAATCATCTCCATCT			:362
TrCHRc13:	CACCTAGAGAAGAGCCTTTTGTGTTACTCTAAACTTTGGGCACACTGAAAATCATCTCCATCT			:362
TrCHRc14:	CACCTAGAGAAGAGCCTTTTGTGTTACTCTAAACTTTGGGCACACTGAAAATCATCTCCATCT			:352
TrCHRc15:	CACCTAGAGAAGAGCCTTTTGTGTTACTCTAAACTTTGGGCACACTGAAAATCATCTCCATCT			:352
TrCHRc16:	CACCTAGAGAAGAGCCTTTTGTGTTACTCTAAACTTTGGGCACACTGAAAATCATCTCCATCT			:338
	*	440	*	480
TrCHRc1:	AGTGTTCTCGTCCTTCAAAAAATCTCAAGAGCTCTTCAATTGGAGGACTTGGACTTGTG			:480
TrCHRc2:	AGTGTTCTCGTCCTTCAAAAAATCTCAAGAGCTCTTCAATTGGAGGACTTGGACTTGTG			:461
TrCHRc3:	AGTGTTCTCGTCCTTCAAAAAATCTCAAGAGCTCTTCAATTGGAGGACTTGGACTTGTG			:433
TrCHRc4:	AGTGTTCTCGTCCTTCAAAAAATCTCAAGAGCTCTTCAATTGGAGGACTTGGACTTGTG			:431
TrCHRc5:	-			:
TrCHRc6:	AGTGTTCTCGTCCTTCAAAAAATCTCAAGAGCTCTTCAATTGGAGGACTTGGACTTGTG			:430
TrCHRc7:	AGTGTTCTCGTCCTTCAAAAAATCTCAAGAGCTCTTCAATTGGAGGACTTGGACTTGTG			:426
TrCHRc8:	AGTGTTCTCGTCCTTCAAAAAATCTCAAGAGCTCTTCAATTGGAGGACTTGGACTTGTG			:423
TrCHRc9:	AGTGTTCTCGTCCTTCAAAAAATCTCAAGAGCTCTTCAATTGGAGGACTTGGACTTGTG			:422
TrCHRc10:	AGTGTTCTCGTCCTTCAAAAAATCTCAAGAGCTCTTCAATTGGAGGACTTGGACTTGTG			:422
TrCHRc11:	AGTGTTCTCGTCCTTCAAAAAATCTCAAGAGCTCTTCAATTGGAGGACTTGGACTTGTG			:422
TrCHRc12:	AGTGTTCTCGTCCTTCAAAAAATCTCAAGAGCTCTTCAATTGGAGGACTTGGACTTGTG			:422
TrCHRc13:	AGTGTTCTCGTCCTTCAAAAAATCTCAAGAGCTCTTCAATTGGAGGACTTGGACTTGTG			:412
TrCHRc14:	AGTGTTCTCGTCCTTCAAAAAATCTCAAGAGCTCTTCAATTGGAGGACTTGGACTTGTG			:412
TrCHRc15:	AGTGTTCTCGTCCTTCAAAAAATCTCAAGAGCTCTTCAATTGGAGGACTTGGACTTGTG			:412
TrCHRc16:	AGTGTTCTCGTCCTTCAAAAAATCTCAAGAGCTCTTCAATTGGAGGACTTGGACTTGTG			:398
	*	500	*	520
TrCHRc1:	TTTGATCCATTGGGCCACTTAGTCTCAGCCCGGAAGAGTTTCATTCCCAATTGAGGTGGG			:540
TrCHRc2:	TTTGATCCATTGGGCCACTTAGTCTCAGCCCGGAAGAGTTTCATTCCCAATTGAGGTGGG			:521
TrCHRc3:	TTTGATCCATTGGGCCACTTAGTCTCAGCCCGGAAGAGTTTCATTCCCAATTGAGGTGGG			:493
TrCHRc4:	TTTGATCCATTGGGCCACTTAGTCTCAGCCCGGAAGAGTTTCATTCCCAATTGAGGTGGG			:491
TrCHRc5:	-			:
TrCHRc6:	TTTGATCCATTGGGCCACTTAGTCTCAGCCCGGAAGAGTTTCATTCCCAATTGAGGTGGG			:490
TrCHRc7:	TTTGATCCATTGGGCCACTTAGTCTCAGCCCGGAAGAGTTTCATTCCCAATTGAGGTGGG			:486
TrCHRc8:	TTTGATCCATTGGGCCACTTAGTCTCAGCCCGGAAGAGTTTCATTCCCAATTGAGGTGGG			:482
TrCHRc9:	TTTGATCCATTGGGCCACTTAGTCTCAGCCCGGAAGAGTTTCATTCCCAATTGAGGTGGG			:482
TrCHRc10:	TTTGATCCATTGGGCCACTTAGTCTCAGCCCGGAAGAGTTTCATTCCCAATTGAGGTGGG			:482
TrCHRc11:	TTTGATCCATTGGGCCACTTAGTCTCAGCCCGGAAGAGTTTCATTCCCAATTGAGGTGGG			:482
TrCHRc12:	TTTGATCCATTGGGCCACTTAGTCTCAGCCCGGAAGAGTTTCATTCCCAATTGAGGTGGG			:472
TrCHRc13:	TTTGATCCATTGGGCCACTTAGTCTCAGCCCGGAAGAGTTTCATTCCCAATTGAGGTGGG			:472
TrCHRc14:	TTTGATCCATTGGGCCACTTAGTCTCAGCCCGGAAGAGTTTCATTCCCAATTGAGGTGGG			:472
TrCHRc15:	TTTGATCCATTGGGCCACTTAGTCTCAGCCCGGAAGAGTTTCATTCCCAATTGAGGTGGG			:472
TrCHRc16:	TTTGATCCATTGGGCCACTTAGTCTCAGCCCGGAAGAGTTTCATTCCCAATTGAGGTGGG			:458

FIGURE 43 (cont)

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      *           560           *           580           *           600
TrChrc1 : AGATCTCTTGCCATTGTGATGGAAGGCTGTTTGGG----- :576
TrChrc2 : AGN----- :524
TrChrc3 : AGATCTCTTGCCATTGTGATGGAAGGCTGTTTGGCAATCCATGGAAGAAGGCTTGAAACT :553
TrChrc4 : AGATCTCTTGCCATTGTGATGGAAGGCTGTTTGGCAATCCATGGAAGAAGGCTTGAAACT :551
TrChrc5 : ----- : -
TrChrc6 : AGATCTCTTGCCATTGTGATGGAAGGCTGTTTGGGAATCCATGGAAGAAANGCTTNAAACT :550
TrChrc7 : AGATCTCTTGCCATTGTGATGGAAGGCTGTTTGGCAATCCATGGAAGAAGGCTTGAAACT :546
TrChrc8 : AGATCTCTTGCCATTGTGATGGAAGGCTGTTTGGGAATCCATGGAAGAAGGCTTGAAACT :543
TrChrc9 : AGATCTCTTGCCATTGTGATGGAAGGCTGTTTGGGAATCCATGGAAGAAGGCTTGAAACT :542
TrChrc10 : AGATCTCTTGCCATTGTGATGGAAGGCTGTTTGGGAATCCATGGAAGAAGGCTTGAAACT :542
TrChrc11 : AGATCTCTTGCCATTGTGATGGAAGGCTGTTTGGGAATCCATGGAAGAAGGCTTGAAACT :542
TrChrc12 : AGATCTCTTGCCATTGTGATGGAAGGCTGTTTGGGAATCCATGGAAGAAGGCTTGAAACT :542
TrChrc13 : AGATCTCTTGCCATTGTGATGGAAGGCTGTTTGGGAATCCATGGAAGAAGGCTTGAAACT :532
TrChrc14 : AGATCTCTTGCCATTGTGATGGAAGGCTGTTTGGGAATCCATGGAAGAAGGCTTGAAACT :532
TrChrc15 : AGATCTCTTGCCATTGTGATGGAAGGCTGTTTGGGAATCCATGGAAGAAGGCTTGAAACT :532
TrChrc16 : AGATCTCTTGCCATTGTGATGGAAGGCTGTTTGGGAATCCATGGAAGAAGGCTTGAAACT :518

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```

      *           620           *           640           *           660
TrChrc1 : ----- : -
TrChrc2 : ----- : -
TrChrc3 : TGGACTCACAAGCTATTGGTGTTAGTAACCTCTCTGTCAAGANN----- :577
TrChrc4 : TGGACTCACAAGCTATTGGTGTTAGTAACCTCTCTGTCAAGANN----- :597
TrChrc5 : ----- : -
TrChrc6 : TGGACTCACAAGCTATTGGTGTTAGTAACCTCTCTGTCAAGAAACTTCAAAATCTTTT :610
TrChrc7 : TGGACTCACAAGCTATTGGTGTTAGTAACCTCTCTGTCAAGAAACTTCAAAATCTTTT :570
TrChrc8 : TGGACTCACAAGCTATTGGTGTTAGTAACCTCTCTGTCAAGAAACTTCAAAATCTTTT :603
TrChrc9 : TGGACTCACAAGCTATTGGTGTTAGTAACCTCTCTGTCAAGAAACTTCAAAATCTTTT :573
TrChrc10 : TGGACTCACAAGCTATTGGTGTTAGTAACCTCTCTGTCAAGAAACTTCAAAATCTTTT :583
TrChrc11 : TGGACTCACAAGCTATTGGTGTTAGTAACCTCTCTGTCAAGAAACTTCAAAATCTTTT :597
TrChrc12 : TGGACTCACAAGCTATTGGTGTTAGTAACCTCTCTGTCAAGAAACTTCAAAATCTTTT :597
TrChrc13 : TGGACTCACAAGCTATTGGTGTTAGTAACCTCTCTGTCAAGAAACTTCAAAATCTTTT :574
TrChrc14 : TGGACTCACAAGCTATTGGTGTTAGTAACCTCTCTGTCAAGAAACTTCAAAATCTTTT :578
TrChrc15 : TGGACTCACAAGCTATTGGTGTTAGTAACCTCTCTGTCAAGAAACTTCAAAATCTTTT :592
TrChrc16 : TGGACTCACAAGCTATTGGTGTTAGTAACCTCTCTGTCAAGAAACTTCAAAATCTTTT :578

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      *           680           *
TrChrc1 : ----- : -
TrChrc2 : ----- : -
TrChrc3 : ----- : -
TrChrc4 : ----- : -
TrChrc5 : ----- : -
TrChrc6 : CTCAGTTGGCCACCGTCTTTCTGCGG----- : 636
TrChrc7 : ----- : -
TrChrc8 : CTCAGTTGGCCACCGTCTT----- : 621
TrChrc9 : ----- : -
TrChrc10 : ----- : -
TrChrc11 : ----- : -
TrChrc12 : ----- : -
TrChrc13 : ----- : -
TrChrc14 : ----- : -
TrChrc15 : CTCAGTTCT----- : 600
TrChrc16 : CTCAGTTGGCCACCGTCTTTCTGCGGCTCAATCAG----- : 612

```

FIGURE 43 (cont)

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TrDFra : GCACACNTTCTTGACTTACCAATTGTAATNCATAATAATNTAAACATGTCAAAAGACAGT : 60
 * 20 * 40 * 60

TrDFra : TTGTGTNACCGGAGCCAGCGGAGCCATCGGTTTCATGGGTGGTTCGCCTCCTCCTCGAAGC : 120
 * 80 * 100 * 120

TrDFra : CGGTACATTGTCCACGCCACCATCCAAGATCTCGAGGATGAGAACGAGACAAAAACATTT : 180
 * 140 * 160 * 180

TrDFra : GGAAGCAATGGAAGGAGCAAAGGGTCATCTCAAATTTTCGAAATGGATCTTCTTAACAG : 240
 * 200 * 220 * 240

TrDFra : CGACTCTATTGCGGCCGCCGTGAAAGGTTGTGCCGGAGTTATACATCTTGCATGTCCTAA : 300
 * 260 * 280 * 300

TrDFra : CATCATTTGGTGAAGTCAAAGACCCGAGAAGCAAATTTTGAACCGCAATTCAAGGAAC : 360
 * 320 * 340 * 360

TrDFra : GGTTAATGTGTTGAAGGTGGCAAAGGAAGCAGGGTGGAGCGTGTTGGCGACATCGTC : 420
 * 380 * 400 * 420

TrDFra : GATCTCCGCCATCATACCGAGTCTTAATTGGCCAGCTGATAAGATTAAGGGAGAAGATTG : 480
 * 440 * 460 * 480

TrDFra : TTGGACAGACCTTGATTATTGCAAGGAAAAGAAGTTATACTACCCCATTGCAAAGACACT : 540
 * 500 * 520 * 540

TrDFra : AGCAGAAAAAGCTGGTTGGGAATTTGCTAAAGAGACCGGTTTTTGATGTTGTTATGATTAA : 600
 * 560 * 580 * 600

TrDFra : CCCTGGTACT : 610
 *

FIGURE 44

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```

      *           20           *           40           *           60
TrDFra : MSKTVCTXTGASGAIGSWVVRLLLERGYIVHATIQDLEDENETKHLAMEGAKGHLKFFEM : 60

      *           80           *           100          *           120
TrDFra : DLLNSDSIAAAVKGCGAGVIHLACPNIIIGEVDPEKQILEPAIQGTVNVLKVAKEAGVERV : 120

      *           140          *           160          *           180
TrDFra : VATSSISAIIPSPNWPADKIKGEDCWTDLDYCKEKKLYYPIAKTLAEKAGWEFAKETGFD : 180

TrDFra : VVMINPGT : 188

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FIGURE 45

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TrDFRa1 : GCACACCTCTTGACITACCAATGTGAATNCATAATAATTTTAAACATGTCAAAGACAGT : 60
TrDFRa2 : GCACACCTCTCTTGACITACCAATGTGAATNCATAATAATTTTAAACATGTCAAAGACAGT : 60
TrDFRa3 : GCACACCTCTCTTGACITACCAATGTGAATNCATAATAATTTTAAACATGTCAAAGGACAGT : 60
TrDFRa4 : GCACACCTCTCTTGACITACCAATGTGAATNCATAATAATTTTAAACATGTCAAAGACAGT : 60
TrDFRa5 : ---CCTGTTCTCTTGACITACCAATGTGAATNCATAATAATTTTAAACATGTCAAAGACAGT : 58
TrDFRa6 : ---CTGTTCTCTTGACITACCAATGTGAATNCATAATAATTTTAAACATGTCAAAGACAGT : 58
TrDFRa7 : ---CCTCTCTTGACITACCAATGTGAATNCATAATAATTTTAAACATGTCAAAGGACAGT : 55
TrDFRa8 : ---CCTCTCTTGACITACCAATGTGAATNCATAATAATTTTAAACATGTCAAAGACAGT : 55
TrDFRa9 : ---TTTCTCTTGACITACCAATGTGAATNCATAATAATTTTAAACATGTCAAAGACAGT : 54
TrDFRa10 : -----NCGG : 5

TrDFRa1 : TTGTGTNACCGGAGCCAGCGGAGCCATCGGTTTCATGGGTGGTTCCGCTCTCTCTCGAAGC : 120
TrDFRa2 : TTGTGTNACCGGAGCCAGCGGAGCCATCGGTTTCATGGGTGGTTCCGCTCTCTCTCGAAGC : 120
TrDFRa3 : TTGTGTNACCGGAGCCAGCGGAGCCATCGGTTTCATGGGTGGTTCCGCTCTCTCTCGAAGC : 120
TrDFRa4 : TTGTGTNACCGGAGCCAGCGGAGCCATCGGTTTCATGGGTGGTTCCGCTCTCTCTCGAAGC : 120
TrDFRa5 : TTGTGTNACCGGAGCCAGCGGAGCCATCGGTTTCATGGGTGGTTCCGCTCTCTCTCGAAGC : 118
TrDFRa6 : TTGTGTNACCGGAGCCAGCGGAGCCATCGGTTTCATGGGTGGTTCCGCTCTCTCTCGAAGC : 118
TrDFRa7 : TTGTGTNACCGGAGCCAGCGGAGCCATCGGTTTCATGGGTGGTTCCGCTCTCTCTCGAAGC : 115
TrDFRa8 : TTGTGTNACCGGAGCCAGCGGAGCCATCGGTTTCATGGGTGGTTCCGCTCTCTCTCGAAGC : 115
TrDFRa9 : TTGTGTNACCGGAGCCAGCGGAGCCATCGGTTTCATGGGTGGTTCCGCTCTCTCTCGAAGC : 114
TrDFRa10 : TTGTGTNACCGGAGCCAGCGGAGCCATCGGTTTCATGGGTGGTTCCGCTCTCTCTCGAAGC : 65

TrDFRa1 : CGGCTACATTTGCCACGCCACCATTCCAAGATCTCGAGGATGAGAACGAGACAAAACATTT : 180
TrDFRa2 : CGGCTACATTTGCCACGCCACCATTCCAAGATCTCGAGGATGAGAACGAGACAAAACATTT : 180
TrDFRa3 : CGGCTACATTTGCCACGCCACCATTCCAAGATCTCGAGGATGAGAACGAGACAAAACATTT : 180
TrDFRa4 : CGGCTACATTTGCCACGCCACCATTCCAAGATCTCGAGGATGAGAACGAGACAAAACATTT : 180
TrDFRa5 : CGGCTACATTTGCCACGCCACCATTCCAAGATCTCGAGGATGAGAACGAGACAAAACATTT : 178
TrDFRa6 : CGGCTACATTTGCCACGCCACCATTCCAAGATCTCGAGGATGAGAACGAGACAAAACATTT : 178
TrDFRa7 : CGGCTACATTTGCCACGCCACCATTCCAAGATCTCGAGGATGAGAACGAGACAAAACATTT : 175
TrDFRa8 : CGGCTACATTTGCCACGCCACCATTCCAAGATCTCGAGGATGAGAACGAGACAAAACATTT : 175
TrDFRa9 : CGGCTACATTTGCCACGCCACCATTCCAAGATCTCGAGGATGAGAACGAGACAAAACATTT : 174
TrDFRa10 : CGGCTACATTTGCCACGCCACCATTCCAAGATCTCGAGGATGAGAACGAGACAAAACATTT : 125

TrDFRa1 : GGAAGCAATGGAAGGAGCAAAAGGGTCATCTCAAATTTTTCGAAATGGATCTTCTTAACAG : 240
TrDFRa2 : GGAAGCAATGGAAGGAGCAAAAGGGTCATCTCAAATTTTTCGAAATGGATCTTCTTAACAG : 240
TrDFRa3 : GGAAGCAATGGAAGGAGCAAAAGGGTCATCTCAAATTTTTCGAAATGGATCTTCTTAACAG : 240
TrDFRa4 : GGAAGCAATGGAAGGAGCAAAAGGGTCATCTCAAATTTTTCGAAATGGATCTTCTTAACAG : 240
TrDFRa5 : GGAAGCAATGGAAGGAGCAAAAGGGTCATCTCAAATTTTTCGAAATGGATCTTCTTAACAG : 238
TrDFRa6 : GGAAGCAATGGAAGGAGCAAAAGGGTCATCTCAAATTTTTCGAAATGGATCTTCTTAACAG : 238
TrDFRa7 : GGAAGCAATGGAAGGAGCAAAAGGGTCATCTCAAATTTTTCGAAATGGATCTTCTTAACAG : 235
TrDFRa8 : GGAAGCAATGGAAGGAGCAAAAGGGTCATCTCAAATTTTTCGAAATGGATCTTCTTAACAG : 235
TrDFRa9 : GGAAGCAATGGAAGGAGCAAAAGGGTCATCTCAAATTTTTCGAAATGGATCTTCTTAACAG : 234
TrDFRa10 : GGAAGCAATGGAAGGAGCAAAAGGGTCATCTCAAATTTTTCGAAATGGATCTTCTTAACAG : 185

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FIGURE 46

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```

                *           260           *           280           *           300
TrDFRa1 : CGACTCTAATTGCGGCCGCCGTGAAAGGTTGTCGCCGGAGTTATACATCTTGCNATGTCCTAAC :300
TrDFRa2 : CGACTCTAATTGCGGCCGCCGTGAAAGGTTGTCGCCGGAGTTATACATCTTGCATGTGCTTAAC :300
TrDFRa3 : CGACTCTAATTGCGGCCGCCGTGAAAGGTTGTCGCCGGAGTTATACATCTTGCATGTGCTTAAC :300
TrDFRa4 : CGACTCTAATTGCGGCCGCCGTGAAAGGTTGTCGCCGGAGTTATACATCTTGCATGTGCTTAAC :300
TrDFRa5 : CGACTCTAATTGCGGCCGCCGTGAAAGGTTGTCGCCGGAGTTATACATCTTGCATGTGCTTAAC :298
TrDFRa6 : CGACTCTAATTGCGGCCGCCGTGAAAGGTTGTCGCCGGAGTTATACATCTTGCATGTGCTTAAC :298
TrDFRa7 : CGACTCTAATTGCGGCCGCCGTGAAAGGTTGTCGCCGGAGTTATACATCTTGCATGTGCTTAAC :295
TrDFRa8 : CGACTCTAATTGCGGCCGCCGTGAAAGGTTGTCGCCGGAGTTATACATCTTGCATGTGCTTAAC :295
TrDFRa9 : CGACTCTAATTGCGGCCGCCGTGAAAGGTTGTCGCCGGAGTTATACATCTTGCATGTGCTTAAC :294
TrDFRa10: CGACTCTAATTGCGGCCGCCGTGAAAGGTTGTCGCCGGAGTTATACATCTTGCATGTGCTTAAC :232

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                *           320           *           340           *           360
TrDFRa1 : CACCTTTGGCGAATCAAGGTTGTCGCCGGAGTTATACATCTTGCNATGTCCTAAC :327
TrDFRa2 : CATCATTTGGTGAAGTCAAAGACCCCGAGAAGCAAAATTTTGGAAACCGCAATTCGAAGGAAC :349
TrDFRa3 : CATCATTTGGTGAAGTCAAAGACCCCGAGAAGCAAAATTTTGGAAACCGCAATTCGAAGGAAC :360
TrDFRa4 : CATCATTTGGTGAAGTCAAAGACCCCGAGAAGCAAAATTTTGGAAACCGCAATTCGAAGGAAC :360
TrDFRa5 : CATCATTTGGTGAAGTCAAAGACCCCGAGAAGCAAAATTTTGGAAACCGCAATTCGAAGGAAC :358
TrDFRa6 : CATCATTTGGTGAAGTCAAAGACCCCGAGAAGCAAAATTTTGGAAACCGCAATTCGAAGGAAC :358
TrDFRa7 : CATCATTTGGTGAAGTCAAAGACCCCGAGAAGCAAAATTTTGGAAACCGCAATTCGAAGGAAC :355
TrDFRa8 : CATCATTTGGTGAAGTCAAAGACCCCGAGAAGCAAAATTTTGGAAACCGCAATTCGAAGGAAC :355
TrDFRa9 : CATCATTTGGTGAAGTCAAAGACCCCGAGAAGCAAAATTTTGGAAACCGCAATTCGAAGGAAC :328
TrDFRa10: CATCATTTGGTGAAGTCAAAGACCCCGAGAAGCAAAATTTTGGAAACCGCAATTCGAAGGAAC :

```

```

                *           380           *           400           *           420
TrDFRa1 : ----- : -
TrDFRa2 : ----- : -
TrDFRa3 : GGTTAATGTGTTGAAGGTGGCAAAGGAAGCAGGGGTGGAGCGTGTGGTGGCGACATCGTC :420
TrDFRa4 : GGTTAATGTGTTGAAGGTGGCAAAGGAAGCAGGGGTGGAGCGTGTGGTGGCGACATCGTC :420
TrDFRa5 : GGTTAATGTGTTGAAGGTGGCAAAGGAAGCAGGGGTGGAGCGTGTGGTGGCGACATCGTC :418
TrDFRa6 : GGTTAATGTGTTGAAGGTGGCAAAGGAAGCAGGGGTGGAGCGTGTGGTGGCGACATCGTC :418
TrDFRa7 : GGTTAATGTGTTGAAGGTGGCAAAGGAAGCAGGGGTGGAGCGTGTGGTGGCGACATCGTC :415
TrDFRa8 : GGTTAATGTGTTGAAGGTGGCAAAGGAAGCAGGGGTGGAGCGTGTGGTGGCGACATCGTC :415
TrDFRa9 : ----- : -
TrDFRa10: ----- : -

```

```

                *           440           *           460           *           480
TrDFRa1 : ----- : -
TrDFRa2 : ----- : -
TrDFRa3 : GATCTCCGCCATCATACCGAGTCTCTAAATGGCCAGCTGATAAGATTAAAGGGAGAAGATTG :480
TrDFRa4 : GATCTCCGCCATCATACCGAGTCTCTAAATGGCCAGCTGATAAGATTAAAGGGAGAAGATTG :480
TrDFRa5 : GATCTCCGCCATCATACCGAGTCTCTAAATGGCCAGCTGATAAGATTAAAGGGAGAAGATTG :478
TrDFRa6 : GATCTCCGCCATCATACCGAGTCTCTAAATGGCCAGCTGATAAGATTAAAGGGAGAAGATTG :478
TrDFRa7 : GATCTCCGCCATCATACCGAGTCTCTAAATGGCCAGCTGATAAGATTAAAGGGAGAAGATTG :475
TrDFRa8 : GATCTCCGCCATCATACCGAGTCTCTAAATGGCCAGCTGATAAGATTAAAGGGAGAAGATTG :475
TrDFRa9 : ----- : -
TrDFRa10: ----- : -

```

FIGURE 46 (cont)

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```

      *           500           *           520           *           540
TrDFRa1 : ----- : -
TrDFRa2 : ----- : -
TrDFRa3 : NTGGACAGACCTTGATTATTGCAANGAAAAAGAAGTTATACTACCCCATTGCAAAAGACATT : 540
TrDFRa4 : TTGGACAGACCTTGATTATTGCAAGGAAAAAGAAGTTATACTACCCCATTGCAAAAGACACT : 540
TrDFRa5 : TTGGACAGACCTTGATTATTGCAAGGAAAAAGAAGTTATACTACCCCATTGCAAAAGACACT : 538
TrDFRa6 : TTGGACAGACCTTGATTATTGCAAGGAAAAAGAAGTTATACTACCCCATTGCAAAAGACACT : 538
TrDFRa7 : TTGGACAGACCTTGATTATTGCAAGGAAAAAGAAGTTATACTACCCCATTGCAAAAGACATT : 535
TrDFRa8 : TTGGACAGACCTTGATTATTGCAAGGAAAAAGAAGTTATACTACCCCATTGCAAAAGACACT : 535
TrDFRa9 : ----- : -
TrDFRa10 : ----- : -

      *           560           *           580           *           600
TrDFRa1 : ----- : -
TrDFRa2 : ----- : -
TrDFRa3 : TNCAGAAAAACCTGGTTGGGAATTTGCTAAAGAGACCCGTTTGATGTTGTT : 592
TrDFRa4 : TGCAGAAAAACCTGGTTGGGAATTTGCTAAAGAGACCCGTTTGATGTTGTTAG : 594
TrDFRa5 : TGCAGAAAAACCTGGTTGGGAATTTGCTAAAGAGACCCGTTTGATGTTGTTAG : 593
TrDFRa6 : TGCAGAAAAACCTGGTTGGGAATTTGCTAAAGAGACCCGTTTGTGATGTTATGATT : 598
TrDFRa7 : TGCAGAAAAACCTGGTTGGGAATTTGCTAAAGAGAC : 571
TrDFRa8 : TGCAGAAAAACCTGGTTGGGAATTTGCTAAAGAGACCCGTTTGATGTTGTA : 586
TrDFRa9 : ----- : -
TrDFRa10 : ----- : -

      *
TrDFRa1 : ----- : -
TrDFRa2 : ----- : -
TrDFRa3 : ----- : -
TrDFRa4 : ----- : -
TrDFRa5 : ----- : -
TrDFRa6 : CCTGGTACT : 608
TrDFRa7 : ----- : -
TrDFRa8 : ----- : -
TrDFRa9 : ----- : -
TrDFRa10 : ----- : -

```

FIGURE 46 (cont)

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```

TrDFRb :   *           20           *           40           *           60
          : ATAAAACCAANCTNCAAAACTGATTGGAATCAGAAAAATAGAAGAAAAGAGATGCCTGA : 60

          *           80           *           100          *           120
TrDFRb :   : GTTTGTGTGTACAGSGGGCACTGGCTTCATAGCAGCCTACCTAGTGAAAGCCTTATTAGA : 120

          *           140          *           160          *           180
TrDFRb :   : AAAGSGTCACACAGTAAGGACTACTGTGAAGAAACCAGATGATTTGGAGAAGGTTGGTTA : 180

          *           200          *           220          *           240
TrDFRb :   : TCTAACTGAACCTAAGTGAAGACAAAGAGAGATTGAAGATTTTAAAGCAGATCTATTGGT : 240

          *           260          *           280          *           300
TrDFRb :   : GGAAGGGGAGTTTGTATGAGGCAGTGAGTGGTGTGTGTTTCATACAGCTTCCCC : 300

          *           320          *           340          *           360
TrDFRb :   : TGTCTCTGTTCCACATGATGACAACATTCAAGTTACTTTGATTGATCCATGTATAAAGG : 360

          *           380          *           400          *           420
TrDFRb :   : AACACAAATGTGCTTAACCTCATGCATCAAAGCAAAGGTGAAACGTGTGGTGTAAACATC : 420

          *           440          *           460          *           480
TrDFRb :   : TTCATGCTCTTCCATAAGATACCGTGACGATGTGCAACAAATTTCCTCTCTAATGAATC : 480

          *           500          *           520          *           540
TrDFRb :   : TCATTGGAGTGATTCTGAATACTGCAAAACGCTATAACCTGTGGTATGCATATGCAAAGAC : 540

          *           560          *           580          *           600
TrDFRb :   : TTTAGGAGAAAAAAGAGCATGGAGGATTGCAAAAGGAAGTGAATTGATCTAGTTGTAGT : 600

          *           620
TrDFRb :   : TAACCCCTCTTTTGTGGTGGTC : 623

```

FIGURE 47

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```

      *           20           *           40           *           60
TrDFRb : MPEFCVTTGGTGFI AAYLVKALLEKGHTVVRTTVRNPDDLEKVGYLTELSEDKERLKILKAD : 60

      *           80           *           100          *           120
TrDFRb : LLVEGSFDEAVSGVDGVFHTASPVLVPHDDNIQVTLIDPCIKGTQNVLNSCIKAKVKRVV : 120

      *           140          *           160          *           180
TrDFRb : LTSSCSSIRYRDDVQQISPLNESHWSDEYCKRYNLWYAYAKTLGEKEAWRIAKESGIDL : 180

      *
TrDFRb : VVVNPSFVGG : 190

```

FIGURE 48

TrDfRb1:	20	40	*	60		
TrDfRb2:	NTAAAAACAANTCTCAAACCTGATTCGAACCTAGAAAAATAGAGAAAAGAGATGCCCTGA				60	
TrDfRb3:	-----GNACTCTGNNAAAAATAGAGAAAAGAGATGCCCTGA				35	
TrDfRb4:	-----GGAAGAGATGCCCTGA-----GAGATGCCCTGA				11	
TrDfRb1:	*	80	*	100	*	120
TrDfRb2:	GTTTGTGTTACAGGGGGCAGCTGGTTCATAGCAGCCTACCTAGTGAAGAGCCTTATTAGA					120
TrDfRb3:	GTTTGTGTTACAGGGGGCAGCTGGTTCATAGCAGCCTACCTAGTGAAGAGCCTTATTAGA					95
TrDfRb4:	GTTTGTGTTACAGGGGGCAGCTGGTTCATAGCAGCCTACCTAGTGAAGAGCCTTATTAGA					71
TrDfRb1:	*	140	*	160	*	180
TrDfRb2:	AAAGGGTCACACAGTAAGGACTACTGTAAGAAACCCAGATGATTTGGAGAAGGTTGGTTTA					180
TrDfRb3:	AAAGGGTCACACAGTAAGGACTACTGTAAGAAACCCAGATGATTTGGAGAAGGTTGGTTTA					155
TrDfRb4:	AAAGGGTCACACAGTAAGGACTACTGTAAGAAACCCAGATGATTTGGAGAAGGTTGGTTTA					131
TrDfRb1:	*	200	*	220	*	240
TrDfRb2:	TCCTAACTGAACCTAAGTCAGACAAAGACAGATTGAAGATTTTAAAGCAGATCTATTGGT					240
TrDfRb3:	TCCTAACTGAACCTAAGTCAGACAAAGACAGATTGAAGATTTTAAAGCAGATCTATTGGT					215
TrDfRb4:	TCCTAACTGAACCTAAGTCAGACAAAGACAGATTGAAGATTTTAAAGCAGATCTATTGGT					191
TrDfRb1:	*	260	*	280	*	300
TrDfRb2:	GGAAGGGAGCTTTTGATGAGGCAGTCAGTGGTGTTCATGGTGTTTCATACAGCTTCCCC					300
TrDfRb3:	GGAAGGGAGCTTTTGATGAGGCAGTCAGTGGTGTTCATGGTGTTTCATACAGCTTCCCC					275
TrDfRb4:	GGAAGGGAGCTTTTGATGAGGCAGTCAGTGGTGTTCATGGTGTTTCATACAGCTTCCCC					256
TrDfRb1:	*	320	*	340	*	360
TrDfRb2:	TGTTCTGTGTCCACATGATGACAAATTCAGGTACTTTGATTGATCCATGTATAAAAGG					360
TrDfRb3:	TGTTCTGTGTCCACATGATGACAAATTCAGGTACTTTGATTGATCCATGTATAAAAGG					335
TrDfRb4:	TGTTCTGTGTCCACATGATGACAAATTCAGGTACTTTGATTGATCCATGTATAAAAGG					311
TrDfRb1:	*	380	*	400	*	420
TrDfRb2:	AACACAAAAGTGCTTTAACTCATGCATCAAGCAAAAGGTGAAACGTGTGGTGTTAACATC					420
TrDfRb3:	AACACAAAAGTGCTTTAACTCATGCATCAAGCAAAAGGTGAAACGTGTGGTGTTAACATC					395
TrDfRb4:	AACACAAAAGTGCTTTAACTCATGCATCAAGCAAAAGGTGAAACGTGTGGTGTTAACATC					371
TrDfRb1:	*	440	*	460	*	480
TrDfRb2:	TTCATGCTCTTCCATAGAGTACCGTGACGATGTGCAACAAATTTCCCTCTTAATGAATC					480
TrDfRb3:	TTCATGCTCTTCCATAGAGTACCGTGACGATGTGCAACAAATTTCCCTCTTAATGAATC					455
TrDfRb4:	TTCATGCTCTTCCATAGAGTACCGTGACGATGTGCAACAAATTTCCCTCTTAATGAATC					431

FIGURE 49

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```

          *           500           *           520           *           540
TrDFRb1: TCATTGGAGCTGATTCTGAATAC TGCAAACGCTATAACCTGTGGTATGCATATGCAAAGAC : 540
TrDFRb2: TCATTGGAGCTGATTCTGAT TACTGCAAACGCTATAACCTGTGGTATGCATATGCAAAGAC : 515
TrDFRb3: TCATTGGAGCTGATTCTGAATAC TGCAAACGCTATAACCTGTGGTATGCATATGCAAAGAC : 496
TrDFRb4: TCATTGGAGCTGATTCTGAATAC TGCAAACGCTATAACCTGTGGTATGCATATGCAAAGAC : 491

```

```

          *           560           *           580           *           600
TrDFRb1: TTTAGGAGAAAAAGAGCATGGAGCATTC ----- : 570
TrDFRb2: TTTAGGAGAAAAAGAGCATGGAGCATTC AAGCGAAAGTCGATTAATCTAGTTCT --- : 572
TrDFRb3: TTTAGGAGAAAAAGAGCATGGAGCATTC AAGCGAAAGTCGAATTGATCTAGTTGTAGT : 556
TrDFRb4: TTTAGGAGAAAAAGAGCATGGAGCATTC AAGCGAAAGTCGAATTGATCTAGTTGTAGT : 551

```

```

          *           620
TrDFRb1 : ----- : -
TrDFRb2 : ----- : -
TrDFRb3 : AAACCCCTCTTTTGTGTT ----- : 572
TrDFRb4 : AAACCCCTCTTTTGTGTTGGTTC : 574

```

FIGURE 49 (cont)

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```

TrDFRC :   *           20           *           40           *           60
          : GNGAAGANCTAGTTTGCCTAACCCGGANCAACGGTTTCATCGGAACATGGCTAGTTAAAA : 60

          *           80           *           100          *           120
TrDFRC : CCTACTCCAAAAACACTACAAAATTACGCCACAATCTTCCCCAATTCCAACGCATCTC : 120

          *           140          *           160          *           180
TrDFRC : ATCTCTTCACACTCCACCCGGAAGCTCAATCCCGGATCACAAATTTTCCCTGTCGATATCC : 180

          *           200          *           220          *           240
TrDFRC : TCGACTCCACCGCCGCTTCTCCGCTATCAATAACTGCTCAGTGCTTTTCATGCCGCTT : 240

          *           260          *           280          *           300
TrDFRC : CTCCATGTACCCTCGAAGATCCAAGTATCCGCAAAAAGAGCTTCTAGAACCTGCTGTAC : 300

          *           320          *           340          *           360
TrDFRC : AAGGAACCCTAATGTTCTAGAAAGCATCCAGCGCGCAGGTACCAAACCTAATTGGCCGG : 360

          *           380          *           400          *           420
TrDFRC : AGAAAAAGGCGATCGATGAGGCGTCTGTGGACGGATGTTGAGTACTGTAAMTTGAGAGGGA : 420

          *           440          *           460          *           480
TrDFRC : AGTGGTATCTGGTGTGAAAAACGGAGGCGGAGAGGCGCTTGGGATTTTCGAGAGAAAA : 480

          *           500          *           520          *           540
TrDFRC : ATGGTGGTGTGTGATGTGGGGGCGGNICATCCGGGACTTGTTTGGGAGAGTTGATACAGA : 540

          *           560          *           580          *           600
TrDFRC : AGGAGTTGAATGCGAGTTTCAGCGGNITTTACAGAGTTGATGATGGGGAGTGAGGATACTC : 600

          *           620          *           640
TrDFRC : AAGAGTGNTATTGGNNGGGGGCTGNNNATGNTAAAGATGN : 641

```

FIGURE 50

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```

      *      20      *      40      *      60
TrDFRc : EXLVCVTRXNGFIGTWLVKTLQKHYKIHATIFPNSNASHLFTLHPEAQSRTIFPVDIL : 60

      *      80      *      100     *      120
TrDFRc : DSTAVFSAINNCSGVFHAASPCTLEDPTDPQKELLEPAVQGTLNVLEASSAQVPPNPWPE : 120

      *      140     *      160     *      180
TrDFRc : KKAIDEASWTDVEYCKLRGKWYLVSKTEAEKAAMDFREKNGGVDVGAXHPGTCLGELIQK : 180

      *      200
TrDFRc : ELNASSALQRLMMGSEDTQEXYWXGG : 206

```

FIGURE 51

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TrDfRd : GCNTGTGACGCGTATNAACACACANGTCTTCCCTTGAGCTCTGTITTCACATGTCTGA : 60
 * 20 * 40 * 60

TrDfRd : AGCTAGTTTTCGCGTCACCGGCGGCAGCGGATGCATCGGTTCATGGCTAGTCCATCTCCTTC : 120
 * 80 * 100 * 120

TrDfRd : TCCTCCGCGGCTACACTGTTACGCGCACCGTCCAAAATCTCAATGATGAGAACGAAACGA : 180
 * 140 * 160 * 180

TrDfRd : AGCATCTAGAAGCTCTCGAAGGAGCACAAATCTCCGTCTCTTCCAGATCGATCTCC : 240
 * 200 * 220 * 240

TrDfRd : TTAACACGACACAACTCTCGTGTCTGCCGCGGTGCGTGGAAATTTCCACCTCGCTT : 300
 * 260 * 280 * 300

TrDfRd : CACCTGCACTGTAGACAAAGTTTCATGATCCTCAGAGGAGCTTTTGGATCTGCAATTA : 360
 * 320 * 340 * 360

TrDfRd : AAGGGACTTTGAATGTGCTTACTGCAGCTAAGGAAGTAGGGGTGAAGCGTGTGTTGTTA : 420
 * 380 * 400 * 420

TrDfRd : CCTCGTCTGTCTCGGCGATTACTCCTAGTCTGATTGGCCTTCTGATGTGTGTTAAAGAG : 480
 * 440 * 460 * 480

TrDfRd : AGGATTGTTGGACTGATGTTGAATATTGCAAGAAAAAGAGTTGGGGTATCCGTTGTCCA : 540
 * 500 * 520 * 540

TrDfRd : AAACATTGGCTGAAAAAGCTGCGTGGGATTTTNCAGAAAAAGATGGTTGGATGTTGTTG : 600
 * 560 * 580 * 600

TrDfRd : NGGTGAATCCCGNACTGNGATGGGTCTGTGTTTTCCACACGGCATAATGCAAGCATGC : 660
 * 620 * 640 * 660

TrDfRd : TCATGCCCTGGGAACTTTTTGAAGGCTGGNNCTGAACAATTTGAAGACTATTTTATGG : 720
 * 680 * 700 * 720

TrDfRd : GATTGCCNCTTTAAAGATGTNGCATGCGNCATNNTTTGGGGTATGAGAACAAANNN : 780
 * 740 * 760 * 780

TrDfRd : CTTGGGANACATNGGNGGTTGAAACTATCNNTCCCTACGG : 822
 * 800 * 820

FIGURE 52

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```

      *           20           *           40           *           60
TrDFRd : MSKLVCVTGGSGCIGSWLVHLLLLRGYTVHATVQNLNDENETKHLEALEGAQTNLRLFQI : 60

      *           80           *           100          *           120
TrDFRd : DLLNYDTILAAVRGCVGIFHLASPCCTVDKVHDPQKELLDPAIKGTNLNVLTAAKEVGVKRV : 120

      *           140          *           160          *           180
TrDFRd : VVTSSVSAITPSPDWPSDVVKREDCWTDVEYCKKKELGYPLSKRTLAEKAANDFXKENGLD : 180

      *           200          *           220          *           240
TrDFRd : VVXVNPXTXMGPFVPPRHNASMLMFWETFLKAXXETFDYFMGLAXFKDXALXHXLYEN : 240

      *
TrDFRd : KXXLGXXXGLKLXXLT : 256

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FIGURE 53

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TrDFrd1:  GCNTTGTATCAGCGTA*      20      *      40      *      60
TrDFrd2:  -----MACANNITCTCCCTTGAGCTCTGTTTCTCCNCAITGCGA : 60
TrDFrd1:  AGCTAGTTTGGCTACCGGGGCGAGCGGATGCATCGGTTTCATGGCTAGTCCATCTCCTTC : 120
TrDFrd2:  AGCTAGTTTGGCTACCGGGGCGAGCGGATGCATCGGTTTCATGGCTAGTCCATCTCCTTC : 99

TrDFrd1:  TCCTCCGGGGTACACTGTTTCACGCCACCGTCCAAAATCTCAATGATGAGAACGAAACG : 180
TrDFrd2:  TCCTCCGGGGTACACTGTTTCACGCCACCGTCCAAAATCTCAATGATGAGAACGAAACG : 159

TrDFrd1:  GCATCTAGAAGCTCTCGAAGGAGCACAACTAATCTCGGTCCTCTCCAGATCGATCTCG : 240
TrDFrd2:  GCATCTAGAAGCTCTCGAAGGAGCACAACTAATCTCGGTCCTCTCCAGATCGATCTCG : 219

TrDFrd1:  TTAACACGACACAATCCTCGCTGCTGTCCCGCGGTTCGGTCGGAAATTTTCCACCTCGCTT : 300
TrDFrd2:  TTAACACGACACAATCCTCGCTGCTGTCCCGCGGTTCGGTCGGAAATTTTCCACCTCGCTT : 279

TrDFrd1:  CACCTTGCACCTGTAGACAAAGTTTCATGATCCTCAGAAGGAGCTTTTGGATCCTGCAATT : 360
TrDFrd2:  CACCTTGCACCTGTAGACAAAGTTTCATGATCCTCAGAAGGAGCTTTTGGATCCTGCAATT : 339

TrDFrd1:  AAGGGACTTTGAAATGTGCTTACTGCAGCTAAGGAAGTAGGGGTGAAGCGTGTGGTTGT : 420
TrDFrd2:  AAGGGACTTTGAAATGTGCTTACTGCAGCTAAGGAAGTAGGGGTGAAGCGTGTGGTTGT : 399

TrDFrd1:  CCTCGTCTGTCTCGGCGATTACTCCTAGTCTTCTGATTGGCCCTCTGATGTTGTAAAAAG : 480
TrDFrd2:  CCTCGTCTGTCTCGGCGATTACTCCTAGTCTTCTGATTGGCCCTCTGATGTTGTAAAAAG : 459

TrDFrd1:  AGGATTGTTGGACTGATGTTGAATATTGCAAGAAAAAAGAGTTTGGTATCCGTT----- : 535
TrDFrd2:  AGGATTGTTGGACTGATGTTGAATATTGCAAGAAAAAAGAGTTGGGGTATCCGTTGTCCT : 519

TrDFrd1:  ----- : -
TrDFrd2:  MNCATTTGGCTGAAAAAGCTGCGTGGGATTTTTCNCAAGAAAAATGGTTTGGATGTTGTC : 579

TrDFrd1:  ----- : -
TrDFrd2:  NGGTGAATCCGGGNACTGNGATGGGTCCTGTGTTTTCACCAACGGCATTAATGCAAGCATGC : 639

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FIGURE 54

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      *           680           *           700           *           720
TrDFRd1: ----- : -
TrDFRd2: TCATGCCTTGGGAAACTTTTGAAGGCTGGNNCTGAAACATTTGAAGACTATTTTATGC : 699

      *           740           *           760           *           780
TrDFRd1: ----- : -
TrDFRd2: GATTGGCCNNCTTTAAAGATGTGTCATGGCNCATNNTTGGGGTATGAGAACAAANANN : 759

      *           800           *           820
TrDFRd1: ----- : -
TrDFRd2: CTTTGGGANACATNGGNGGGTGAACATATCNCCTTACGG : 801

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FIGURE 54 (cont)

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TrDFre :   *           20           *           40           *           60
          GTCAC TTAGAAATGGAACACAAAGGTGGAGACAAAGTATGTGTGACAGGGGCATCAGGC : 60

          *           80           *           100          *           120
TrDFre :   TTTT TAGCATCTTGGCTTATTAAAGAACTTCTTTTGTCTGGCTATCAAGTCATTGGAACA : 120

          *           140          *           160          *           180
TrDFre :   GTTAGAGATTTAGGGAAGAAAGAAAGTTGAACATTTATGGAAATTGGAAGGAGCAACA : 180

          *           200          *           220          *           240
TrDFre :   GAAAGACTAGAACTAATCCAAGCTGATTTAATGGAAGAAAATAGTTTCGACAAAGCGATC : 240

          *           260          *           280          *           300
TrDFre :   ATGGGATGCAAAGGTGTCTTCCACATTGCCTCTCCAGTACTCAATCATATATCAGATAAT : 300

          *           320          *           340          *           360
TrDFre :   CCTAAGCGGAAATCTTGAACCGGCAGTCCAAGGTACGCTAAATGTGTTGCGTTCCTTGT : 360

          *           380          *           400          *           420
TrDFre :   AAGAGGAACCCGATCTTGTTCGAGTGGTGCTACCTCATCATCTTCGGCTGTAGAGTA : 420

          *           440          *           460          *           480
TrDFre :   AGAGCTGATTTTGATCCAAGCATACCAATTGATGAATCATCTTGGAGCTCCTTGGAAATG : 480

          *           500          *           520          *           540
TrDFre :   TCGAGAAACTCAAGGCATGGTACCCAATGTCAAAGACAATGGCAGAAAAAGCAGCTTGG : 540

          *           560          *           580
TrDFre :   GAATATAGCAAAGAGAATGGAATAGACTTAGTGACTATTTTC : 582

```

FIGURE 55

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```

      *           20           *           40           *           60
TrDFre : MEHKGDKVCVTGASGFLASWLIKLLLSGYQVIGTVRDLGKKKKVEHLWKLEGATERLE : 60

      *           80           *           100          *           120
TrDFre : LIQADLMEENSFDKAIMOCKGVFHIA SPVLNHISDNPKAEILEPAVQGTLNVLRSCRNP : 120

      *           140          *           160          *           180
TrDFre : DLVRVVLA SSSAVRVRADFDPSIPIDESSWSSELC EKLKAWYPMSKTMAEKAWEYSK : 180

      *
TrDFre : ENGIDLVTIF : 190

```

FIGURE 56

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TrDFRf :   *           20           *           40           *           60
TNCNNGCTNCNTNCGGCAGAGANTTTCCTGACCTATNTGTACTNAAGAATATTTCTA : 60

TrDFRf :   *           80           *           100          *           120
TATATATATTTGTGTTCAAGAACCCAAAAATAGAAATAGTGAGTGGAAAGGAGTTGCAAG : 120

TrDFRf :   *           140          *           160          *           180
GTTTGTGTCACCGGTGCTGCTGTTATATTGGTTCTCTTTTAGTCAAAAAGCTTTTGGAA : 180

TrDFRf :   *           200          *           220          *           240
AAGGTTACACCGTTCATGCTACTCTTAGAAACTTGAAGGACGAATCCAAAGTAGATTTT : 240

TrDFRf :   *           260          *           280          *           300
TTGAGAGGCTTTCCACATGCAGATACTAGACTTATGTTATTTGAAGCTGATATATACAAA : 300

TrDFRf :   *           320          *           340          *           360
TCAGATGAATTTTGGCCCGCAATTCAAGGTTGTGAGTTTGTTTTCACCTTGTCTACTCCT : 360

TrDFRf :   *           380          *           400          *           420
TTTCAACATCAAACGTGATTCTCAGTTTAAGAGCATAGAGGAAGCTGCAATAGCAGGGGTA : 420

TrDFRf :   *           440          *           460          *           480
AAAAGCATAGCTGAAAATTGCATAAAATCAGGAACAGTGAGAAAATTGATATACACTGGA : 480

TrDFRf :   *           500          *           520          *           540
ACTGTAATTGCTTCTTCTCTCTGAAAGATGATGGAGTGCGCTACAAAGACTTCATTGAT : 540

TrDFRf :   *           560          *
GAAACTTGTGGACACCTCTCCATCTTCTCT : 572

```

FIGURE 57

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TrDFRf : MERSCKVCTGGAGYIGSLLVKKLLEKGYTVHATLRNLKDESKVDFLRGFPHADTRLMLF : 60

TrDFRf : EADIYKSEDEFWPAIQGCEVFVHATPFQHQTDSPKSIIEAAIAGVKSAENCIKSGTVR : 120

TrDFRf : KLIYTGTVIASSSLKDDGSGYKDFIDETCWTPLHLP : 156

FIGURE 58

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```

      *           20           *           40           *           60
TrDFRg : GCCNTTGCCCTACTACTAACTATATATTATTATATATATATGATGATACATAGTGACA : 60

      *           80           *           100          *           120
TrDFRg : TTAATAARTTGAAGGGAGATAAATAGTTGAAAAACACACAGTTGGAGTGTTTTGTGTGT : 120

      *           140          *           160          *           180
TrDFRg : TAAAGAAGCTNGAAAAATGGAGGAAGCNACAAAGATGGTGAAAAAGAGTGGACAAATTGTT : 180

      *           200          *           220          *           240
TrDFRg : CCTACTGCCAAATACTGTGTTACAGGAGCAACAGGCTATATTGGTTCATGCTTGTGTTGAA : 240

      *           260          *           280          *           300
TrDFRg : GCTCTTCTTCAAAGAGGTTGCACTGTTCTATGCTACTGTTAGAGATCCTGAAAAATCGTTA : 300

      *           320          *           340          *           360
TrDFRg : CACCTCCTGTCTGTTGTGGAAAGGTAGTAGCCAATTGAGAATTTCCGTGCGGATTGCGAA : 360

      *           380          *           400          *           420
TrDFRg : GAAGAAGGAAGTTTCGATGATGCCGTAAGAGGATGTATTGGTGTGTTCATGTTGCAGCT : 420

      *           440          *           460          *           480
TrDFRg : TCAATGCAATTCAATATTAGTGACAAAGAAAAACACTGAGGACTTTGTTGAAGCAAAATATA : 480

      *           500          *           520          *           540
TrDFRg : ATTGACCCGCAATCAAAGGAACCATAAATCTTCTCAAATCATGCTTGAATCAAATTCA : 540

      *           560          *           580          *           600
TrDFRg : GTGAAAAGGGTTGTTTTTCACATCTTCCATAAGTACTATTACTGCTAAAGCAACGACGGA : 600

      *           620          *           640          *           660
TrDFRg : AAATGGAAACCTATTGTTGATGAATCTTGCCAAACAAAACCTGAGATTCTGTGGAAATACA : 660

      *           680          *           700          *
TrDFRg : CAACCAAGTGGATGGGTTTATGCACCTTCAAAGCTTCATGCAGAGAAGCGGCT : 714

```

FIGURE 59

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```

      *           20           *           40           *           60
TrDFRg : MVKKSQQIVPTAKYCVTGATGYIGSWLVEALLQRGCTVHATVRDPEKSLHLLSLWKGSQ : 60

      *           80           *           100          *           120
TrDFRg : LRIFRADLQEEGSPDDAVKGCIGVFHVAASMQFNISDKENTEDFVEANIIDPAIKGTINL : 120

      *           140          *           160          *           180
TrDFRg : LKSLKSNVSKRVVFTSSISTITAKDNDGKWKPIVDESCQTKTEILWNTQPSGHWYALSK : 180

TrDFRg : LHABEAA : 187

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FIGURE 60

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[illegible]

FIGURE 61

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	*	560	*	580	*	600	
TrDFRg1:	-----						:
TrDFRg2:	GTGAAAAGGGTTGTTTTCACATCTTCCATAAGTACTATTTACTGCTAAAGACAACGACGG						: 477
TrDFRg3:	GTGAAAAGGGTTGTTTTCACATCTTCCATAAGTACTATTTACTGCTAAAGACAACGACGG						: 472

	*	620	*	640	*	660	
TrDFRg1:	-----						:
TrDFRg2:	JJJTTGGAACCTATTGTTGATGAATCTTGCCAAACAAAACTGAGATTCTGTGGAATAC						: 537
TrDFRg3:	JJJTTGGAACCTATTGTTGATGAATCTTGCCAAACAAAACTGAGATTCTGTGGAATAC						: 532

	*	680	*	700	*		
TrDFRg1:	-----					:	-
TrDFRg2:	CAACCAAGTGGATGGGTTTATGCACCTTCAAAGCTTCAATGCAGAAGAAGCGGCT					: 591	
TrDFRg3:	CAACCAAGTGGATGGGTTTATGCACCTTCAAAGCTTCATC-----					: 572	

FIGURE 61 (cont)

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TrDFRh : * 20 * 40 * 60
 GNNGNGTCTCCGTTNAATTNAGNCTATATTGAAAAGGAAAAAAGAGTAGAGAAAGTGA : 60

TrDFRh : * 80 * 100 * 120
 AGTGAAGTGAAAACATACATGGGTCCGAATCAGAAATAGTTTGTGTTACCGGAGCTTCA : 120

TrDFRh : * 140 * 160 * 180
 GGTTTCATCGGATCGTGGCTTGTATGAGACTTATAGAGCGTGGCTACACGGTTCGAGCC : 180

TrDFRh : * 200 * 220 * 240
 ACCGTCGCGACCCAGATAACATGAAGAAGGTGAAGCATTTGGTGGAACTGCCGGGTGCA : 240

TrDFRh : * 260 * 280 * 300
 AAAAGCAAATTGTCTCTTTGGAAGGCTGATCTTGATAAAGAGGGGAGTTTGTATGAAGCA : 300

TrDFRh : * 320 * 340 * 360
 ATTAAAGGGTGCACAGGAGTTTTCATGTTGCTACACCAATGGATTTTGAATCCAAGGAC : 360

TrDFRh : * 380 * 400 * 420
 CCTGAGAANTGAAGTGATAAAGCCTACAATAAATGGATTAATAGACATACTGAAAGCATGC : 420

TrDFRh : * 440 * 460 * 480
 GAAAAGGCAAAAACAGTTAGAAAAATGGTTTTCACATCATCGGCTGGAAGTGTGGACGTT : 480

TrDFRh : * 500 * 520 * 540
 ACTGAACATCCAAAGTCTATTATTGATGAAACATGCTGGAGTGACGTTGACTTTTGCCGT : 540

TrDFRh : * 560 * 580 * 600
 AGAGTCAAGATGACCGGTTGGATGTATTTGTTTCAAAGACCCTAGCAGAGCAAGAAGCT : 600

TrDFRh : * 620 * 640 * 660
 TGGAGTATTCGAAAGAGCACAACATAGACTTTGTCTCCATCATCCACCTCTTGTGTT : 660

TrDFRh : * 680 * 700 * 720
 GGCCCTTCTTATGGCCTCAATGCCACCTAGTCTAATCACTGCTCTTCTCTTATCACA : 720

TrDFRh : * 740 * 760 * 780
 GGAAATGAGGCCCATCTACTCAATCATAAAGCAAGGCAATACGTCCATTAGATGACCTT : 780

TrDFRh : * 800 * 820 * 840
 TGTCTTGCTCATATATTTCTGTATGAGAATCCAAAAGCTCAAGGGAGATACATTGTGCT : 840

FIGURE 62

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TrDFRh : TCACATGAAGCAACCATTTCATCAAGTTGCAAAACTTATTAAGAAAAATACCCAGAGTTC : 900

TrDFRh : AATGTCCCAACAAAATTCATGATATCCAGATGAANTGGAAATTATTAAATTTTCTAAA : 960

TrDFRh : AAGAAGATCACAGACT : 976

FIGURE 62 (cont)

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```

      *           20           *           40           *           60
TrDFRh : MGSESEIVCVTGASGFIGSWLVMLRIERGYTVRATVRDPDNMKVKHLVELPGAKSKLSL : 60

      *           80           *           100          *           120
TrDFRh : WKADLDKEGSFDEAIKGCTGVFHVATPMDFESKDPENEVIKPTINGLIDILKACEKAKTV : 120

      *           140          *           160          *           180
TrDFRh : RKLVTSSAGTVDVTEHPKSIIDETCNSDVDFCRRVKMTGWMYFVSKTLAEQEAWKYSKE : 180

      *           200          *           220          *           240
TrDFRh : HNIDFVSIIPPLVVGPFMLMASMPPSLITALSLITGNEAHYSIIKQGQYVHLDLCLAHIF : 240

      *           260          *           280          *
TrDFRh : LYENPKAQGRYICCSHEATHQVAKLIKEKYPEFNVPTKFNNDIPDELEIIKFSKKKID : 299

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FIGURE 63

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      *           20           *           40           *           60
TrDFRh1 : GNNCTTCTCTCCGCTTNAATTTNAGNCTATATTGAAAAAGAAAAAAGAGTAGNNNANNGA : 60
TrDFRh2 : ---GNGCTCTCCGCTTNAATTTNAGNCTATATTGAAAAAGAAAAAAGAGTAGNNNANNG : 59
TrDFRh3 : ---GNGCTCTCCGCTTNAATTTNAGNCTATATTGAAAAAGAAAAAAGAGTAGNNNANNG : 57
TrDFRh4 : ---GNGCTCTCCGCTTNAATTTNAGNCTATATTGAAAAAGAAAAAAGAGTAGNNNANNG : 57
TrDFRh5 : ---GNGCTCTCCGCTTNAATTTNAGNCTATATTGAAAAAGAAAAAAGAGTAGNNNANNG : 57
TrDFRh6 : ---GNGCTCTCCGCTTNAATTTNAGNCTATATTGAAAAAGAAAAAAGAGTAGNNNANNG : 57
TrDFRh7 : ---GNGCTCTCCGCTTNAATTTNAGNCTATATTGAAAAAGAAAAAAGAGTAGNNNANNG : 57
TrDFRh8 : ---GCTCTCCGCTTNAATTTNAGNCTATATTGAAAAAGAAAAAAGAGTAGNNNANNG : 56
TrDFRh9 : ---GCTCTCCGCTTNAATTTNAGNCTATATTGAAAAAGAAAAAAGAGTAGNNNANNG : 56
TrDFRh10 : ---GCTCTCCGCTTNAATTTNAGNCTATATTGAAAAAGAAAAAAGAGTAGNNNANNG : 56
TrDFRh11 : ---GCTCTCCGCTTNAATTTNAGNCTATATTGAAAAAGAAAAAAGAGTAGNNNANNG : 55
TrDFRh12 : ---GCTCTCCGCTTNAATTTNAGNCTATATTGAAAAAGAAAAAAGAGTAGNNNANNG : 55
TrDFRh13 : ---GCTCTCCGCTTNAATTTNAGNCTATATTGAAAAAGAAAAAAGAGTAGNNNANNG : 52
TrDFRh14 : ---GCTCTCCGCTTNAATTTNAGNCTATATTGAAAAAGAAAAAAGAGTAGNNNANNG : 12
TrDFRh15 : -----GAGAGACTG : -

      *           80           *           100          *           120
TrDFRh1 : AGTGAAGTGA AAAACATACATGGGTTCCGAATCAGAAATAGTTTG GTGTACCGGAGCTTC : 120
TrDFRh2 : ---AGTGAAGTGA AAAACATACATGGGTTCCGAATCAGAAATAGTTTG GTGTACCGGAGCTTC : 119
TrDFRh3 : AGTGAAGTGA AAAACATACATGGGTTCCGAATCAGAAATAGTTTG GTGTACCGGAGCTTC : 117
TrDFRh4 : AGTGAAGTGA AAAACATACATGGGTTCCGAATCAGAAATAGTTTG GTGTACCGGAGCTTC : 117
TrDFRh5 : AGTGAAGTGA AAAACATACATGGGTTCCGAATCAGAAATAGTTTG GTGTACCGGAGCTTC : 117
TrDFRh6 : AGTGAAGTGA AAAACATACATGGGTTCCGAATCAGAAATAGTTTG GTGTACCGGAGCTTC : 117
TrDFRh7 : AGTGAAGTGA AAAACATACATGGGTTCCGAATCAGAAATAGTTTG GTGTACCGGAGCTTC : 117
TrDFRh8 : AGTGAAGTGA AAAACATACATGGGTTCCGAATCAGAAATAGTTTG GTGTACCGGAGCTTC : 116
TrDFRh9 : AGTGAAGTGA AAAACATACATGGGTTCCGAATCAGAAATAGTTTG GTGTACCGGAGCTTC : 116
TrDFRh10 : AGTGAAGTGA AAAACATACATGGGTTCCGAATCAGAAATAGTTTG GTGTACCGGAGCTTC : 116
TrDFRh11 : AGTGAAGTGA AAAACATACATGGGTTCCGAATCAGAAATAGTTTG GTGTACCGGAGCTTC : 115
TrDFRh12 : AGTGAAGTGA AAAACATACATGGGTTCCGAATCAGAAATAGTTTG GTGTACCGGAGCTTC : 115
TrDFRh13 : AGTGAAGTGA AAAACATACATGGGTTCCGAATCAGAAATAGTTTG GTGTACCGGAGCTTC : 112
TrDFRh14 : AGTGAAGTGA AAAACATACATGGGTTCCGAATCAGAAATAGTTTG GTGTACCGGAGCTTC : 72
TrDFRh15 : -----GAGAGACTG : -

      *           140          *           160          *           180
TrDFRh1 : GGTTCATCGGATCGTGCGCTTGTATGAGACTTATAGAGCGTGGCTACACGGTTCGAGCC : 180
TrDFRh2 : GGTTCATCGGATCGTGCGCTTGTATGAGACTTATAGAGCGTGGCTACACGGTTCGAGCC : 179
TrDFRh3 : GGTTCATCGGATCGTGCGCTTGTATGAGACTTATAGAGCGTGGCTACACGGTTCGAGCC : 177
TrDFRh4 : GGTTCATCGGATCGTGCGCTTGTATGAGACTTATAGAGCGTGGCTACACGGTTCGAGCC : 177
TrDFRh5 : GGTTCATCGGATCGTGCGCTTGTATGAGACTTATAGAGCGTGGCTACACGGTTCGAGCC : 177
TrDFRh6 : GGTTCATCGGATCGTGCGCTTGTATGAGACTTATAGAGCGTGGCTACACGGTTCGAGCC : 177
TrDFRh7 : GGTTCATCGGATCGTGCGCTTGTATGAGACTTATAGAGCGTGGCTACACGGTTCGAGCC : 177
TrDFRh8 : GGTTCATCGGATCGTGCGCTTGTATGAGACTTATAGAGCGTGGCTACACGGTTCGAGCC : 176
TrDFRh9 : GGTTCATCGGATCGTGCGCTTGTATGAGACTTATAGAGCGTGGCTACACGGTTCGAGCC : 176
TrDFRh10 : GGTTCATCGGATCGTGCGCTTGTATGAGACTTATAGAGCGTGGCTACACGGTTCGAGCC : 176
TrDFRh11 : GGTTCATCGGATCGTGCGCTTGTATGAGACTTATAGAGCGTGGCTACACGGTTCGAGCC : 175
TrDFRh12 : GGTTCATCGGATCGTGCGCTTGTATGAGACTTATAGAGCGTGGCTACACGGTTCGAGCC : 175
TrDFRh13 : GGTTCATCGGATCGTGCGCTTGTATGAGACTTATAGAGCGTGGCTACACGGTTCGAGCC : 172
TrDFRh14 : GGTTCATCGGATCGTGCGCTTGTATGAGACTTATAGAGCGTGGCTACACGGTTCGAGCC : 132
TrDFRh15 : -----GAGAGACTG : -

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FIGURE 64

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      *           200           *           220           *           240
TrDFRn1: ACCGTTCGGGACCCAGATAACATGAAGAAGGTGAAGCATTTGGTGGAACTGCCGGGTGCA :240
TrDFRn2: ACCGTTCGGGACCCAGATAACATGAAGAAGGTGAAGCATTTGGTGGAACTGCCGGGTGCA :239
TrDFRn3: ACCGTTCGGGACCCAGATAACATGAAGAAGGTGAAGCATTTGGTGGAACTGCCGGGTGCA :237
TrDFRn4: ACCGTTCGGGACCCAGATAACATGAAGAAGGTGAAGCATTTGGTGGAACTGCCGGGTGCA :237
TrDFRn5: ACCGTTCGGGACCCAGATAACATGAAGAAGGTGAAGCATTTGGTGGAACTGCCGGGTGCA :237
TrDFRn6: ACCGTTCGGGACCCAGATAACATGAAGAAGGTGAAGCATTTGGTGGAACTGCCGGGTGCA :237
TrDFRn7: ACCGTTCGGGACCCAGATAACATGAAGAAGGTGAAGCATTTGGTGGAACTGCCGGGTGCA :237
TrDFRn8: ACCGTTCGGGACCCAGATAACATGAAGAAGGTGAAGCATTTGGTGGAACTGCCGGGTGCA :236
TrDFRn9: ACCGTTCGGGACCCAGATAACATGAAGAAGGTGAAGCATTTGGTGGAACTGCCGGGTGCA :236
TrDFRn10: ACCGTTCGGGACCCAGATAACATGAAGAAGGTGAAGCATTTGGTGGAACTGCCGGGTGCA :236
TrDFRn11: ACCGTTCGGGACCCAGATAACATGAAGAAGGTGAAGCATTTGGTGGAACTGCCGGGTGCA :235
TrDFRn12: ACCGTTCGGGACCCAGATAACATGAAGAAGGTGAAGCATTTGGTGGAACTGCCGGGTGCA :235
TrDFRn13: ACCGTTCGGGACCCAGATAACATGAAGAAGGTGAAGCATTTGGTGGAACTGCCGGGTGCA :235
TrDFRn14: ACCGTTCGGGACCCAGATAACATGAAGAAGGTGAAGCATTTGGTGGAACTGCCGGGTGCA :192
TrDFRn15: -----: -

      *           260           *           280           *           300
TrDFRn1: AAAAGCAAATTGTCTCTTTGGAAGGCTGATCTTGATAAAGAGGGGGAGTTTGATGAAGCA :300
TrDFRn2: AAAAGCAAATTGTCTCTTTGGAAGGCTGATCTTGATAAAGAGGGGGAGTTTGATGAAGCA :299
TrDFRn3: AAAAGCAAATTGTCTCTTTGGAAGGCTGATCTTGATAAAGAGGGGGAGTTTGATGAAGCA :297
TrDFRn4: AAAAGCAAATTGTCTCTTTGGAAGGCTGATCTTGATAAAGAGGGGGAGTTTGATGAAGCA :297
TrDFRn5: AAAAGCAAATTGTCTCTTTGGAAGGCTGATCTTGATAAAGAGGGGGAGTTTGATGAAGCA :297
TrDFRn6: AAAAGCAAATTGTCTCTTTGGAAGGCTGATCTTGATAAAGAGGGGGAGTTTGATGAAGCA :297
TrDFRn7: AAAAGCAAATTGTCTCTTTGGAAGGCTGATCTTGATAAAGAGGGGGAGTTTGATGAAGCA :297
TrDFRn8: AAAAGCAAATTGTCTCTTTGGAAGGCTGATCTTGATAAAGAGGGGGAGTTTGATGAAGCA :296
TrDFRn9: AAAAGCAAATTGTCTCTTTGGAAGGCTGATCTTGATAAAGAGGGGGAGTTTGATGAAGCA :296
TrDFRn10: AAAAGCAAATTGTCTCTTTGGAAGGCTGATCTTGATAAAGAGGGGGAGTTTGATGAAGCA :296
TrDFRn11: AAAAGCAAATTGTCTCTTTGGAAGGCTGATCTTGATAAAGAGGGGGAGTTTGATGAAGCA :295
TrDFRn12: AAAAGCAAATTGTCTCTTTGGAAGGCTGATCTTGATAAAGAGGGGGAGTTTGATGAAGCA :295
TrDFRn13: AAAAGCAAATTGTCTCTTTGGAAGGCTGATCTTGATAAAGAGGGGGAGTTTGATGAAGCA :292
TrDFRn14: AAAAGCAAATTGTCTCTTTGGAAGGCTGATCTTGATAAAGAGGGGGAGTTTGATGAAGCA :252
TrDFRn15: -----: -

      *           320           *           340           *           360
TrDFRn1: MTAAAGGGTGCACAGGAGTTTTTCATGTTGCTACACCAATGGATTTTGAATCCAAGGAC :360
TrDFRn2: MTAAAGGGTGCACAGGAGTTTTTCATGTTGCTACACCAATGGATTTTGAATCCAAGGAC :359
TrDFRn3: MTAAAGGGTGCACAGGAGTTTTTCATGTTGCTACACCAATGGATTTTGAATCCAAGGAC :357
TrDFRn4: MTAAAGGGTGCACAGGAGTTTTTCATGTTGCTACACCAATGGATTTTGAATCCAAGGAC :357
TrDFRn5: MTAAAGGGTGCACAGGAGTTTTTCATGTTGCTACACCAATGGATTTTGAATCCAAGGAC :357
TrDFRn6: MTAAAGGGTGCACAGGAGTTTTTCATGTTGCTACACCAATGGATTTTGAATCCAAGGAC :357
TrDFRn7: MTAAAGGGTGCACAGGAGTTTTTCATGTTGCTACACCAATGGATTTTGAATCCAAGGAC :357
TrDFRn8: MTAAAGGGTGCACAGGAGTTTTTCATGTTGCTACACCAATGGATTTTGAATCCAAGGAC :356
TrDFRn9: MTAAAGGGTGCACAGGAGTTTTTCATGTTGCTACACCAATGGATTTTGAATCCAAGGAC :356
TrDFRn10: MTAAAGGGTGCACAGGAGTTTTTCATGTTGCTACACCAATGGATTTTGAATCCAAGGAC :356
TrDFRn11: MTAAAGGGTGCACAGGAGTTTTTCATGTTGCTACACCAATGGATTTTGAATCCAAGGAC :355
TrDFRn12: MTAAAGGGTGCACAGGAGTTTTTCATGTTGCTACACCAATGGATTTTGAATCCAAGGAC :355
TrDFRn13: MTAAAGGGTGCACAGGAGTTTTTCATGTTGCTACACCAATGGATTTTGAATCCAAGGAC :352
TrDFRn14: MTAAAGGGTGCACAGGAGTTTTTCATGTTGCTACACCAATGGATTTTGAATCCAAGGAC :352
TrDFRn15: -----: -

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FIGURE 64 (cont)

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      *               380               *               400               *               420
TrDFRh1:  CCTGAGAATGAAGTGATAAAGCCTACAATAAATGGATTAATAGACATACCTGAAAGCATGC : 420
TrDFRh2:  CCTGAGAATGAAGTGATAAAGCCTACAATAAATGGATTAATAGACATACCTGAAAGCATGC : 419
TrDFRh3:  CCTGAGAATGAAGTGATAAAGCCTACAATAAATGGATTAATAGACATACCTGAAAGCATGC : 417
TrDFRh4:  CCTGAGAATGAAGTGATAAAGCCTACAATAAATGGATTAATAGACATACCTGAAAGCATGC : 417
TrDFRh5:  CCTGAGAATGAAGTGATAAAGCCTACAATAAATGGATTAATAGACATACCTGAAAGCATGC : 417
TrDFRh6:  CCTGAGAATGAAGTGATAAAGCCTACAATAAATGGATTAATAGACATACCTGAAAGCATGC : 417
TrDFRh7:  CCTGAGAATGAAGTGATAAAGCCTACAATAAATGGATTAATAGACATACCTGAAAGCATGC : 417
TrDFRh8:  CCTGAGAATGAAGTGATAAAGCCTACAATAAATGGATTAATAGACATACCTGAAAGCATGC : 416
TrDFRh9:  CCTGAGAATGAAGTGATAAAGCCTACAATAAATGGATTAATAGACATACCTGAAAGCATGC : 416
TrDFRh10: CCTGAGAATGAAGTGATAAAGCCTACAATAAATGGATTAATAGACATACCTGAAAGCATGC : 416
TrDFRh11: CCTGAGAATGAAGTGATAAAGCCTACAATAAATGGATTAATAGACATACCTGAAAGCATGC : 415
TrDFRh12: CCTGAGAATGAAGTGATAAAGCCTACAATAAATGGATTAATAGACATACCTGAAAGCATGC : 415
TrDFRh13: CCTGAGAATGAAGTGATAAAGCCTACAATAAATGGATTAATAGACATACCTGAAAGCATGC : 412
TrDFRh14: CCTGAGAATGAAGTGATAAAGCCTACAATAAATGGATTAATAGACATACCTGAAAGCATGC : 372
TrDFRh15: CCTGAGAATGAAGTGATAAAGCCTACAATAAATGGATTAATAGACATACCTGAAAGCATGC : 14

      *               440               *               460               *               480
TrDFRh1:  GAAAGGCCAAAAACAGTTAGAAAAATTGGTTTTCACATCATCGGCTGGAACCTGTGGACGTT : 480
TrDFRh2:  GAAAGGCCAAAAACAGTTAGAAAAATTGGTTTTCACATCATCGGCTGGAACCTGTGGACGTT : 479
TrDFRh3:  GAAAGGCCAAAAACAGTTAGAAAAATTGGTTTTCACATCATCGGCTGGAACCTGTGGACGTT : 477
TrDFRh4:  GAAAGGCCAAAAACAGTTAGAAAAATTGGTTTTCACATCATCGGCTGGAACCTGTGGACGTT : 477
TrDFRh5:  GAAAGGCCAAAAACAGTTAGAAAAATTGGTTTTCACATCATCGGCTGGAACCTGTGGACGTT : 477
TrDFRh6:  GAAAGGCCAAAAACAGTTAGAAAAATTGGTTTTCACATCATCGGCTGGAACCTGTGGACGTT : 477
TrDFRh7:  GAAAGGCCAAAAACAGTTAGAAAAATTGGTTTTCACATCATCGGCTGGAACCTGTGGACGTT : 477
TrDFRh8:  GAAAGGCCAAAAACAGTTAGAAAAATTGGTTTTCACATCATCGGCTGGAACCTGTGGACGTT : 476
TrDFRh9:  GAAAGGCCAAAAACAGTTAGAAAAATTGGTTTTCACATCATCGGCTGGAACCTGTGGACGTT : 476
TrDFRh10: GAAAGGCCAAAAACAGTTAGAAAAATTGGTTTTCACATCATCGGCTGGAACCTGTGGACGTT : 476
TrDFRh11: GAAAGGCCAAAAACAGTTAGAAAAATTGGTTTTCACATCATCGGCTGGAACCTGTGGACGTT : 475
TrDFRh12: GAAAGGCCAAAAACAGTTAGAAAAATTGGTTTTCACATCATCGGCTGGAACCTGTGGACGTT : 475
TrDFRh13: GAAAGGCCAAAAACAGTTAGAAAAATTGGTTTTCACATCATCGGCTGGAACCTGTGGACGTT : 472
TrDFRh14: GAAAGGCCAAAAACAGTTAGAAAAATTGGTTTTCACATCATCGGCTGGAACCTGTGGACGTT : 432
TrDFRh15: GAAAGGCCAAAAACAGTTAGAAAAATTGGTTTTCACATCATCGGCTGGAACCTGTGGACGTT : 74

      *               500               *               520               *               540
TrDFRh1:  CTGGAACATCCAAAGTCATTATTGATGAAACATGCTGGAGTGACGTTGACCTTTTGCCGT : 540
TrDFRh2:  CTGGAACATCCAAAGTCATTATTGATGAAACATGCTGGAGTGACGTTGACCTTTTGCCGT : 539
TrDFRh3:  CTGGAACATCCAAAGTCATTATTGATGAAACATGCTGGAGTGACGTTGACCTTTTGCCGT : 493
TrDFRh4:  CTGGAACATCCAAAGTCATTATTGATGAAACATGCTGGAGTGACGTTGACCTTTTGCCGT : 537
TrDFRh5:  CTGGAACATCCAAAGTCATTATTGATGAAACATGCTGGAGTGACGTTGACCTTTTGCCGT : 537
TrDFRh6:  CTGGAACATCCAAAGTCATTATTGATGAAACATGCTGGAGTGACGTTGACCTTTTGCCGT : 537
TrDFRh7:  CTGGAACATCCAAAGTCATTATTGATGAAACATGCTGGAGTGACGTTGACCTTTTGCCGT : 537
TrDFRh8:  CTGGAACATCCAAAGTCATTATTGATGAAACATGCTGGAGTGACGTTGACCTTTTGCCGT : 536
TrDFRh9:  CTGGAACATCCAAAGTCATTATTGATGAAACATGCTGGAGTGACGTTGACCTTTTGCCGT : 536
TrDFRh10: CTGGAACATCCAAAGTCATTATTGATGAAACATGCTGGAGTGACGTTGACCTTTTGCCGT : 536
TrDFRh11: CTGGAACATCCAAAGTCATTATTGATGAAACATGCTGGAGTGACGTTGACCTTTTGCCGT : 535
TrDFRh12: CTGGAACATCCAAAGTCATTATTGATGAAACATGCTGGAGTGACGTTGACCTTTTGCCGT : 535
TrDFRh13: CTGGAACATCCAAAGTCATTATTGATGAAACATGCTGGAGTGACGTTGACCTTTTGCCGT : 532
TrDFRh14: CTGGAACATCCAAAGTCATTATTGATGAAACATGCTGGAGTGACGTTGACCTTTTGCCGT : 492
TrDFRh15: CTGGAACATCCAAAGTCATTATTGATGAAACATGCTGGAGTGACGTTGACCTTTTGCCGT : 134

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FIGURE 64 (cont)

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	*	560	*	580	*	600	
TrDFRh1 :		AGAGTCAAGATGACCGGTTCGGATGTA	TTTGTTC	AAAGACCC	TAC		: 586
TrDFRh2 :		AGAGTCAAAATGACCGGTTCGGATGTA	TTTT				: 569
TrDFRh3 :							: -
TrDFRh4 :		ANAGTCAAAATGACCGGTTCGGATGTA	TTTGTTC	AAANAGCC			: 580
TrDFRh5 :		AGAGTCAAGATGACCGGTTCGGATGTA	TTTGTTC	AAAGACCC			: 581
TrDFRh6 :		AGAGTCAAGATGACCGGTTCGGATGTA	TTTGTTC	AAAGACCC	TAGCAGAGCAAG		: 592
TrDFRh7 :		AGAGTCAAGATGACCGGTTCGGATGTA	TTTGTTC	AAAGACCC	TAGCAGAGCAAGAAGCT		: 597
TrDFRh8 :		AGAGTCAAAATGACCGGTTCGGATGTA	TTTGTTC	AAAG			: 576
TrDFRh9 :		AGAGTCAAGATGACCGGTTCGGATGTA	TTTGTTC	AAAGACCC	TAGCAGAG		: 587
TrDFRh10 :		AGAGTCAAGATGACCGGTTCGGATGTA	TTTGTTC	AAAGACCC	TAGCAGAGCAAGAAGCT		: 596
TrDFRh11 :		AGAGTCAAAATGACCGGTTCGGATGTA	TTTGTTC	AAAGACCC			: 579
TrDFRh12 :		AGAGTCAAGATGACCGGTTCGGATGTA	TTTGTTC	AAAGACCC	TAGCAGAGCAAGAAGCT		: 595
TrDFRh13 :		AGAGTCAAAATGACCGGTTCGGATGTA	TTTGTTC	AAAGACCC	TAGCAGAGCAAG		: 586
TrDFRh14 :		AGAGTCAAAATGACCGGTTCGGATGTA	TTTGTTC	AAAGACCC	TAGCAGAGCAAGAAGCT		: 552
TrDFRh15 :		AGAGTCAAAATGACCGGTTCGGATGTA	TTTGTTC	AAAGACCC	TAGCAGAGCAAGAAGCT		: 194

	*	620	*	640	*	660	
TrDFRh1 :							: -
TrDFRh2 :							: -
TrDFRh3 :							: -
TrDFRh4 :							: -
TrDFRh5 :							: -
TrDFRh6 :							: -
TrDFRh7 :		T					: 598
TrDFRh8 :							: -
TrDFRh9 :							: -
TrDFRh10 :		TGGAAGTATTC	AAAAGAGCACAACATAGACTTTC				: 630
TrDFRh11 :							: -
TrDFRh12 :		TGGAAGTAT					: 604
TrDFRh13 :							: -
TrDFRh14 :		TGGAAGTATTCGAAAAGAGCACAACATAGACTTTC					: 586
TrDFRh15 :		TGGAAGTATTCGAAAAGAGCACAACATAGACTTTGCTCGATCAITCCACCTCTTGTTGT					: 254

	*	680	*	700	*	720	
TrDFRh1 :							: -
TrDFRh2 :							: -
TrDFRh3 :							: -
TrDFRh4 :							: -
TrDFRh5 :							: -
TrDFRh6 :							: -
TrDFRh7 :							: -
TrDFRh8 :							: -
TrDFRh9 :							: -
TrDFRh10 :							: -
TrDFRh11 :							: -
TrDFRh12 :							: -
TrDFRh13 :							: -
TrDFRh14 :							: -
TrDFRh15 :		GGCCCCTTTCCTATATGGCTCAATGCCACCTAGTCTAATCACTGCTCTTCTCTTATCAC					: 314

FIGURE 64 (cont)

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		*	740	*	760	*	780	
TrDFRh1 :	-----							:
TrDFRh2 :	-----							:
TrDFRh3 :	-----							:
TrDFRh4 :	-----							:
TrDFRh5 :	-----							:
TrDFRh6 :	-----							:
TrDFRh7 :	-----							:
TrDFRh8 :	-----							:
TrDFRh9 :	-----							:
TrDFRh10 :	-----							:
TrDFRh11 :	-----							:
TrDFRh12 :	-----							:
TrDFRh13 :	-----							:
TrDFRh14 :	-----							:
TrDFRh15 :	GGAAATGAGGCCCATTTACTCAATCATAAAGCAAGGSCAATACGTCGATTTAGATGACCTT							: 374
		*	800	*	820	*	840	
TrDFRh1 :	-----							:
TrDFRh2 :	-----							:
TrDFRh3 :	-----							:
TrDFRh4 :	-----							:
TrDFRh5 :	-----							:
TrDFRh6 :	-----							:
TrDFRh7 :	-----							:
TrDFRh8 :	-----							:
TrDFRh9 :	-----							:
TrDFRh10 :	-----							:
TrDFRh11 :	-----							:
TrDFRh12 :	-----							:
TrDFRh13 :	-----							:
TrDFRh14 :	-----							:
TrDFRh15 :	TGCTTGCTCATATATTTCTGTAAGAGAAATCCAAAAGCTCAAGGAGATACATTTGCTGT							: 434
		*	860	*	880	*	900	
TrDFRh1 :	-----							:
TrDFRh2 :	-----							:
TrDFRh3 :	-----							:
TrDFRh4 :	-----							:
TrDFRh5 :	-----							:
TrDFRh6 :	-----							:
TrDFRh7 :	-----							:
TrDFRh8 :	-----							:
TrDFRh9 :	-----							:
TrDFRh10 :	-----							:
TrDFRh11 :	-----							:
TrDFRh12 :	-----							:
TrDFRh13 :	-----							:
TrDFRh14 :	-----							:
TrDFRh15 :	TCACATGAAGCAACCATTTCAACAAGTTGCAAAACTTTATTAAGAAAAATACCCAGAGTTC							: 494

FIGURE 64 (cont)

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	*	920	*	940	*	960	
TrDFRh1 :	-----		-----		-----		;
TrDFRh2 :	-----		-----		-----		;
TrDFRh3 :	-----		-----		-----		;
TrDFRh4 :	-----		-----		-----		;
TrDFRh5 :	-----		-----		-----		;
TrDFRh6 :	-----		-----		-----		;
TrDFRh7 :	-----		-----		-----		;
TrDFRh8 :	-----		-----		-----		;
TrDFRh9 :	-----		-----		-----		;
TrDFRh10 :	-----		-----		-----		;
TrDFRh11 :	-----		-----		-----		;
TrDFRh12 :	-----		-----		-----		;
TrDFRh13 :	-----		-----		-----		;
TrDFRh14 :	-----		-----		-----		;
TrDFRh15 :	AATGTCCCAACAAAATTCAATGATATCCAGATGAATTGGAAATTATTAATTTTCTTAA						;

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	*		
TrDFRh1 :	-----	;	-
TrDFRh2 :	-----	;	-
TrDFRh3 :	-----	;	-
TrDFRh4 :	-----	;	-
TrDFRh5 :	-----	;	-
TrDFRh6 :	-----	;	-
TrDFRh7 :	-----	;	-
TrDFRh8 :	-----	;	-
TrDFRh9 :	-----	;	-
TrDFRh10 :	-----	;	-
TrDFRh11 :	-----	;	-
TrDFRh12 :	-----	;	-
TrDFRh13 :	-----	;	-
TrDFRh14 :	-----	;	-
TrDFRh15 :	GAAGATCACAGAC	;	570

FIGURE 64 (cont)

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TrLCRa : GGNCAATAAACTGCACTAGTGTGTATAAGTTTNTTAGTGAAAAAGAGTGTGTAAATTA : 60
          *          20          *          40          *          60
TrLCRa : ACATCATGGCTAGTATCAAAACAATTGGAACAAGAAAGCATGTGTGTGGTGCGACTG : 120
          *          80          *          100          *          120
TrLCRa : GTTTGTGTGCATCTATGTTGATCAAAACAGTTACTTGAAGGGTTATGCTGTTAATACTA : 180
          *          140          *          160          *          180
TrLCRa : CTGTTAGAGACCCAGATAGTCTTAAGAAAATATCTCACCTAGTGGCACTGCAAGTTTGG : 240
          *          200          *          220          *          240
TrLCRa : GGGAACTGAATCTATTTAGAGCAGACTTAAACAGTTGAAGAAGATTTTGATGCTCCTATAG : 300
          *          260          *          280          *          300
TrLCRa : CAGGATGTGAGCTGTGTTTCAACTTGCTACACCTGTGAACCTTTGCTTCTCAAGATCCTG : 360
          *          320          *          340          *          360
TrLCRa : AGAATGACATGATAAAGCCAGCAATCAAGGTTGTGTTGAATGTGTTGAAGCAAGTGCAA : 420
          *          380          *          400          *          420
TrLCRa : GAGCAAAAGAAGTCAAAAGAGTTATCTTAAACATCTTCGGCAGCCGCGGTGACTATAAATG : 480
          *          440          *          460          *          480
TrLCRa : AACTCAAAAGGGACAGGTCATGTTATGGATGAAACCAACTGGTCAGATGTTGAATTTCTGA : 540
          *          500          *          520          *          540
TrLCRa : ACACTGCAAAAGCCACCCACTTGGGGTTATCCTGCTTCAAAAATGCTAGCTGAAAAGGCTG : 600
          *          560          *          580          *          600
TrLCRa : CATGGAATTTGCTGAAGAAAAATGACATTGATCTAATCACTGTGATACCTAGTTTAACAA : 660
          *          620          *          640          *          660
TrLCRa : CTGGTCCTTCTCTCACACCAGATATCCCATCTAGTGTGGCTTGGCAATGTCTCTTAATAA : 720
          *          680          *          700          *          720
TrLCRa : CAGGCAATGATTTCTCTATAAATGCTCTGAAAGGAATGCAATTTCTGTGCGGTTCTGTTAT : 780
          *          740          *          760          *          780
TrLCRa : CCATCACTCATGTTGAGGATATTGGCCGAGCTCATATATTTCTGGCAGAGAAG : 833
          *          800          *          820          *

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FIGURE 65

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      *           20           *           40           *           60
TrLCRa : MASIKQIGNKKACVIGGTGFVASMLIKQLLEKGYAVNTTVRDPDSPKKISHLVALQSLGE : 60

      *           80           *           100          *           120
TrLCRa : LNLFRADLTVEEDFDAPIAGCELVFQLATPVNFASQDPENDMIKPAIKGVNLNVLKASARA : 120

      *           140          *           160          *           180
TrLCRa : KEVKRVILTSSAAAVTINELKGTGHVMDETNWSDSVEFLNTAKPPTWGYPAKMLAEKAAM : 180

      *           200          *           220          *           240
TrLCRa : KFAEENDIDLITVIPSLTTGPSLTPDIPSSVGLAMSLITGNDFLINALKGMQFLSGSLSI : 240

      *
TrLCRa : THVEDICRAHIFLAEK : 256

```

FIGURE 66

	*	20	*	40	*	60	
TrLCRa1:	<u>GGNCATAAAAACTGCACCTAGTGTGTAAGAATTTC</u> TACTGCAAAAAGAGTGTTGTAATAATTC						: 60
TrLCRa2:	<u>GGNCATAAAAACTGCACCTAGTGTGTAAGAATTTC</u> TACTGCAAAAAGAGTGTTGTAATAATTC						: 60
TrLCRa3:	-----TAAAAAAGCTGACCTGCTGTGTAAGAATTTC						: 55
TrLCRa4:	-----TAAAAAAGCTGACCTGCTGTGTAAGAATTTC						: 55
TrLCRa5:	-----TAAAAAAGCTGACCTGCTGTGTAAGAATTTC						: 55
TrLCRa6:	-----TAAAAAAGCTGACCTGCTGTGTAAGAATTTC						: 47
TrLCRa7:	-----TAAAAAAGCTGACCTGCTGTGTAAGAATTTC						: -
	*	80	*	100	*	120	
TrLCRa1:	<u>GCATCATGCGCTAGTATCAACAAGAAATTTGGAACAAGAAAGCATGCTGATTTGGTGGCAGCTC</u>						: 120
TrLCRa2:	<u>GCATCATGCGCTAGTATCAACAAGAAATTTGGAACAAGAAAGCATGCTGATTTGGTGGCAGCTC</u>						: 120
TrLCRa3:	<u>GCATCATGCGCTAGTATCAACAAGAAATTTGGAACAAGAAAGCATGCTGATTTGGTGGCAGCTC</u>						: 115
TrLCRa4:	<u>GCATCATGCGCTAGTATCAACAAGAAATTTGGAACAAGAAAGCATGCTGATTTGGTGGCAGCTC</u>						: 120
TrLCRa5:	<u>GCATCATGCGCTAGTATCAACAAGAAATTTGGAACAAGAAAGCATGCTGATTTGGTGGCAGCTC</u>						: 115
TrLCRa6:	<u>GCATCATGCGCTAGTATCAACAAGAAATTTGGAACAAGAAAGCATGCTGATTTGGTGGCAGCTC</u>						: 107
TrLCRa7:	-----TAAAAAAGCTGACCTGCTGTGTAAGAATTTC						: -
	*	140	*	160	*	180	
TrLCRa1:	<u>GTTTTGTTGTCATCTATGTTGATCAACAGTTACTT</u> TGAAAAGGGTTATGCTGTTAATACTA						: 180
TrLCRa2:	<u>GTTTTGTTGTCATCTATGTTGATCAACAGTTACTT</u> TGAAAAGGGTTATGCTGTTAATACTA						: 180
TrLCRa3:	<u>GTTTTGTTGTCATCTATGTTGATCAACAGTTACTT</u> TGAAAAGGGTTATGCTGTTAATACTA						: 175
TrLCRa4:	<u>GTTTTGTTGTCATCTATGTTGATCAACAGTTACTT</u> TGAAAAGGGTTATGCTGTTAATACTA						: 175
TrLCRa5:	<u>GTTTTGTTGTCATCTATGTTGATCAACAGTTACTT</u> TGAAAAGGGTTATGCTGTTAATACTA						: 175
TrLCRa6:	<u>GTTTTGTTGTCATCTATGTTGATCAACAGTTACTT</u> TGAAAAGGGTTATGCTGTTAATACTA						: 167
TrLCRa7:	-----TAAAAAAGCTGACCTGCTGTGTAAGAATTTC						: -
	*	200	*	220	*	240	
TrLCRa1:	<u>CTGTTTAGAGACCAGATAGTCTTAAGAAAATATCTCCACCTAGTGGCACTGCAAAGTTTGG</u>						: 240
TrLCRa2:	<u>CTGTTTAGAGACCAGATAGTCTTAAGAAAATATCTCCACCTAGTGGCACTGCAAAGTTTGG</u>						: 240
TrLCRa3:	<u>CTGTTTAGAGACCAGATAGTCTTAAGAAAATATCTCCACCTAGTGGCACTGCAAAGTTTGG</u>						: 235
TrLCRa4:	<u>CTGTTTAGAGACCAGATAGTCTTAAGAAAATATCTCCACCTAGTGGCACTGCAAAGTTTGG</u>						: 235
TrLCRa5:	<u>CTGTTTAGAGACCAGATAGTCTTAAGAAAATATCTCCACCTAGTGGCACTGCAAAGTTTGG</u>						: 227
TrLCRa6:	<u>CTGTTTAGAGACCAGATAGTCTTAAGAAAATATCTCCACCTAGTGGCACTGCAAAGTTTGG</u>						: 1
TrLCRa7:	-----TAAAAAAGCTGACCTGCTGTGTAAGAATTTC						: -
	*	260	*	280	*	300	
TrLCRa1:	<u>GGGAAGCTGAATCTATTTTAGAGCAGACTTAACAGTTGAAGAAGATTTTGATGCTCCCTATAG</u>						: 300
TrLCRa2:	<u>GGGAAGCTGAATCTATTTTAGAGCAGACTTAACAGTTGAAGAAGATTTTGATGCTCCCTATAG</u>						: 300
TrLCRa3:	<u>GGGAAGCTGAATCTATTTTAGAGCAGACTTAACAGTTGAAGAAGATTTTGATGCTCCCTATAG</u>						: 295
TrLCRa4:	<u>GGGAAGCTGAATCTATTTTAGAGCAGACTTAACAGTTGAAGAAGATTTTGATGCTCCCTATAG</u>						: 295
TrLCRa5:	<u>GGGAAGCTGAATCTATTTTAGAGCAGACTTAACAGTTGAAGAAGATTTTGATGCTCCCTATAG</u>						: 287
TrLCRa6:	<u>GGGAAGCTGAATCTATTTTAGAGCAGACTTAACAGTTGAAGAAGATTTTGATGCTCCCTATAG</u>						: 61
TrLCRa7:	<u>GGGAAGCTGAATCTATTTTAGAGCAGACTTAACAGTTGAAGAAGATTTTGATGCTCCCTATAG</u>						: 34
	*	320	*	340	*	360	
TrLCRa1:	<u>CAGGATGTGAGCTGTGTTTTCAACTTGTCTACACCTGTGAACCTTGCTCTCTCAAGATCCTG</u>						: 360
TrLCRa2:	<u>CAGGATGTGAGCTGTGTTTTCAACTTGTCTACACCTGTGAACCTTGCTCTCTCAAGATCCTG</u>						: 360
TrLCRa3:	<u>CAGGATGTGAGCTGTGTTTTCAACTTGTCTACACCTGTGAACCTTGCTCTCTCAAGATCCTG</u>						: 355
TrLCRa4:	<u>CAGGATGTGAGCTGTGTTTTCAACTTGTCTACACCTGTGAACCTTGCTCTCTCAAGATCCTG</u>						: 355
TrLCRa5:	<u>CAGGATGTGAGCTGTGTTTTCAACTTGTCTACACCTGTGAACCTTGCTCTCTCAAGATCCTG</u>						: 347
TrLCRa6:	<u>CAGGATGTGAGCTGTGTTTTCAACTTGTCTACACCTGTGAACCTTGCTCTCTCAAGATCCTG</u>						: 121
TrLCRa7:	<u>CAGGATGTGAGCTGTGTTTTCAACTTGTCTACACCTGTGAACCTTGCTCTCTCAAGATCCTG</u>						: 94

FIGURE 67

[illegible]

FIGURE 67 (cont)

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```

          *           740           *           760           *           780
TrLCRa1: ----- : -
TrLCRa2: ----- : -
TrLCRa3: ----- : -
TrLCRa4: ----- : -
TrLCRa5: ----- : -
TrLCRa6: CAGGCAATGATTTCTCATAAATGCTCTGAAAGGAATGCAATTTCTGTCGGGTTCGTTAT : 541
TrLCRa7: CAGGCAATGATTTCTCATAAATGCTCTGAAAGGAATGCAATTTCTGTCGGGTTCGTTAT : 514

          *           800           *           820           *
TrLCRa1: ----- : -
TrLCRa2: ----- : -
TrLCRa3: ----- : -
TrLCRa4: ----- : -
TrLCRa5: ----- : -
TrLCRa6: CCATCACTCATGTTGAGGATATTTGCCGAGCTCATATATTTCTGG----- : 586
TrLCRa7: CCATCACTCATGTTGAGGATATTTGCCGAGCTCATATATTTCTGCCAGAGAAG : 567

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FIGURE 67 (cont)

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```

      *           20           *           40           *           60
TrF3'5'Ha: GGAACCAATTGTGTCGGACTTTTTCCTCGGGTTGGCCCGGATTCGATTTGCAGGGTGTGGTG : 60

      *           80           *           100          *           120
TrF3'5'Ha: AAAGAGATGGATGTCTTGGTTCACGTTTGTATAGCATATTGAAAAAATGATTGGTGAA :120

      *           140          *           160          *           180
TrF3'5'Ha: CGTAAGAAGAAGGAAGTGGAGGGGAAAGAAAATGAAAGTAAGGATTTTCTGCAGTTTTTG :180

      *           200          *           220          *           240
TrF3'5'Ha: TTGAATTTGAAGGATGAGGGTGATTCTAAGACTCCATTCACAATTACCCATGTTAAGGCT :240

      *           260          *           280          *           300
TrF3'5'Ha: CTACTCATGGACATGGTTGTGGGTGGATCAGACACATCCTCCAACACAATTGAGTTTGCA :300

      *           320          *           340          *           360
TrF3'5'Ha: TTGGCAGAAATGATGAACAACCCAGAAGTAATGAGGAAGGTTCAAGAGGAMTTAGAAGAT :360

      *           380          *           400          *           420
TrF3'5'Ha: GTAGTTGGGAAAGATAACTTAGTAGAAGAGTCTCACATTCTAAGCTACCTACTTGCAT :420

      *           440          *           460          *           480
TrF3'5'Ha: GCAGTGATGAAAGAAACACTTCGTTTACACCCAGCACTTCCACTTTTAGTCCCTCACTGT :480

      *           500          *           520          *           540
TrF3'5'Ha: CCAAGTGAAACCAATGTGTGGAGGCTACACAATTCCAAAGGGATCTCGTGTGTTTGTG :540

      *           560          *           580          *
TrF3'5'Ha: AACGTTTGGGCTATTCTATAGAGACCCCTTCCATTGGGAGAAACCACTAGAATTGTGAT :597

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FIGURE 68

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      *           20           *           40           *           60
TrF3'5'Ha: GTNLSDFPGLARFDLQGVVKEMDVLVPRPDSIFEKMMIGERKKKKEVEGKENSKDPLQFL : 60

      *           80           *           100          *           120
TrF3'5'Ha: LNLKDEGDSKTPFTTITHVKALLMDMVVGGSDTSSNTIEFALAEMNNPEVMRKVQEELED :120

      *           140          *           160          *           180
TrF3'5'Ha: VVGKDNLVVEESHIHKLPYLHAVMKETLRLHPALPLLVPFCPSETTNVGGYTIPKGSRVFV :180

      *
TrF3'5'Ha: NVWAIHRDPSIWEKPLEFD :199

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FIGURE 69

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      *           20           *           40           *           60
TrF3'5'Hb: GNAATCCACNAATCTCTTGAANTAATACCATTTCTTTACAAGAACTTAACCATGGTGATG : 60

      *           80           *           100          *           120
TrF3'5'Hb: ATCACTCAATACCAAACCTTCCTTTACAAAGAACTTTCTATATCCTTTTTCATTTTCTTG :120

      *           140          *           160           *           180
TrF3'5'Hb: ATAACCCATTTTCATCATAAGTTTTTCTCTTCAAAAAAATCTCAAAAAAATTCACACGAGC :180

      *           200          *           220           *           240
TrF3'5'Hb: CCAAAAGGTTTTCCAGTTGTTGGTGCACCCCACATAATGGGATCCATGCCTCATGTTACC :240

      *           260          *           280           *           300
TrF3'5'Hb: CTATTCAAAATGTCACAAAAATATGGTCCCATAAATGTACCTAAAAATGGGATCAAAATAAC :300

      *           320          *           340           *           360
TrF3'5'Hb: ATGGTTGTAGCATCAACTCCTTCTTCAGCCAAAGCATTCTCAAAACACTTGACCTAAT :360

      *           380          *           400           *           420
TrF3'5'Hb: TTCTCCAATAGACCCGCGAACGCTGGCGCAACTCACCTAGCTTATGATTACAAAGACTTG :420

      *           440          *           460           *           480
TrF3'5'Hb: GPTTTCGCCGACTATGGATCTAGGTGGAAATTACTTAGGAAACTAAAGTAACATTGCACATG :480

      *           500          *           520           *           540
TrF3'5'Hb: CTCGGCGGAAAAAGCCCTCGAAAAATGGTCGAAAGTTCGTGAGATTGAAATGGGTCACATG :540

      *           560          *           580           *           600
TrF3'5'Hb: ATTCGTACAATTGTACGATTGTAGCAAGAAAGACGAATCCGTTGTGTGCGCCGAAATGTTG :600

      *           620          *           640           *           660
TrF3'5'Hb: ACATATGCTATGGCCARTATGATAGGTCAAGTTATATTAGTCGTCGCGTGTTCGAGACA :660

      *           680          *           700
TrF3'5'Hb: AAAGGTAGTGACTCAAAATGAATTTAAGGATATGGTTGTMGTG :700

```

FIGURE 70

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      *           20           *           40           *           60
TrF3'5'Hb: MVMITQVQTFLYKELSSISFFIFLITHFIIISPLFKKNLKKLPPGPKGFPVVGALPLMGSM : 60

      *           80           *           100          *           120
TrF3'5'Hb: HVTLFKMSQKYGPIMYLMGSSNNMVVASTPSSAKAFLKTLDLNFSNRPPNAGATHLAYDS :120

      *           140          *           160          *           180
TrF3'5'Hb: QDLVPADYGSRWKLLRKLSNLHMLGGKALENWSKVREIEMGHMIRTWYDCSKKDESVVVA :180

      *           200          *
TrF3'5'Hb: EMLTYAMANMIGQVILSRRVPFETKGSDSNEFKDMVX :216

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FIGURE 71

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TrF3'5'Hb1:	CNAATCCACNAAATCTCTGAATTAATNCCATTCTTTTACAAGAACTTTTCATATCCCTTTTTCATTTCCTTG	: 60
TrF3'5'Hb2:	-----CAATCTCTCTGAAATAANNCCATTCTTTTACAAGAACTTTAACCAATCGGTGATG	: 54
TrF3'5'Hb3:	-----CNAATCTCTGAATTAATACCAATTTCTTTTACAAGAACTTTAACCTTCGTGATG	: 52
TrF3'5'Hb4:	-----TCTCTTCTCTTATATACCAATTTCTTTTACAAGAACTTTAACCTTCGTGATG	: 48
TrF3'5'Hb1:	ATCACTCAATACCAAACCTTCTCTTTTACAAGAACTTTTCATATCCCTTTTTCATTTCCTTG	: 120
TrF3'5'Hb2:	ATCACTCAATACCAAACCTTCTCTTTTACAAGAACTTTTCATATCCCTTTTTCATTTCCTTG	: 114
TrF3'5'Hb3:	ATNNCTCAATACCAAACCTTCTCTTTTACAAGAACTTTTCATATCCCTTTTTCATTTCCTTG	: 112
TrF3'5'Hb4:	ATNNCTCAATACCAAACCTTCTCTTTTACAAGAACTTTTCATATCCCTTTTTCATTTCCTTG	: 108
TrF3'5'Hb1:	ATAACCCCTTTTCATCATTAAGTTTCTCTTTCAAAAAAAATCTCAAAAAATCTCCACCAGGC	: 180
TrF3'5'Hb2:	ATAACCCCTTTTCATCATTAAGTTTCTCTTTCAAAAAAAATCTCAAAAAATCTCCACCAGGC	: 174
TrF3'5'Hb3:	ATAACCCCTTTTCATCATTAAGTTTCTCTTTCAAAAAAAATCTCAAAAAATCTCCACCAGGC	: 172
TrF3'5'Hb4:	ATAACCCCTTTTCATCATTAAGTTTCTCTTTCAAAAAAAATCTCAAAAAATCTCCACCAGGC	: 168
TrF3'5'Hb1:	CCAAAGGTTTTCAGTTGTTGGTGCACTCCCACTAATGGGATCCATGCCATCATGTATCC	: 240
TrF3'5'Hb2:	CCAAAGGTTTTCAGTTGTTGGTGCACTCCCACTAATGGGATCCATGCCATCATGTATCC	: 234
TrF3'5'Hb3:	CCAAAGGTTTTCAGTTGTTGGTGCACTCCCACTAATGGGATCCATGCCATCATGTATCC	: 232
TrF3'5'Hb4:	CCAAAGGTTTTCAGTTGTTGGTGCACTCCCACTAATGGGATCCATGCCATCATGTATCC	: 228
TrF3'5'Hb1:	CTATTCAAAATGTACAAAAATATGGTCCCAATAATGTACCTAAAAATGGGATCAAAATAC	: 300
TrF3'5'Hb2:	CTATTCAAAATGTACAAAAATATGGTCCCAATAATGTACCTAAAAATGGGATCAAAATAC	: 294
TrF3'5'Hb3:	CTATTCAAAATGTACAAAAATATGGTCCCAATAATGTACCTAAAAATGGGATCAAAATAC	: 292
TrF3'5'Hb4:	CTATTCAAAATGTACAAAAATATGGTCCCAATAATGTACCTAAAAATGGGATCAAAATAC	: 288
TrF3'5'Hb1:	ATGGTTCTAGCATCAACTCTCTCTTCAGCCAAAGCAATTTCTCAAAACACTTGACCTAAAT	: 360
TrF3'5'Hb2:	ATGGTTCTAGCATCAACTCTCTCTTCAGCCAAAGCAATTTCTCAAAACACTTGACCTAAAT	: 354
TrF3'5'Hb3:	ATGGTTCTAGCATCAACTCTCTCTTCAGCCAAAGCAATTTCTCAAAACACTTGACCTAAAT	: 352
TrF3'5'Hb4:	ATGGTTCTAGCATCAACTCTCTCTTCAGCCAAAGCAATTTCTCAAAACACTTGACCTAAAT	: 348
TrF3'5'Hb1:	TTCTCCAAATAGACCGCGGAACGCTGGCGCTACTCACCAGCTTATGATTCACAAGACTTG	: 420
TrF3'5'Hb2:	TTCTCCAAATAGACCGCGGAACGCTGGCGCTACTCACCAGCTTATGATTCACAAGACTTG	: 414
TrF3'5'Hb3:	TTCTCCAAATAGACCGCGGAACGCTGGCGCTACTCACCAGCTTATGATTCACAAGACTTG	: 412
TrF3'5'Hb4:	TTCTCCAAATAGACCGCGGAACGCTGGCGCTACTCACCAGCTTATGATTCACAAGACTTG	: 408
TrF3'5'Hb1:	GTTTTCGCCGCACTATGGATCTAGGTGGAAATTTACTTAGGAAACTAAGTAACCTTGCACATG	: 480
TrF3'5'Hb2:	GTTTTCGCCGCACTATGGATCTAGGTGGAAATTTACTTAGGAAACTAAGTAACCTTGCACATG	: 474
TrF3'5'Hb3:	GTTTTCGCCGCACTATGGATCTAGGTGGAAATTTACTTAGGAAACTAAGTAACCTTGCACATG	: 472
TrF3'5'Hb4:	GTTTTCGCCGCACTATGGATCTAGGTGGAAATTTACTTAGGAAACTAAGTAACCTTGCACATG	: 468
TrF3'5'Hb1:	CTCGGCGGAAAAGCCCTCGAAATTTGGTTCGAAAGTTCTGTGAGATTGAAATGGGTACACATG	: 540
TrF3'5'Hb2:	CTCGGCGGAAAAGCCCTCGAAATTTGGTTCGAAAGTTCTGTGAGATTGAAATGGGTACACATG	: 534
TrF3'5'Hb3:	CTCGGCGGAAAAGCCCTCGAAATTTGGTTCGAAAGTTCTGTGAGATTGAAATGGGTACACATG	: 532
TrF3'5'Hb4:	CTCGGCGGAAAAGCCCTCGAAATTTGGTTCGAAAGTTCTGTGAGATTGAAATGGGTACACATG	: 528

FIGURE 72

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```

      *           560           *           580           *           600
TrF3'5'Hb1:  ATTCGTACAAATGTATGATTGTAGCAAGAAAGACGAATCCGTTG-----:584
TrF3'5'Hb2:  ATTCGTACAAATGTACGATTGTAGCAAGAAAGACGAATCCGTTGTTGGCCGAAATGTTG-----:594
TrF3'5'Hb3:  ATTCGTACAAATGTACGATTGTAGCAAGAAAGACGAATATGTTGTTGTC-----:580
TrF3'5'Hb4:  ATTCGTACAAATGTACGATTGTAGCAAGAAAGACGAATCCGTTGNTG-----: 74

      *           620           *           640           *           660
TrF3'5'Hb1:  -----: -
TrF3'5'Hb2:  ACATATGCTATGGCCAATATGATAGGTCAAGTTATATTGAGTCGTCGGCTGTTTCGAGAC-----:654
TrF3'5'Hb3:  -----: -
TrF3'5'Hb4:  -----: -

      *           680           *           700
TrF3'5'Hb1:  -----: -
TrF3'5'Hb2:  TTTGGTAGTGACTCAAATGAAATTAAAGGATATGGTTGNTG-----:694
TrF3'5'Hb3:  -----: -
TrF3'5'Hb4:  -----: -

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FIGURE 72 (cont)

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      *           20           *           40           *           60
TrF3Ha : GCACACNTCTATTTATTTCTACTTAAACCTNACAAAAAATAANACCCACAAAAACACAAAC : 60

      *           80           *           100          *           120
TrF3Ha : ACCACAAACACCAAAACCGAGTCCGTTTCTTNNTCNAACATGGCACCAGGCCAAACTCTA : 120

      *           140          *           160          *           180
TrF3Ha : AGTTATCTCTCACAAACAACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT : 180

      *           200          *           220          *           240
TrF3Ha : CCAAAAGTTGCCTACAATAACTTCAGCAACGAGATTCCAATCATTCTCTTGCTGGAATT : 240

      *           260          *           280          *           300
TrF3Ha : GATGAGGTTGATGGTCGTAGAACAGAGATATGTAACAGATTGTTGAAGCTTGTGAGAAT : 300

      *           320          *           340          *           360
TrF3Ha : TGGGSTATTTTTCAGGTTGTTGATCATGGTGTGATACAAAACCTTGTTTCGAGATGACC : 360

      *           380          *           400          *           420
TrF3Ha : CGTTTGTCTAGAGAGTTTTTTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC : 420

      *           440          *           460          *           480
TrF3Ha : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTCCAAGGAGAAGCAGTGAAGGAT : 480

      *           500          *           520          *           540
TrF3Ha : TGSAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAAGAGATTATTCAGGTGG : 540

      *           560          *           580          *           600
TrF3Ha : CCAGACAAGCCAGAAGGATGGAAAGAGGTAAACAGAAAAATACAGTGAACCTAATGAAT : 600

      *           620          *           640          *           660
TrF3Ha : TTAGCTTGCAAACTATTGGAAGTTTATCAGAAGCAATGGGTTTAGAAAAAGAAAGCTCTA : 660

      *           680          *           700          *           720
TrF3Ha : ACAAAGCATGTGTTGATATGGATCAAAAAGTTGTTATAAAATTATTACCCAAAATGCCCT : 720

      *           740          *           760          *           780
TrF3Ha : GAACCTGACCTCACACTTGGCCTTAAACGTCACACTGACCTGGCACAATTACTCTTTTG : 780

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FIGURE 73

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```

      *           800           *           820           *           840
TrF3Ha :  CTTCAAGATCAAGTTGGTGGCCTTCAAGCTACCAAAGATAATGGTAAGACGTGGATTACA : 840

      *           860           *           880           *           900
TrF3Ha :  GTTCAACCAAGTTGAAGGTGCTTTTGTGTTAATCTTGAGACCATGGTCACTATCTAAGT : 900

      *           920           *           940           *           960
TrF3Ha :  AATGGACGGTTCAAAAATGCTGACCACCAAGCAGTGGTGAATTCGAACTACAGCCGNTTA : 960

      *           980           *          1000           *          1020
TrF3Ha :  TCAATAGCAACATTTCAAATCCAGCTCCCGATGCAACTGTATACCCCTTTGAAGATTAGA : 1020

      *          1040           *          1060           *          1080
TrF3Ha :  GAGGGTGAAAAATCTGTGTTGGAAGAACCAATCACTTTTGCTGAAATGTATAGAAGGAAG : 1080

      *          1100           *          1120           *          1140
TrF3Ha :  ATGACCAAAGACCTTGAAATTGCTAGGATGAAGAAGTTGGCTAAGGAACAACAACCTTAGG : 1140

      *          1160           *          1180           *          1200
TrF3Ha :  GACTTGGAGGAGAACAGACTAAATATGAGGCCAAACCTTTGAATGAGATCTTTTGCTTAA : 1200

      *          1220           *          1240           *          1260
TrF3Ha :  TTAATTAGTCTTAATTTAAATAATTAATAAATTTTAGACTTAAATTTACATATAATAATTT : 1260

TrF3Ha : T : 1261

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FIGURE 73 (cont)

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      *           20           *           40           *           6
TrF3Ha : MAPSQTL SYLSQQNTLESSFVREEDERPKVAYNNFNSNEIPIISLAGIDEVDGRRTBICNK : 59

      *           80           *           100          *           120
TrF3Ha : IVEACENWGIFQVVDHGVDTKLVSEMTRFAREFFALPPEEKLRFDMSGGKKGGFIVSSHL : 120

      *           140          *           160          *           180
TrF3Ha : QGEAVKDWRELVTYFSYPIKQRDYSRWPDKPEGWKEVTEKYSENLMNLACKLLEVLSEAM : 180

      *           200          *           220          *           240
TrF3Ha : GLEKEALTKACVDMQKVVINYPKCEPDLTLGLKRHTDPGTITLLQDQVGGLQATKD : 240

      *           260          *           280          *           300
TrF3Ha : NGKTWITVQPVEGAFVVNLGDHGHYLSNGRPFKNADHQAVVNSNYXLSIATFQNPAPDAT : 300

      *           320          *           340          *           360
TrF3Ha : VYPLKIREGKSVLEEPITFAEMYRRKMTKDLEIARMKKLAKEQQLRDLEENKTKYEAKP : 360

TrF3Ha : LNEIFA : 366

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FIGURE 74

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      *           20           *           40           *           60
TrF3Ha1 : GCACACNICATTTTATTTCCTACTTAAACCTGACAAAAATTAACCCACAACACACAAAC : 59
TrF3Ha2 : GCACACNICATTTTATTTCCTACTTAAACCTTAAAAATTAACCCACAACACACAAAC : 52
TrF3Ha3 : CACACNICATTTTATTTCCTACTTAAACCTTACAAAAAATAANACCCACAACACACAAAC : 59
TrF3Ha4 : GCGCTCTATTATTTCCTACTTAAACCTTNNCAAAAAATTAANACCCACAACACACAAAC : 58
TrF3Ha5 : -----GTTAACACACCTTCAACACAAAC : 22
TrF3Ha6 : -----GNAACCCACAACACACAAAC : 20
TrF3Ha7 : -----CACACAAATTCACAAAC : 16
TrF3Ha8 : -----CACACAAATTCACAAAC : 16
TrF3Ha9 : -----CCACANGACACAAAC : 13
TrF3Ha10 : -----GGAACACACAAAC : 13
TrF3Ha11 : -----GNAACACACAAAC : 13
TrF3Ha12 : -----GGTAACACAAAC : 9
TrF3Ha13 : -----TGTAAACACAAAC : 12
TrF3Ha14 : -----TCAACACAAAC : 12
TrF3Ha15 : -----GNAATCTAAAC : 11
TrF3Ha16 : -----GAACCTAAAC : 10
TrF3Ha17 : -----AACCTAAAC : 9
TrF3Ha18 : -----GACCTAAAC : 8
TrF3Ha19 : -----ACCTAAAC : 5
TrF3Ha20 : -----GCTAAAC : 6
TrF3Ha21 : -----GCTAAAC : 5
TrF3Ha22 : -----GCTAAAC : 4
TrF3Ha23 : -----GCTAAAC : 3
TrF3Ha24 : -----GCTAAAC : 3
TrF3Ha25 : -----GCTAAAC : 2
TrF3Ha26 : -----GCTAAAC : 2
TrF3Ha27 : -----GCTAAAC : 2
TrF3Ha28 : -----GCTAAAC : 2
TrF3Ha29 : -----GCTAAAC : 1
TrF3Ha30 : -----GCTAAAC : -
TrF3Ha31 : -----GCTAAAC : -
TrF3Ha32 : -----GCTAAAC : -
TrF3Ha33 : -----GCTAAAC : -
TrF3Ha34 : -----GCTAAAC : -
TrF3Ha35 : -----GCTAAAC : -
TrF3Ha36 : -----GCTAAAC : -
TrF3Ha37 : -----GCTAAAC : -
TrF3Ha38 : -----GCTAAAC : -
TrF3Ha39 : -----GCTAAAC : -
TrF3Ha40 : -----GCTAAAC : -
TrF3Ha41 : -----GCTAAAC : -

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FIGURE 75

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```

      *               80               *               100               *               120
TrF3Ha1 : ACCAATAACAG--AGG--CCGTTTCCATCTGCTG---A---AACATGGCACCAAGCCAAACTCTT : 113
TrF3Ha2 : ACCAATAACAG--AGG--CCGTTTCCATCTGCTG---A---AACATGGCACCAAGCCAAACTCTT : 106
TrF3Ha3 : ACCAATAACAG--AGG--CCGTTTCCATCTGCTG---A---AACATGGCACCAAGCCAAACTCTT : 119
TrF3Ha4 : AACACAATAACAG--AGG--CCGTTTCCATCTGCTG---A---AACATGGCACCAAGCCAAACTCTT : 118
TrF3Ha5 : ACCAATAACAG--AGG--CCGTTTCCATCTGCTG---A---AACATGGCACCAAGCCAAACTCTT : 78
TrF3Ha6 : AACACAATAACAG--AGG--CCGTTTCCATCTGCTG---A---AACATGGCACCAAGCCAAACTCTT : 71
TrF3Ha7 : ACCAATAACAG--AGG--CCGTTTCCATCTGCTG---A---AACATGGCACCAAGCCAAACTCTT : 73
TrF3Ha8 : ACCAATAACAG--AGG--CCGTTTCCATCTGCTG---A---AACATGGCACCAAGCCAAACTCTT : 72
TrF3Ha9 : AACACAATAACAG--AGG--CCGTTTCCATCTGCTG---A---AACATGGCACCAAGCCAAACTCTT : 70
TrF3Ha10 : AACACAATAACAG--AGG--CCGTTTCCATCTGCTG---A---AACATGGCACCAAGCCAAACTCTT : 73
TrF3Ha11 : ACCAATAACAG--AGG--CCGTTTCCATCTGCTG---A---AACATGGCACCAAGCCAAACTCTT : 66
TrF3Ha12 : ACCAATAACAG--AGG--CCGTTTCCATCTGCTG---A---AACATGGCACCAAGCCAAACTCTT : 57
TrF3Ha13 : ACCAATAACAG--AGG--CCGTTTCCATCTGCTG---A---AACATGGCACCAAGCCAAACTCTT : 64
TrF3Ha14 : ACCAATAACAG--AGG--CCGTTTCCATCTGCTG---A---AACATGGCACCAAGCCAAACTCTT : 69
TrF3Ha15 : AACACAATAACAG--AGG--CCGTTTCCATCTGCTG---A---AACATGGCACCAAGCCAAACTCTT : 71
TrF3Ha16 : AACACAATAACAG--AGG--CCGTTTCCATCTGCTG---A---AACATGGCACCAAGCCAAACTCTT : 67
TrF3Ha17 : AACACAATAACAG--AGG--CCGTTTCCATCTGCTG---A---AACATGGCACCAAGCCAAACTCTT : 69
TrF3Ha18 : AACACAATAACAG--AGG--CCGTTTCCATCTGCTG---A---AACATGGCACCAAGCCAAACTCTT : 68
TrF3Ha19 : AACACAATAACAG--AGG--CCGTTTCCATCTGCTG---A---AACATGGCACCAAGCCAAACTCTT : 60
TrF3Ha20 : AACACAATAACAG--AGG--CCGTTTCCATCTGCTG---A---AACATGGCACCAAGCCAAACTCTT : 66
TrF3Ha21 : AACACAATAACAG--AGG--CCGTTTCCATCTGCTG---A---AACATGGCACCAAGCCAAACTCTT : 66
TrF3Ha22 : AACACAATAACAG--AGG--CCGTTTCCATCTGCTG---A---AACATGGCACCAAGCCAAACTCTT : 62
TrF3Ha23 : AACACAATAACAG--AGG--CCGTTTCCATCTGCTG---A---AACATGGCACCAAGCCAAACTCTT : 60
TrF3Ha24 : AACACAATAACAG--AGG--CCGTTTCCATCTGCTG---A---AACATGGCACCAAGCCAAACTCTT : 58
TrF3Ha25 : AACACAATAACAG--AGG--CCGTTTCCATCTGCTG---A---AACATGGCACCAAGCCAAACTCTT : 59
TrF3Ha26 : AACACAATAACAG--AGG--CCGTTTCCATCTGCTG---A---AACATGGCACCAAGCCAAACTCTT : 59
TrF3Ha27 : AACACAATAACAG--AGG--CCGTTTCCATCTGCTG---A---AACATGGCACCAAGCCAAACTCTT : 62
TrF3Ha28 : AACACAATAACAG--AGG--CCGTTTCCATCTGCTG---A---AACATGGCACCAAGCCAAACTCTT : 62
TrF3Ha29 : AACACAATAACAG--AGG--CCGTTTCCATCTGCTG---A---AACATGGCACCAAGCCAAACTCTT : 51
TrF3Ha30 : AACACAATAACAG--AGG--CCGTTTCCATCTGCTG---A---AACATGGCACCAAGCCAAACTCTT : 55
TrF3Ha31 : AACACAATAACAG--AGG--CCGTTTCCATCTGCTG---A---AACATGGCACCAAGCCAAACTCTT : 59
TrF3Ha32 : AACACAATAACAG--AGG--CCGTTTCCATCTGCTG---A---AACATGGCACCAAGCCAAACTCTT : 56
TrF3Ha33 : AACACAATAACAG--AGG--CCGTTTCCATCTGCTG---A---AACATGGCACCAAGCCAAACTCTT : 52
TrF3Ha34 : AACACAATAACAG--AGG--CCGTTTCCATCTGCTG---A---AACATGGCACCAAGCCAAACTCTT : 51
TrF3Ha35 : AACACAATAACAG--AGG--CCGTTTCCATCTGCTG---A---AACATGGCACCAAGCCAAACTCTT : 54
TrF3Ha36 : AACACAATAACAG--AGG--CCGTTTCCATCTGCTG---A---AACATGGCACCAAGCCAAACTCTT : 53
TrF3Ha37 : AACACAATAACAG--AGG--CCGTTTCCATCTGCTG---A---AACATGGCACCAAGCCAAACTCTT : 52
TrF3Ha38 : AACACAATAACAG--AGG--CCGTTTCCATCTGCTG---A---AACATGGCACCAAGCCAAACTCTT : 52
TrF3Ha39 : AACACAATAACAG--AGG--CCGTTTCCATCTGCTG---A---AACATGGCACCAAGCCAAACTCTT : 1
TrF3Ha40 : AACACAATAACAG--AGG--CCGTTTCCATCTGCTG---A---AACATGGCACCAAGCCAAACTCTT : -
TrF3Ha41 : AACACAATAACAG--AGG--CCGTTTCCATCTGCTG---A---AACATGGCACCAAGCCAAACTCTT : -

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FIGURE 75 (cont)

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      *           140           *           160           *           180
TrF3Ha1 : AGTTATCTCTCCACAACAAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :173
TrF3Ha2 : AGTTATCTCTCCACAACAAAAAGACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :166
TrF3Ha3 : AGTTATCTCTCCACAACAAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :179
TrF3Ha4 : AGTTATCTCTCCACAACAAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :178
TrF3Ha5 : AGTTATCTCTCCACAACAAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :131
TrF3Ha6 : AGTTATCTCTCCACAACAAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :133
TrF3Ha7 : AGTTATCTCTCCACAACAAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :132
TrF3Ha8 : AGTTATCTCTCCACAACAAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :133
TrF3Ha9 : AGTTATCTCTCCACAACAAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :130
TrF3Ha10 : AGTTATCTCTCCACAACAAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :133
TrF3Ha11 : AGTTATCTCTCCACAACAAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :126
TrF3Ha12 : AGTTATCTCTCTCCACAACAAAAAGACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :116
TrF3Ha13 : AGTTATCTCTCTCCACAACAAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :124
TrF3Ha14 : AGTTATCTCTCTCCACAACAAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :129
TrF3Ha15 : AGTTATCTCTCTCCACAACAAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :131
TrF3Ha16 : AGTTATCTCTCTCCACAACAAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :127
TrF3Ha17 : AGTTATCTCTCTCCACAACAAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :129
TrF3Ha18 : AGTTATCTCTCTCCACAACAAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :128
TrF3Ha19 : AGTTATCTCTCTCCACAACAAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :120
TrF3Ha20 : AGTTATCTCTCTCCACAACAAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :126
TrF3Ha21 : AGTTATCTCTCTCCACAACAAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :126
TrF3Ha22 : AGTTATCTCTCTCCACAACAAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :122
TrF3Ha23 : AGTTATCTCTCTCCACAACAAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :119
TrF3Ha24 : AGTTATCTCTCTCCACAACAAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :117
TrF3Ha25 : AGTTATCTCTCTCCACAACAAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :118
TrF3Ha26 : AGTTATCTCTCTCCACAACAAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :119
TrF3Ha27 : AGTTATCTCTCTCCACAACAAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :122
TrF3Ha28 : AGTTATCTCTCTCCACAACAAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :122
TrF3Ha29 : AGTTATCTCTCTCCACAACAAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :110
TrF3Ha30 : AGTTATCTCTCTCCACAACAAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :115
TrF3Ha31 : AGTTATCTCTCTCCACAACAAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :119
TrF3Ha32 : AGTTATCTCTCTCCACAACAAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :116
TrF3Ha33 : AGTTATCTCTCTCCACAACAAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :112
TrF3Ha34 : AGTTATCTCTCTCCACAACAAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :109
TrF3Ha35 : AGTTATCTCTCTCCACAACAAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :114
TrF3Ha36 : AGTTATCTCTCTCCACAACAAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :113
TrF3Ha37 : AGTTATCTCTCTCCACAACAAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :112
TrF3Ha38 : AGTTATCTCTCTCCACAACAAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT :112
TrF3Ha39 : AGTTATCTCTCTCCACAACAAAAACACTCTTGAGTCAAGTTTCGTTAGGGAAGAAGATGAGCGT : 61
TrF3Ha40 : ----- : -
TrF3Ha41 : ----- : -

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FIGURE 75 (cont)

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	*	200	*	320	*	240	
TrF3Ha1 :	CCAAAAGT	TGCGTACAATAA	AGCTTCAGCAACGAGAT	TCCAATCA	TTTCTCT	TGCTGGAATT	:233
TrF3Ha2 :	CCAAAAGT	TGCGTACAATAA	AGCTTCAGCAACGAGAT	TCCAATCA	TTTCTCT	TGCTGGAATT	:226
TrF3Ha3 :	CCAAAAGT	TGCGTACAATAA	AGCTTCAGCAACGAGAT	TCCAATCA	TTTCTCT	TGCTGGAATT	:239
TrF3Ha4 :	CCAAAAGT	TGCGTACAATAA	AGCTTCAGCAACGAGAT	TCCAATCA	TTTCTCT	TGCTGGAATT	:238
TrF3Ha5 :	CCAAAAGT	TGCGTACAATAA	AGCTTCAGCAACGAGAT	TCCAATCA	TTTCTCT	TGCTGGAATT	:198
TrF3Ha6 :	CCAAAAGT	TGCGTACAATAA	AGCTTCAGCAACGAGAT	TCCAATCA	TTTCTCT	TGCTGGAATT	:191
TrF3Ha7 :	CCAAAAGT	TGCGTACAATAA	AGCTTCAGCAACGAGAT	TCCAATCA	TTTCTCT	TGCTGGAATT	:193
TrF3Ha8 :	CCAAAAGT	TGCGTACAATAA	AGCTTCAGCAACGAGAT	TCCAATCA	TTTCTCT	TGCTGGAATT	:192
TrF3Ha9 :	CCAAAAGT	TGCGTACAATAA	AGCTTCAGCAACGAGAT	TCCAATCA	TTTCTCT	TGCTGGAATT	:190
TrF3Ha10 :	CCAAAAGT	TGCGTACAATAA	AGCTTCAGCAACGAGAT	TCCAATCA	TTTCTCT	TGCTGGAATT	:193
TrF3Ha11 :	CCAAAAGT	TGCGTACAATAA	AGCTTCAGCAACGAGAT	TCCAATCA	TTTCTCT	TGCTGGAATT	:186
TrF3Ha12 :	CCAAAAGT	TGCGTACAATAA	AGCTTCAGCAACGAGAT	TCCAATCA	TTTCTCT	TGCTGGAATT	:176
TrF3Ha13 :	CCAAAAGT	TGCGTACAATAA	AGCTTCAGCAACGAGAT	TCCAATCA	TTTCTCT	TGCTGGAATT	:184
TrF3Ha14 :	CCAAAAGT	TGCGTACAATAA	AGCTTCAGCAACGAGAT	TCCAATCA	TTTCTCT	TGCTGGAATT	:189
TrF3Ha15 :	CCAAAAGT	TGCGTACAATAA	AGCTTCAGCAACGAGAT	TCCAATCA	TTTCTCT	TGCTGGAATT	:191
TrF3Ha16 :	CCAAAAGT	TGCGTACAATAA	AGCTTCAGCAACGAGAT	TCCAATCA	TTTCTCT	TGCTGGAATT	:187
TrF3Ha17 :	CCAAAAGT	TGCGTACAATAA	AGCTTCAGCAACGAGAT	TCCAATCA	TTTCTCT	TGCTGGAATT	:189
TrF3Ha18 :	CCAAAAGT	TGCGTACAATAA	AGCTTCAGCAACGAGAT	TCCAATCA	TTTCTCT	TGCTGGAATT	:188
TrF3Ha19 :	CCAAAAGT	TGCGTACAATAA	AGCTTCAGCAACGAGAT	TCCAATCA	TTTCTCT	TGCTGGAATT	:180
TrF3Ha20 :	CCAAAAGT	TGCGTACAATAA	AGCTTCAGCAACGAGAT	TCCAATCA	TTTCTCT	TGCTGGAATT	:186
TrF3Ha21 :	CCAAAAGT	TGCGTACAATAA	AGCTTCAGCAACGAGAT	TCCAATCA	TTTCTCT	TGCTGGAATT	:186
TrF3Ha22 :	CCAAAAGT	TGCGTACAATAA	AGCTTCAGCAACGAGAT	TCCAATCA	TTTCTCT	TGCTGGAATT	:182
TrF3Ha23 :	CCAAAAGT	TGCGTACAATAA	AGCTTCAGCAACGAGAT	TCCAATCA	TTTCTCT	TGCTGGAATT	:179
TrF3Ha24 :	CCAAAAGT	TGCGTACAATAA	AGCTTCAGCAACGAGAT	TCCAATCA	TTTCTCT	TGCTGGAATT	:177
TrF3Ha25 :	CCAAAAGT	TGCGTACAATAA	AGCTTCAGCAACGAGAT	TCCAATCA	TTTCTCT	TGCTGGAATT	:178
TrF3Ha26 :	CCAAAAGT	TGCGTACAATAA	AGCTTCAGCAACGAGAT	TCCAATCA	TTTCTCT	TGCTGGAATT	:179
TrF3Ha27 :	CCAAAAGT	TGCGTACAATAA	AGCTTCAGCAACGAGAT	TCCAATCA	TTTCTCT	TGCTGGAATT	:182
TrF3Ha28 :	CCAAAAGT	TGCGTACAATAA	AGCTTCAGCAACGAGAT	TCCAATCA	TTTCTCT	TGCTGGAATT	:182
TrF3Ha29 :	CCAAAAGT	TGCGTACAATAA	AGCTTCAGCAACGAGAT	TCCAATCA	TTTCTCT	TGCTGGAATT	:170
TrF3Ha30 :	CCAAAAGT	TGCGTACAATAA	AGCTTCAGCAACGAGAT	TCCAATCA	TTTCTCT	TGCTGGAATT	:175
TrF3Ha31 :	CCAAAAGT	TGCGTACAATAA	AGCTTCAGCAACGAGAT	TCCAATCA	TTTCTCT	TGCTGGAATT	:179
TrF3Ha32 :	CCAAAAGT	TGCGTACAATAA	AGCTTCAGCAACGAGAT	TCCAATCA	TTTCTCT	TGCTGGAATT	:176
TrF3Ha33 :	CCAAAAGT	TGCGTACAATAA	AGCTTCAGCAACGAGAT	TCCAATCA	TTTCTCT	TGCTGGAATT	:172
TrF3Ha34 :	CCAAAAGT	TGCGTACAATAA	AGCTTCAGCAACGAGAT	TCCAATCA	TTTCTCT	TGCTGGAATT	:169
TrF3Ha35 :	CCAAAAGT	TGCGTACAATAA	AGCTTCAGCAACGAGAT	TCCAATCA	TTTCTCT	TGCTGGAATT	:174
TrF3Ha36 :	CCAAAAGT	TGCGTACAATAA	AGCTTCAGCAACGAGAT	TCCAATCA	TTTCTCT	TGCTGGAATT	:173
TrF3Ha37 :	CCAAAAGT	TGCGTACAATAA	AGCTTCAGCAACGAGAT	TCCAATCA	TTTCTCT	TGCTGGAATT	:172
TrF3Ha38 :	CCAAAAGT	TGCGTACAATAA	AGCTTCAGCAACGAGAT	TCCAATCA	TTTCTCT	TGCTGGAATT	:172
TrF3Ha39 :	CCAAAAGT	TGCGTACAATAA	AGCTTCAGCAACGAGAT	TCCAATCA	TTTCTCT	TGCTGGAATT	:121
TrF3Ha40 :	-----	-----	-----	-----	-----	-----	:-
TrF3Ha41 :	-----	-----	-----	-----	-----	-----	:-

FIGURE 75 (cont)

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      *           260           *           280           *           300
TrF3Ha1 : GATGAGGTTGATGGTTCGTAGAACAGAGATATGTAACAAAGATTGTTGAAGCTTGTGAGAAAT : 293
TrF3Ha2 : GATGAGGTTGATGGTTCGTAGAACAGAGATATGTAACAAAGATTGTTGAAGCTTGTGAGAAAT : 286
TrF3Ha3 : GATGAGGTTGATGGTTCGTAGAACAGAGATATGTAACAAAGATTGTTGAAGCTTGTGAGAAAT : 299
TrF3Ha4 : GATGAGGTTGATGGTTCGTAGAACAGAGATATGTAACAAAGATTGTTGAAGCTTGTGAGAAAT : 298
TrF3Ha5 : GATGAGGTTGATGGTTCGTAGAACAGAGATATGTAACAAAGATTGTTGAAGCTTGTGAGAAAT : 258
TrF3Ha6 : GATGAGGTTGATGGTTCGTAGAACAGAGATATGTAACAAAGATTGTTGAAGCTTGTGAGAAAT : 251
TrF3Ha7 : GATGAGGTTGATGGTTCGTAGAACAGAGATATGTAACAAAGATTGTTGAAGCTTGTGAGAAAT : 253
TrF3Ha8 : GATGAGGTTGATGGTTCGTAGAACAGAGATATGTAACAAAGATTGTTGAAGCTTGTGAGAAAT : 252
TrF3Ha9 : GATGAGGTTGATGGTTCGTAGAACAGAGATATGTAACAAAGATTGTTGAAGCTTGTGAGAAAT : 250
TrF3Ha10 : GATGAGGTTGATGGTTCGTAGAACAGAGATATGTAACAAAGATTGTTGAAGCTTGTGAGAAAT : 253
TrF3Ha11 : GATGAGGTTGATGGTTCGTAGAACAGAGATATGTAACAAAGATTGTTGAAGCTTGTGAGAAAT : 246
TrF3Ha12 : GATGAGGTTGATGGTTCGTAGAACAGAGATATGTAACAAAGATTGTTGAAGCTTGTGAGAAAT : 236
TrF3Ha13 : GATGAGGTTGATGGTTCGTAGAACAGAGATATGTAACAAAGATTGTTGAAGCTTGTGAGAAAT : 244
TrF3Ha14 : GATGAGGTTGATGGTTCGTAGAACAGAGATATGTAACAAAGATTGTTGAAGCTTGTGAGAAAT : 249
TrF3Ha15 : GATGAGGTTGATGGTTCGTAGAACAGAGATATGTAACAAAGATTGTTGAAGCTTGTGAGAAAT : 251
TrF3Ha16 : GATGAGGTTGATGGTTCGTAGAACAGAGATATGTAACAAAGATTGTTGAAGCTTGTGAGAAAT : 247
TrF3Ha17 : GATGAGGTTGATGGTTCGTAGAACAGAGATATGTAACAAAGATTGTTGAAGCTTGTGAGAAAT : 249
TrF3Ha18 : GATGAGGTTGATGGTTCGTAGAACAGAGATATGTAACAAAGATTGTTGAAGCTTGTGAGAAAT : 236
TrF3Ha19 : GATGAGGTTGATGGTTCGTAGAACAGAGATATGTAACAAAGATTGTTGAAGCTTGTGAGAAAT : 240
TrF3Ha20 : GATGAGGTTGATGGTTCGTAGAACAGAGATATGTAACAAAGATTGTTGAAGCTTGTGAGAAAT : 246
TrF3Ha21 : GATGAGGTTGATGGTTCGTAGAACAGAGATATGTAACAAAGATTGTTGAAGCTTGTGAGAAAT : 246
TrF3Ha22 : GATGAGGTTGATGGTTCGTAGAACAGAGATATGTAACAAAGATTGTTGAAGCTTGTGAGAAAT : 242
TrF3Ha23 : GATGAGGTTGATGGTTCGTAGAACAGAGATATGTAACAAAGATTGTTGAAGCTTGTGAGAAAT : 239
TrF3Ha24 : GATGAGGTTGATGGTTCGTAGAACAGAGATATGTAACAAAGATTGTTGAAGCTTGTGAGAAAT : 237
TrF3Ha25 : GATGAGGTTGATGGTTCGTAGAACAGAGATATGTAACAAAGATTGTTGAAGCTTGTGAGAAAT : 238
TrF3Ha26 : GATGAGGTTGATGGTTCGTAGAACAGAGATATGTAACAAAGATTGTTGAAGCTTGTGAGAAAT : 239
TrF3Ha27 : GATGAGGTTGATGGTTCGTAGAACAGAGATATGTAACAAAGATTGTTGAAGCTTGTGAGAAAT : 242
TrF3Ha28 : GATGAGGTTGATGGTTCGTAGAACAGAGATATGTAACAAAGATTGTTGAAGCTTGTGAGAAAT : 242
TrF3Ha29 : GATGAGGTTGATGGTTCGTAGAACAGAGATATGTAACAAAGATTGTTGAAGCTTGTGAGAAAT : 230
TrF3Ha30 : GATGAGGTTGATGGTTCGTAGAACAGAGATATGTAACAAAGATTGTTGAAGCTTGTGAGAAAT : 235
TrF3Ha31 : GATGAGGTTGATGGTTCGTAGAACAGAGATATGTAACAAAGATTGTTGAAGCTTGTGAGAAAT : 239
TrF3Ha32 : GATGAGGTTGATGGTTCGTAGAACAGAGATATGTAACAAAGATTGTTGAAGCTTGTGAGAAAT : 236
TrF3Ha33 : GATGAGGTTGATGGTTCGTAGAACAGAGATATGTAACAAAGATTGTTGAAGCTTGTGAGAAAT : 232
TrF3Ha34 : GATGAGGTTGATGGTTCGTAGAACAGAGATATGTAACAAAGATTGTTGAAGCTTGTGAGAAAT : 229
TrF3Ha35 : GATGAGGTTGATGGTTCGTAGAACAGAGATATGTAACAAAGATTGTTGAAGCTTGTGAGAAAT : 234
TrF3Ha36 : GATGAGGTTGATGGTTCGTAGAACAGAGATATGTAACAAAGATTGTTGAAGCTTGTGAGAAAT : 233
TrF3Ha37 : GATGAGGTTGATGGTTCGTAGAACAGAGATATGTAACAAAGATTGTTGAAGCTTGTGAGAAAT : 233
TrF3Ha38 : GATGAGGTTGATGGTTCGTAGAACAGAGATATGTAACAAAGATTGTTGAAGCTTGTGAGAAAT : 232
TrF3Ha39 : GATGAGGTTGATGGTTCGTAGAACAGAGATATGTAACAAAGATTGTTGAAGCTTGTGAGAAAT : 181
TrF3Ha40 : GATGAGGTTGATGGTTCGTAGAACAGAGATATGTAACAAAGATTGTTGAAGCTTGTGAGAAAT : 28
TrF3Ha41 : ----- : -

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FIGURE 75 (cont)

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		*	320	*	340	*	360	
TrF3Ha1 :	TCGGGGTATTTTTCAGGTTGTTGATCATGGTGTGATACAAAACCTGTTTCTGAGATGACC							: 353
TrF3Ha2 :	TCGGGGTATTTTTCAGGTTGTTGATCATGGTGTGATACAAAACCTGTTTCTGAGATGACC							: 346
TrF3Ha3 :	TCGGGGTATTTTTCAGGTTGTTGATCATGGTGTGATACAAAACCTGTTTCTGAGATGACC							: 359
TrF3Ha4 :	TCGGGGTATTTTTCAGGTTGTTGATCATGGTGTGATACAAAACCTGTTTCTGAGATGACC							: 358
TrF3Ha5 :	TCGGGGTATTTTTCAGGTTGTTGATCATGGTGTGATACAAAACCTGTTTCTGAGATGACC							: 318
TrF3Ha6 :	TCGGGGTATTTTTCAGGTTGTTGATCATGGTGTGATACAAAACCTGTTTCTGAGATGACC							: 311
TrF3Ha7 :	TCGGGGTATTTTTCAGGTTGTTGATCATGGTGTGATACAAAACCTGTTTCTGAGATGACC							: 313
TrF3Ha8 :	TCGGGGTATTTTTCAGGTTGTTGATCATGGTGTGATACAAAACCTGTTTCTGAGATGACC							: 312
TrF3Ha9 :	TCGGGGTATTTTTCAGGTTGTTGATCATGGTGTGATACAAAACCTGTTTCTGAGATGACC							: 309
TrF3Ha10 :	TCGGGGTATTTTTCAGGTTGTTGATCATGGTGTGATACAAAACCTGTTTCTGAGATGACC							: 267
TrF3Ha11 :	TCGGGGTATTTTTCAGGTTGTTGATCATGGTGTGATACAAAACCTGTTTCTGAGATGACC							: 306
TrF3Ha12 :	TCGGGGTATTTTTCAGGTTGTTGATCATGGTGTGATACAAAACCTGTTTCTGAGATGACC							: 296
TrF3Ha13 :	TCGGGGTATTTTTCAGGTTGTTGATCATGGTGTGATACAAAACCTGTTTCTGAGATGACC							: 304
TrF3Ha14 :	TCGGGGTATTTTTCAGGTTGTTGATCATGGTGTGATACAAAACCTGTTTCTGAGATGACC							: 309
TrF3Ha15 :	TCGGGGTATTTTTCAGGTTGTTGATCATGGTGTGATACAAAACCTGTTTCTGAGATGACC							: 311
TrF3Ha16 :	TCGGGGTATTTTTCAGGTTGTTGATCATGGTGTGATACAAAACCTGTTTCTGAGATGACC							: 317
TrF3Ha17 :	TCGGGGTATTTTTCAGGTTGTTGATCATGGTGTGATACAAAACCTGTTTCTGAGATGACC							: 309
TrF3Ha18 :	TCGGGGTATTTTTCAGGTTGTTGATCATGGTGTGATACAAAACCTGTTTCTGAGATGACC							: -
TrF3Ha19 :	TCGGGGTATTTTTCAGGTTGTTGATCATGGTGTGATACAAAACCTGTTTCTGAGATGACC							: 273
TrF3Ha20 :	TCGGGGTATTTTTCAGGTTGTTGATCATGGTGTGATACAAAACCTGTTTCTGAGATGACC							: 306
TrF3Ha21 :	TCGGGGTATTTTTCAGGTTGTTGATCATGGTGTGATACAAAACCTGTTTCTGAGATGACC							: 306
TrF3Ha22 :	TCGGGGTATTTTTCAGGTTGTTGATCATGGTGTGATACAAAACCTGTTTCTGAGATGACC							: 302
TrF3Ha23 :	TCGGGGTATTTTTCAGGTTGTTGATCATGGTGTGATACAAAACCTGTTTCTGAGATGACC							: 299
TrF3Ha24 :	TCGGGGTATTTTTCAGGTTGTTGATCATGGTGTGATACAAAACCTGTTTCTGAGATGACC							: 297
TrF3Ha25 :	TCGGGGTATTTTTCAGGTTGTTGATCATGGTGTGATACAAAACCTGTTTCTGAGATGACC							: 298
TrF3Ha26 :	TCGGGGTATTTTTCAGGTTGTTGATCATGGTGTGATACAAAACCTGTTTCTGAGATGACC							: 299
TrF3Ha27 :	TCGGGGTATTTTTCAGGTTGTTGATCATGGTGTGATACAAAACCTGTTTCTGAGATGACC							: 302
TrF3Ha28 :	TCGGGGTATTTTTCAGGTTGTTGATCATGGTGTGATACAAAACCTGTTTCTGAGATGACC							: 302
TrF3Ha29 :	TCGGGGTATTTTTCAGGTTGTTGATCATGGTGTGATACAAAACCTGTTTCTGAGATGACC							: 290
TrF3Ha30 :	TCGGGGTATTTTTCAGGTTGTTGATCATGGTGTGATACAAAACCTGTTTCTGAGATGACC							: 295
TrF3Ha31 :	TCGGGGTATTTTTCAGGTTGTTGATCATGGTGTGATACAAAACCTGTTTCTGAGATGACC							: 299
TrF3Ha32 :	TCGGGGTATTTTTCAGGTTGTTGATCATGGTGTGATACAAAACCTGTTTCTGAGATGACC							: 296
TrF3Ha33 :	TCGGGGTATTTTTCAGGTTGTTGATCATGGTGTGATACAAAACCTGTTTCTGAGATGACC							: 292
TrF3Ha34 :	TCGGGGTATTTTTCAGGTTGTTGATCATGGTGTGATACAAAACCTGTTTCTGAGATGACC							: 289
TrF3Ha35 :	TCGGGGTATTTTTCAGGTTGTTGATCATGGTGTGATACAAAACCTGTTTCTGAGATGACC							: 294
TrF3Ha36 :	TCGGGGTATTTTTCAGGTTGTTGATCATGGTGTGATACAAAACCTGTTTCTGAGATGACC							: 293
TrF3Ha37 :	TCGGGGTATTTTTCAGGTTGTTGATCATGGTGTGATACAAAACCTGTTTCTGAGATGACC							: 292
TrF3Ha38 :	TCGGGGTATTTTTCAGGTTGTTGATCATGGTGTGATACAAAACCTGTTTCTGAGATGACC							: 292
TrF3Ha39 :	TCGGGGTATTTTTCAGGTTGTTGATCATGGTGTGATACAAAACCTGTTTCTGAGATGACC							: 241
TrF3Ha40 :	TCGGGGTATTTTTCAGGTTGTTGATCATGGTGTGATACAAAACCTGTTTCTGAGATGACC							: 88
TrF3Ha41 :	TCGGGGTATTTTTCAGGTTGTTGATCATGGTGTGATACAAAACCTGTTTCTGAGATGACC							: -

FIGURE 75 (cont)

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      *               380               *               400               *               420
TrF3Ha1 : CGTTTGTCTAGAGAGTTTTTGTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :413
TrF3Ha2 : CGTTTGTCTAGAGAGTTTTTGTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :406
TrF3Ha3 : CGTTTGTCTAGAGAGTTTTTGTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :419
TrF3Ha4 : CGTTTGTCTAGAGAGTTTTTGTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :418
TrF3Ha5 : CGTTTGTCTAGAGAGTTTTTGTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :378
TrF3Ha6 : CGTTTGTCTAGAGAGTTTTTGTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :371
TrF3Ha7 : CGTTTGTCTAGAGAGTTTTTGTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :373
TrF3Ha8 : CGTTTGTCTAGAGAGTTTTTGTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :372
TrF3Ha9 : CTTTTGTGTAAGAGTTTTTGTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :369
TrF3Ha10 : ----- : -
TrF3Ha11 : CGTTTGTCTAGAGAGTTTTTGTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :366
TrF3Ha12 : CGTTTGTCTAGAGAGTTTTTGTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :366
TrF3Ha13 : CGTTTGTCTAGAGAGTTTTTGTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :364
TrF3Ha14 : CGTTTGTCTAGAGAGTTTTTGTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :369
TrF3Ha15 : CGTTTGTCTAGAGAGTTTTTGTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :371
TrF3Ha16 : CGTTTGTCTAGAGAGTTTTTGTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :367
TrF3Ha17 : CGTTTGTCTAGAGAGTTTTTGTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :369
TrF3Ha18 : ----- : -
TrF3Ha19 : ----- : -
TrF3Ha20 : CGTTTGTCTAGAGAGTTTTTGTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :366
TrF3Ha21 : CGTTTGTCTAGAGAGTTTTTGTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :366
TrF3Ha22 : CGTTTGTCTAGAGAGTTTTTGTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :362
TrF3Ha23 : CGTTTGTCTAGAGAGTTTTTGTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :359
TrF3Ha24 : CGTTTGTCTAGAGAGTTTTTGTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :357
TrF3Ha25 : CGTTTGTCTAGAGAGTTTTTGTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :358
TrF3Ha26 : CGTTTGTCTAGAGAGTTTTTGTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :359
TrF3Ha27 : CGTTTGTCTAGAGAGTTTTTGTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :362
TrF3Ha28 : CGTTTGTCTAGAGAGTTTTTGTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :362
TrF3Ha29 : CGTTTGTCTAGAGAGTTTTTGTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :350
TrF3Ha30 : CGTTTGTCTAGAGAGTTTTTGTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :355
TrF3Ha31 : CGTTTGTCTAGAGAGTTTTTGTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :359
TrF3Ha32 : CGTTTGTCTAGAGAGTTTTTGTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :356
TrF3Ha33 : CGTTTGTCTAGAGAGTTTTTGTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :352
TrF3Ha34 : CGTTTGTCTAGAGAGTTTTTGTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :349
TrF3Ha35 : CGTTTGTCTAGAGAGTTTTTGTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :354
TrF3Ha36 : CGTTTGTCTAGAGAGTTTTTGTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :353
TrF3Ha37 : CGTTTGTCTAGAGAGTTTTTGTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :352
TrF3Ha38 : CGTTTGTCTAGAGAGTTTTTGTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :352
TrF3Ha39 : CGTTTGTCTAGAGAGTTTTTGTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :301
TrF3Ha40 : CGTTTGTCTAGAGAGTTTTTGTGCTTTGCCACCGGAAGAGAAGCTCCGGTTTGACATGTCC :148
TrF3Ha41 : ----- : -

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FIGURE 75 (cont)

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TrF3Ha1 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :473
TrF3Ha2 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :474
TrF3Ha3 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :475
TrF3Ha4 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :476
TrF3Ha5 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :477
TrF3Ha6 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :478
TrF3Ha7 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :479
TrF3Ha8 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :480
TrF3Ha9 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :481
TrF3Ha10 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :482
TrF3Ha11 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :483
TrF3Ha12 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :484
TrF3Ha13 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :485
TrF3Ha14 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :486
TrF3Ha15 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :487
TrF3Ha16 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :488
TrF3Ha17 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :489
TrF3Ha18 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :490
TrF3Ha19 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :491
TrF3Ha20 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :492
TrF3Ha21 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :493
TrF3Ha22 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :494
TrF3Ha23 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :495
TrF3Ha24 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :496
TrF3Ha25 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :497
TrF3Ha26 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :498
TrF3Ha27 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :499
TrF3Ha28 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :500
TrF3Ha29 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :501
TrF3Ha30 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :502
TrF3Ha31 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :503
TrF3Ha32 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :504
TrF3Ha33 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :505
TrF3Ha34 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :506
TrF3Ha35 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :507
TrF3Ha36 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :508
TrF3Ha37 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :509
TrF3Ha38 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :510
TrF3Ha39 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :511
TrF3Ha40 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :512
TrF3Ha41 : GGTGGTAAAAAGGGTGGTTTCATTGTCTCTAGTCATCTTCAAGGAGAAGCAGTGAAGGAT :513

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FIGURE 75 (cont)

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      *           500           *           520           *           540
TrF3Ha1 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :533
TrF3Ha2 : TGGAGAGAGGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :526
TrF3Ha3 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :539
TrF3Ha4 : TGGAGAGAGCTATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :492
TrF3Ha5 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :498
TrF3Ha6 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :491
TrF3Ha7 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :493
TrF3Ha8 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :492
TrF3Ha9 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :493
TrF3Ha10 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :486
TrF3Ha11 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :476
TrF3Ha12 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :450
TrF3Ha13 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :489
TrF3Ha14 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :491
TrF3Ha15 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :487
TrF3Ha16 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :489
TrF3Ha17 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :489
TrF3Ha18 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :489
TrF3Ha19 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :486
TrF3Ha20 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :486
TrF3Ha21 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :482
TrF3Ha22 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :479
TrF3Ha23 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :477
TrF3Ha24 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :478
TrF3Ha25 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :479
TrF3Ha26 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :482
TrF3Ha27 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :482
TrF3Ha28 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :470
TrF3Ha29 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :478
TrF3Ha30 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :476
TrF3Ha31 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :472
TrF3Ha32 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :469
TrF3Ha33 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :474
TrF3Ha34 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :473
TrF3Ha35 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :472
TrF3Ha36 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :472
TrF3Ha37 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :421
TrF3Ha38 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :268
TrF3Ha39 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :268
TrF3Ha40 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :268
TrF3Ha41 : TGGAGAGAGCTAGTGACATATTTTTCATACCCAATTAAACAAAGAGATTATTCAAGGTGG :268

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FIGURE 75 (cont)

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      *           560           *           580           *           600
TrF3Ha1 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTTAATGAAT : 586
TrF3Ha2 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTTAATGAAT : 586
TrF3Ha3 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTTAATGAAT : 599
TrF3Ha4 : ----- : -
TrF3Ha5 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTTAATGAAT : 558
TrF3Ha6 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTTAATGAAT : 551
TrF3Ha7 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTTAATGAAT : 553
TrF3Ha8 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTTAATGAAT : 552
TrF3Ha9 : ----- : -
TrF3Ha10 : ----- : -
TrF3Ha11 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTTAATGAAT : 546
TrF3Ha12 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTTAATGAAT : 536
TrF3Ha13 : ----- : -
TrF3Ha14 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTTAATGAAT : 549
TrF3Ha15 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTTAATGAAT : 551
TrF3Ha16 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTTAATGAAT : 547
TrF3Ha17 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTTAATGAAT : 549
TrF3Ha18 : ----- : -
TrF3Ha19 : ----- : -
TrF3Ha20 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTTAATGAAT : 546
TrF3Ha21 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTTAATGAAT : 546
TrF3Ha22 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTTAATGAAT : 542
TrF3Ha23 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTTAATGAAT : 539
TrF3Ha24 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTTAATGAAT : 535
TrF3Ha25 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTTAATGAAT : 538
TrF3Ha26 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTTAATGAAT : 539
TrF3Ha27 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTTAATGAAT : 542
TrF3Ha28 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTTAATGAAT : 542
TrF3Ha29 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTTAATGAAT : 530
TrF3Ha30 : ----- : -
TrF3Ha31 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTTAATGAAT : 539
TrF3Ha32 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTTAATGAAT : 536
TrF3Ha33 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTTAATGAAT : 532
TrF3Ha34 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTTAATGAAT : 529
TrF3Ha35 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTTAATGAAT : 534
TrF3Ha36 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTTAATGAAT : 533
TrF3Ha37 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTTAATGAAT : 532
TrF3Ha38 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTTAATGAAT : 532
TrF3Ha39 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTTAATGAAT : 481
TrF3Ha40 : CCAGACAAGCCAGAAGGATGGAAAGAGGTAACAGAAAAATACAGTGAAAACCTTAATGAAT : 328
TrF3Ha41 : ----- : -

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FIGURE 75 (cont)

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          *          620          *          640          *          660
TrF3Ha1 : ----- : -
TrF3Ha2 : TTAGCTTGCAG----- : 597
TrF3Ha3 : TTAGCTT----- : 605
TrF3Ha4 : ----- : -
TrF3Ha5 : TTAGCTTGCAAACTATTGGAAGTTTATCAGAAGCAATGGGTTAGAAAAAGAAGCTCTA : 618
TrF3Ha6 : TTAGCTTGCAAACTATTGGAAG----- : 573
TrF3Ha7 : TTAGCTTGCAAACTATTGGAAGTTTATCAGAAGCAATGGGTTAGAAAAAGAAGCTCTA : 613
TrF3Ha8 : TTAGCTTGCAAACTATTGGAAGTTTATCAGAAGCAATGGGTTAGAAAAAGAAGCTCTA : 612
TrF3Ha9 : ----- : -
TrF3Ha10 : ----- : -
TrF3Ha11 : TTAGCTTGCAAACTATTGGAAGTTTATCAGAAG----- : 580
TrF3Ha12 : TTAGCTTGCAAACTATTGGAAGTTTATCAGAAGCAATGGGTTAGAAAA----- : 586
TrF3Ha13 : ----- : -
TrF3Ha14 : TTAGCTTGCAAACTATTGGAAGTTTATCAGAAGCAATGGGTTAGAAAAAGAAGCTCTA : 609
TrF3Ha15 : TTAGCTTGCAAACTATTGGAAGTTTATCAG----- : 592
TrF3Ha16 : TTAGCTTGCAAACTATTGGAAGTTTATCAGAAGCAATGGGTTAGAAAAAGAAGCTCTA : 607
TrF3Ha17 : TTAGCTTGCAAACTATTGGAAGTTTATCAGAAGCAATGGGTT----- : 593
TrF3Ha18 : ----- : -
TrF3Ha19 : ----- : -
TrF3Ha20 : TTAGCTTGCAAACTATTGGAAGTTT----- : 572
TrF3Ha21 : TTAGCTTGCAAACTATTGGAAGTTTATC----- : 575
TrF3Ha22 : TTAGCTTGCAAACTATTGGAAGTTTATCAGAAGCAATGGGTTAGAAAAAGAG----- : 596
TrF3Ha23 : TTAGCTTGCAAACTATTGGAAGTTTATCAGAAGCAATGGGTTAGAAAAAGAAGCTCTA : 599
TrF3Ha24 : ----- : -
TrF3Ha25 : TTAGCTTGCAAACTATTGGAAGTT----- : 559
TrF3Ha26 : TTAGCTTGCAAACTATTGGAAGTTT----- : 565
TrF3Ha27 : TTAGCTTGCAAACTATTGGAAGTTTATCAGAAGCAATGGGTTAGAAAA----- : 591
TrF3Ha28 : TTAGCTTGCAAACTATTGGAAGTTTATCAGAAGCAATGGGTTAGAAAAAGAAGCTCTA : 602
TrF3Ha29 : TTAGCTTGCAAACTATTGGAAGTTTATCAGAAGCAATGGGTTAGAAAAAGAAGCTCTA : 590
TrF3Ha30 : ----- : -
TrF3Ha31 : TTAGCTTGCAAACTATTGGAAGTTTATCAG----- : 570
TrF3Ha32 : TTAGCTTGCAAACTATTGGAAGTTTATCAGAAGCAATGGGTTAGAAAAAGAAGCTCTA : 596
TrF3Ha33 : TTAGCTTGCAAACTATTGGAAGTTTATCAGAAGCAATGGGTTAGAAAAAGAAGCTCTA : 592
TrF3Ha34 : TTAGCTT----- : 536
TrF3Ha35 : TTAGCTTGCAAACTATTGGAAGTTTATCAGAAGCAAT----- : 572
TrF3Ha36 : TTAGCTTGCAAACTATTGGAAGTTTATCAGAAGCAATGG----- : 573
TrF3Ha37 : TTAGCTTGCAAACTATTGGAAGTTTATCAGAAGCAATGG----- : 573
TrF3Ha38 : TTAGCTTGCAAACTATTGGAAGTTTATCAGAAGCAATGGGTTAGAAAAAG----- : 584
TrF3Ha39 : TTAGCTTGCAAACTATTGGAAGTTTATCAGAAGCAATGGGTTAGAAAAAG----- : 529
TrF3Ha40 : TTAGCTTGCAAACTATTGGAAGTTTATCAGAAGCAATGGGTTAGAAAAAGAAGCTCTA : 388
TrF3Ha41 : ----- : -

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FIGURE 75 (cont)

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		*	680	*	700	*	720	
TrF3Ha1	:	-----	-----	-----	-----	-----	-----	:
TrF3Ha2	:	-----	-----	-----	-----	-----	-----	:
TrF3Ha3	:	-----	-----	-----	-----	-----	-----	:
TrF3Ha4	:	-----	-----	-----	-----	-----	-----	:
TrF3Ha5	:	ACAAAAGCATGTGTGATATGGATCAAAAAGTTGTTATAAAATTATTACCCAAAATGCCCT						: 678
TrF3Ha6	:	-----	-----	-----	-----	-----	-----	:
TrF3Ha7	:	ACAAAAGCATGTGTGATATGGATCAAAAAGTTGTTATAAAATTATTACCCAAAATGCCCT						: 673
TrF3Ha8	:	ACAAAAGCATGTGTGATATGGATCAAAAAGTTGTTATAAAATTATTACCCAAAATGCCCT						: 672
TrF3Ha9	:	-----	-----	-----	-----	-----	-----	:
TrF3Ha10	:	-----	-----	-----	-----	-----	-----	:
TrF3Ha11	:	-----	-----	-----	-----	-----	-----	:
TrF3Ha12	:	-----	-----	-----	-----	-----	-----	:
TrF3Ha13	:	-----	-----	-----	-----	-----	-----	:
TrF3Ha14	:	ACAAAAGCATGTGTGATATGGATCAAAAAGTTGTTATAAAATTATTACCCAAAATGCCCT						: 669
TrF3Ha15	:	-----	-----	-----	-----	-----	-----	:
TrF3Ha16	:	ACA						: 610
TrF3Ha17	:	-----	-----	-----	-----	-----	-----	:
TrF3Ha18	:	-----	-----	-----	-----	-----	-----	:
TrF3Ha19	:	-----	-----	-----	-----	-----	-----	:
TrF3Ha20	:	-----	-----	-----	-----	-----	-----	:
TrF3Ha21	:	-----	-----	-----	-----	-----	-----	:
TrF3Ha22	:	-----	-----	-----	-----	-----	-----	:
TrF3Ha23	:	ACAAAAGCATGTC						: 612
TrF3Ha24	:	-----	-----	-----	-----	-----	-----	:
TrF3Ha25	:	-----	-----	-----	-----	-----	-----	:
TrF3Ha26	:	-----	-----	-----	-----	-----	-----	:
TrF3Ha27	:	-----	-----	-----	-----	-----	-----	:
TrF3Ha28	:	ACAAAAG						: 609
TrF3Ha29	:	ACAAAAG						: 597
TrF3Ha30	:	-----	-----	-----	-----	-----	-----	:
TrF3Ha31	:	-----	-----	-----	-----	-----	-----	:
TrF3Ha32	:	ACAAAAGCATGT						: 608
TrF3Ha33	:	ACAAAAGCATGT						: 602
TrF3Ha34	:	-----	-----	-----	-----	-----	-----	:
TrF3Ha35	:	-----	-----	-----	-----	-----	-----	:
TrF3Ha36	:	-----	-----	-----	-----	-----	-----	:
TrF3Ha37	:	-----	-----	-----	-----	-----	-----	:
TrF3Ha38	:	-----	-----	-----	-----	-----	-----	:
TrF3Ha39	:	-----	-----	-----	-----	-----	-----	:
TrF3Ha40	:	ACAAAAGCATGTGTGATATGGATCAAAAAGTTGTTATAAAATTATTACCCAAAATGCCCT						: 448
TrF3Ha41	:	-----	-----	ATCAAAAAGTTGTTATAAAATTATTACCCAAAATGCCCT				: 38

FIGURE 75 (cont)

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	*	740	*	760	*	780	
TrF3Ha1 :	-----						:-
TrF3Ha2 :	-----						:-
TrF3Ha3 :	-----						:-
TrF3Ha4 :	-----						:-
TrF3Ha5 :	GAACCTGACCTC						:690
TrF3Ha6 :	-----						:-
TrF3Ha7 :	GAACCTGACCTC	GCACCTT	GCCTTAAACG	TCACACTG	ACCCNCA		:716
TrF3Ha8 :	GAACCTGACCTC	CACACTTGGCCTTAAACG	TCACACTG	ACCCCTGG	CACAN		:721
TrF3Ha9 :	-----						:-
TrF3Ha10 :	-----						:-
TrF3Ha11 :	-----						:-
TrF3Ha12 :	-----						:-
TrF3Ha13 :	-----						:-
TrF3Ha14 :	GAACCTGACCTC						:681
TrF3Ha15 :	-----						:-
TrF3Ha16 :	-----						:-
TrF3Ha17 :	-----						:-
TrF3Ha18 :	-----						:-
TrF3Ha19 :	-----						:-
TrF3Ha20 :	-----						:-
TrF3Ha21 :	-----						:-
TrF3Ha22 :	-----						:-
TrF3Ha23 :	-----						:-
TrF3Ha24 :	-----						:-
TrF3Ha25 :	-----						:-
TrF3Ha26 :	-----						:-
TrF3Ha27 :	-----						:-
TrF3Ha28 :	-----						:-
TrF3Ha29 :	-----						:-
TrF3Ha30 :	-----						:-
TrF3Ha31 :	-----						:-
TrF3Ha32 :	-----						:-
TrF3Ha33 :	-----						:-
TrF3Ha34 :	-----						:-
TrF3Ha35 :	-----						:-
TrF3Ha36 :	-----						:-
TrF3Ha37 :	-----						:-
TrF3Ha38 :	-----						:-
TrF3Ha39 :	-----						:-
TrF3Ha40 :	GAACCTGACCTC	CACACTTGGCCTTAAACG	TCACACTG	ACCCCTGG	CACAA	TACTCTTTTC	:508
TrF3Ha41 :	GAACCTGACCTC	CACACTTGGCCTTAAAC	TCACACTG	ACCCCTGG	CACAA	TACTCTTTTC	:98

FIGURE 75 (cont)

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	*	800	*	820	*	840	
TrF3Ha1	:	-----	:	-----	:	-----	:
TrF3Ha2	:	-----	:	-----	:	-----	:
TrF3Ha3	:	-----	:	-----	:	-----	:
TrF3Ha4	:	-----	:	-----	:	-----	:
TrF3Ha5	:	-----	:	-----	:	-----	:
TrF3Ha6	:	-----	:	-----	:	-----	:
TrF3Ha7	:	-----	:	-----	:	-----	:
TrF3Ha8	:	-----	:	-----	:	-----	:
TrF3Ha9	:	-----	:	-----	:	-----	:
TrF3Ha10	:	-----	:	-----	:	-----	:
TrF3Ha11	:	-----	:	-----	:	-----	:
TrF3Ha12	:	-----	:	-----	:	-----	:
TrF3Ha13	:	-----	:	-----	:	-----	:
TrF3Ha14	:	-----	:	-----	:	-----	:
TrF3Ha15	:	-----	:	-----	:	-----	:
TrF3Ha16	:	-----	:	-----	:	-----	:
TrF3Ha17	:	-----	:	-----	:	-----	:
TrF3Ha18	:	-----	:	-----	:	-----	:
TrF3Ha19	:	-----	:	-----	:	-----	:
TrF3Ha20	:	-----	:	-----	:	-----	:
TrF3Ha21	:	-----	:	-----	:	-----	:
TrF3Ha22	:	-----	:	-----	:	-----	:
TrF3Ha23	:	-----	:	-----	:	-----	:
TrF3Ha24	:	-----	:	-----	:	-----	:
TrF3Ha25	:	-----	:	-----	:	-----	:
TrF3Ha26	:	-----	:	-----	:	-----	:
TrF3Ha27	:	-----	:	-----	:	-----	:
TrF3Ha28	:	-----	:	-----	:	-----	:
TrF3Ha29	:	-----	:	-----	:	-----	:
TrF3Ha30	:	-----	:	-----	:	-----	:
TrF3Ha31	:	-----	:	-----	:	-----	:
TrF3Ha32	:	-----	:	-----	:	-----	:
TrF3Ha33	:	-----	:	-----	:	-----	:
TrF3Ha34	:	-----	:	-----	:	-----	:
TrF3Ha35	:	-----	:	-----	:	-----	:
TrF3Ha36	:	-----	:	-----	:	-----	:
TrF3Ha37	:	-----	:	-----	:	-----	:
TrF3Ha38	:	-----	:	-----	:	-----	:
TrF3Ha39	:	-----	:	-----	:	-----	:
TrF3Ha40	:	CTTCAAGATCAAGTTGGTGGCTTCAAGCTACCAAGATAATGGTAAGACGTGGATTAC	:	-----	:	-----	: 568
TrF3Ha41	:	CTTCAAGATCAAGTTGGTGGCTTCAAGCTACCAAGATAATGGTAAGACGTGGATTAC	:	-----	:	-----	: 158

FIGURE 75 (cont)

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	*	860	*	880	*	900	
TrF3Ha1 :	-----		-----		-----		:-
TrF3Ha2 :	-----		-----		-----		:-
TrF3Ha3 :	-----		-----		-----		:-
TrF3Ha4 :	-----		-----		-----		:-
TrF3Ha5 :	-----		-----		-----		:-
TrF3Ha6 :	-----		-----		-----		:-
TrF3Ha7 :	-----		-----		-----		:-
TrF3Ha8 :	-----		-----		-----		:-
TrF3Ha9 :	-----		-----		-----		:-
TrF3Ha10 :	-----		-----		-----		:-
TrF3Ha11 :	-----		-----		-----		:-
TrF3Ha12 :	-----		-----		-----		:-
TrF3Ha13 :	-----		-----		-----		:-
TrF3Ha14 :	-----		-----		-----		:-
TrF3Ha15 :	-----		-----		-----		:-
TrF3Ha16 :	-----		-----		-----		:-
TrF3Ha17 :	-----		-----		-----		:-
TrF3Ha18 :	-----		-----		-----		:-
TrF3Ha19 :	-----		-----		-----		:-
TrF3Ha20 :	-----		-----		-----		:-
TrF3Ha21 :	-----		-----		-----		:-
TrF3Ha22 :	-----		-----		-----		:-
TrF3Ha23 :	-----		-----		-----		:-
TrF3Ha24 :	-----		-----		-----		:-
TrF3Ha25 :	-----		-----		-----		:-
TrF3Ha26 :	-----		-----		-----		:-
TrF3Ha27 :	-----		-----		-----		:-
TrF3Ha28 :	-----		-----		-----		:-
TrF3Ha29 :	-----		-----		-----		:-
TrF3Ha30 :	-----		-----		-----		:-
TrF3Ha31 :	-----		-----		-----		:-
TrF3Ha32 :	-----		-----		-----		:-
TrF3Ha33 :	-----		-----		-----		:-
TrF3Ha34 :	-----		-----		-----		:-
TrF3Ha35 :	-----		-----		-----		:-
TrF3Ha36 :	-----		-----		-----		:-
TrF3Ha37 :	-----		-----		-----		:-
TrF3Ha38 :	-----		-----		-----		:-
TrF3Ha39 :	-----		-----		-----		:-
TrF3Ha40 :	-----		-----		-----		:-
TrF3Ha41 :	-----		-----		-----		:-

GTTCAACCAGTTGAAGGTGCTTTTGTGTTAATCTTGGAGACCATGGTCACATATCTAAGT 628
 GTTCAACCAGTTGAAGGTGCTTTTGTGTTAATCTTGGAGACCATGGTCATATCTAAGT 218

FIGURE 75 (cont)

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	920	*	940	*	960
TrF3Ha1	:				:
TrF3Ha2	:				:
TrF3Ha3	:				:
TrF3Ha4	:				:
TrF3Ha5	:				:
TrF3Ha6	:				:
TrF3Ha7	:				:
TrF3Ha8	:				:
TrF3Ha9	:				:
TrF3Ha10	:				:
TrF3Ha11	:				:
TrF3Ha12	:				:
TrF3Ha13	:				:
TrF3Ha14	:				:
TrF3Ha15	:				:
TrF3Ha16	:				:
TrF3Ha17	:				:
TrF3Ha18	:				:
TrF3Ha19	:				:
TrF3Ha20	:				:
TrF3Ha21	:				:
TrF3Ha22	:				:
TrF3Ha23	:				:
TrF3Ha24	:				:
TrF3Ha25	:				:
TrF3Ha26	:				:
TrF3Ha27	:				:
TrF3Ha28	:				:
TrF3Ha29	:				:
TrF3Ha30	:				:
TrF3Ha31	:				:
TrF3Ha32	:				:
TrF3Ha33	:				:
TrF3Ha34	:				:
TrF3Ha35	:				:
TrF3Ha36	:				:
TrF3Ha37	:				:
TrF3Ha38	:				:
TrF3Ha39	:				:
TrF3Ha40	:				:
TrF3Ha41	:				:

ATGGACGGTTCAAAAATGCTGACCAACAGCAGTGGTGAATTCGAACACACGCCGNTTT
ATGGACGGTTCAAAAATGCTGACCACCAAGCAGTGGTGAATTCGAACACACGCCGNTTT

FIGURE 75 (cont)

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	*	980	*	1000	*	1020	
TrF3Ha1 :	-----		-----		-----		:-
TrF3Ha2 :	-----		-----		-----		:-
TrF3Ha3 :	-----		-----		-----		:-
TrF3Ha4 :	-----		-----		-----		:-
TrF3Ha5 :	-----		-----		-----		:-
TrF3Ha6 :	-----		-----		-----		:-
TrF3Ha7 :	-----		-----		-----		:-
TrF3Ha8 :	-----		-----		-----		:-
TrF3Ha9 :	-----		-----		-----		:-
TrF3Ha10 :	-----		-----		-----		:-
TrF3Ha11 :	-----		-----		-----		:-
TrF3Ha12 :	-----		-----		-----		:-
TrF3Ha13 :	-----		-----		-----		:-
TrF3Ha14 :	-----		-----		-----		:-
TrF3Ha15 :	-----		-----		-----		:-
TrF3Ha16 :	-----		-----		-----		:-
TrF3Ha17 :	-----		-----		-----		:-
TrF3Ha18 :	-----		-----		-----		:-
TrF3Ha19 :	-----		-----		-----		:-
TrF3Ha20 :	-----		-----		-----		:-
TrF3Ha21 :	-----		-----		-----		:-
TrF3Ha22 :	-----		-----		-----		:-
TrF3Ha23 :	-----		-----		-----		:-
TrF3Ha24 :	-----		-----		-----		:-
TrF3Ha25 :	-----		-----		-----		:-
TrF3Ha26 :	-----		-----		-----		:-
TrF3Ha27 :	-----		-----		-----		:-
TrF3Ha28 :	-----		-----		-----		:-
TrF3Ha29 :	-----		-----		-----		:-
TrF3Ha30 :	-----		-----		-----		:-
TrF3Ha31 :	-----		-----		-----		:-
TrF3Ha32 :	-----		-----		-----		:-
TrF3Ha33 :	-----		-----		-----		:-
TrF3Ha34 :	-----		-----		-----		:-
TrF3Ha35 :	-----		-----		-----		:-
TrF3Ha36 :	-----		-----		-----		:-
TrF3Ha37 :	-----		-----		-----		:-
TrF3Ha38 :	-----		-----		-----		:-
TrF3Ha39 :	-----		-----		-----		:-
TrF3Ha40 :	-----		-----		-----		:-
TrF3Ha41 :	-----		-----		-----		:-
	TC	CAATAGC	CA				:698
	TC	CAATAGCAACATTT	C	AAAA	TCCAGCTCCC	GATGCAACTGTATACCC	TTTGAAGATTAGT
							:338

FIGURE 75 (cont)

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	*	1040	*	1060	*	1080	
TrF3Ha1	:	-----	:	-----	:	-----	:
TrF3Ha2	:	-----	:	-----	:	-----	:
TrF3Ha3	:	-----	:	-----	:	-----	:
TrF3Ha4	:	-----	:	-----	:	-----	:
TrF3Ha5	:	-----	:	-----	:	-----	:
TrF3Ha6	:	-----	:	-----	:	-----	:
TrF3Ha7	:	-----	:	-----	:	-----	:
TrF3Ha8	:	-----	:	-----	:	-----	:
TrF3Ha9	:	-----	:	-----	:	-----	:
TrF3Ha10	:	-----	:	-----	:	-----	:
TrF3Ha11	:	-----	:	-----	:	-----	:
TrF3Ha12	:	-----	:	-----	:	-----	:
TrF3Ha13	:	-----	:	-----	:	-----	:
TrF3Ha14	:	-----	:	-----	:	-----	:
TrF3Ha15	:	-----	:	-----	:	-----	:
TrF3Ha16	:	-----	:	-----	:	-----	:
TrF3Ha17	:	-----	:	-----	:	-----	:
TrF3Ha18	:	-----	:	-----	:	-----	:
TrF3Ha19	:	-----	:	-----	:	-----	:
TrF3Ha20	:	-----	:	-----	:	-----	:
TrF3Ha21	:	-----	:	-----	:	-----	:
TrF3Ha22	:	-----	:	-----	:	-----	:
TrF3Ha23	:	-----	:	-----	:	-----	:
TrF3Ha24	:	-----	:	-----	:	-----	:
TrF3Ha25	:	-----	:	-----	:	-----	:
TrF3Ha26	:	-----	:	-----	:	-----	:
TrF3Ha27	:	-----	:	-----	:	-----	:
TrF3Ha28	:	-----	:	-----	:	-----	:
TrF3Ha29	:	-----	:	-----	:	-----	:
TrF3Ha30	:	-----	:	-----	:	-----	:
TrF3Ha31	:	-----	:	-----	:	-----	:
TrF3Ha32	:	-----	:	-----	:	-----	:
TrF3Ha33	:	-----	:	-----	:	-----	:
TrF3Ha34	:	-----	:	-----	:	-----	:
TrF3Ha35	:	-----	:	-----	:	-----	:
TrF3Ha36	:	-----	:	-----	:	-----	:
TrF3Ha37	:	-----	:	-----	:	-----	:
TrF3Ha38	:	-----	:	-----	:	-----	:
TrF3Ha39	:	-----	:	-----	:	-----	:
TrF3Ha40	:	-----	:	-----	:	-----	:
TrF3Ha41	:	GAGGGTGAAAAATCTGTGTGGAAGAACAATGACITTTTGCCTGAAATGTATAGAAAGGAAC					:398

FIGURE 75 (cont)

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		*	1100	*	1120	*	1140	
TrF3Ha1	:	-----		-----		-----		:
TrF3Ha2	:	-----		-----		-----		:
TrF3Ha3	:	-----		-----		-----		:
TrF3Ha4	:	-----		-----		-----		:
TrF3Ha5	:	-----		-----		-----		:
TrF3Ha6	:	-----		-----		-----		:
TrF3Ha7	:	-----		-----		-----		:
TrF3Ha8	:	-----		-----		-----		:
TrF3Ha9	:	-----		-----		-----		:
TrF3Ha10	:	-----		-----		-----		:
TrF3Ha11	:	-----		-----		-----		:
TrF3Ha12	:	-----		-----		-----		:
TrF3Ha13	:	-----		-----		-----		:
TrF3Ha14	:	-----		-----		-----		:
TrF3Ha15	:	-----		-----		-----		:
TrF3Ha16	:	-----		-----		-----		:
TrF3Ha17	:	-----		-----		-----		:
TrF3Ha18	:	-----		-----		-----		:
TrF3Ha19	:	-----		-----		-----		:
TrF3Ha20	:	-----		-----		-----		:
TrF3Ha21	:	-----		-----		-----		:
TrF3Ha22	:	-----		-----		-----		:
TrF3Ha23	:	-----		-----		-----		:
TrF3Ha24	:	-----		-----		-----		:
TrF3Ha25	:	-----		-----		-----		:
TrF3Ha26	:	-----		-----		-----		:
TrF3Ha27	:	-----		-----		-----		:
TrF3Ha28	:	-----		-----		-----		:
TrF3Ha29	:	-----		-----		-----		:
TrF3Ha30	:	-----		-----		-----		:
TrF3Ha31	:	-----		-----		-----		:
TrF3Ha32	:	-----		-----		-----		:
TrF3Ha33	:	-----		-----		-----		:
TrF3Ha34	:	-----		-----		-----		:
TrF3Ha35	:	-----		-----		-----		:
TrF3Ha36	:	-----		-----		-----		:
TrF3Ha37	:	-----		-----		-----		:
TrF3Ha38	:	-----		-----		-----		:
TrF3Ha39	:	-----		-----		-----		:
TrF3Ha40	:	-----		-----		-----		:
TrF3Ha41	:	ATGACCAAGACCTTGAAATGCTAGGATGAAGAACTGGCTAAGGAACAACAACCTTAGG						: 458

FIGURE 75 (cont)

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	*	1160	*	1180	*	1200	
TrF3Ha1 :	-----		-----		-----		:-
TrF3Ha2 :	-----		-----		-----		:-
TrF3Ha3 :	-----		-----		-----		:-
TrF3Ha4 :	-----		-----		-----		:-
TrF3Ha5 :	-----		-----		-----		:-
TrF3Ha6 :	-----		-----		-----		:-
TrF3Ha7 :	-----		-----		-----		:-
TrF3Ha8 :	-----		-----		-----		:-
TrF3Ha9 :	-----		-----		-----		:-
TrF3Ha10 :	-----		-----		-----		:-
TrF3Ha11 :	-----		-----		-----		:-
TrF3Ha12 :	-----		-----		-----		:-
TrF3Ha13 :	-----		-----		-----		:-
TrF3Ha14 :	-----		-----		-----		:-
TrF3Ha15 :	-----		-----		-----		:-
TrF3Ha16 :	-----		-----		-----		:-
TrF3Ha17 :	-----		-----		-----		:-
TrF3Ha18 :	-----		-----		-----		:-
TrF3Ha19 :	-----		-----		-----		:-
TrF3Ha20 :	-----		-----		-----		:-
TrF3Ha21 :	-----		-----		-----		:-
TrF3Ha22 :	-----		-----		-----		:-
TrF3Ha23 :	-----		-----		-----		:-
TrF3Ha24 :	-----		-----		-----		:-
TrF3Ha25 :	-----		-----		-----		:-
TrF3Ha26 :	-----		-----		-----		:-
TrF3Ha27 :	-----		-----		-----		:-
TrF3Ha28 :	-----		-----		-----		:-
TrF3Ha29 :	-----		-----		-----		:-
TrF3Ha30 :	-----		-----		-----		:-
TrF3Ha31 :	-----		-----		-----		:-
TrF3Ha32 :	-----		-----		-----		:-
TrF3Ha33 :	-----		-----		-----		:-
TrF3Ha34 :	-----		-----		-----		:-
TrF3Ha35 :	-----		-----		-----		:-
TrF3Ha36 :	-----		-----		-----		:-
TrF3Ha37 :	-----		-----		-----		:-
TrF3Ha38 :	-----		-----		-----		:-
TrF3Ha39 :	-----		-----		-----		:-
TrF3Ha40 :	-----		-----		-----		:-
TrF3Ha41 :	GACTTGGAGGAGAACAGACTAAATATGAGGCCAAACCTTTGAATGAGATCTTTGCCTAT						:518

FIGURE 75 (cont)

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	*	1220	*	1240	*	1260	
TrF3Ha1	:	-----		-----		-----	:
TrF3Ha2	:	-----		-----		-----	:
TrF3Ha3	:	-----		-----		-----	:
TrF3Ha4	:	-----		-----		-----	:
TrF3Ha5	:	-----		-----		-----	:
TrF3Ha6	:	-----		-----		-----	:
TrF3Ha7	:	-----		-----		-----	:
TrF3Ha8	:	-----		-----		-----	:
TrF3Ha9	:	-----		-----		-----	:
TrF3Ha10	:	-----		-----		-----	:
TrF3Ha11	:	-----		-----		-----	:
TrF3Ha12	:	-----		-----		-----	:
TrF3Ha13	:	-----		-----		-----	:
TrF3Ha14	:	-----		-----		-----	:
TrF3Ha15	:	-----		-----		-----	:
TrF3Ha16	:	-----		-----		-----	:
TrF3Ha17	:	-----		-----		-----	:
TrF3Ha18	:	-----		-----		-----	:
TrF3Ha19	:	-----		-----		-----	:
TrF3Ha20	:	-----		-----		-----	:
TrF3Ha21	:	-----		-----		-----	:
TrF3Ha22	:	-----		-----		-----	:
TrF3Ha23	:	-----		-----		-----	:
TrF3Ha24	:	-----		-----		-----	:
TrF3Ha25	:	-----		-----		-----	:
TrF3Ha26	:	-----		-----		-----	:
TrF3Ha27	:	-----		-----		-----	:
TrF3Ha28	:	-----		-----		-----	:
TrF3Ha29	:	-----		-----		-----	:
TrF3Ha30	:	-----		-----		-----	:
TrF3Ha31	:	-----		-----		-----	:
TrF3Ha32	:	-----		-----		-----	:
TrF3Ha33	:	-----		-----		-----	:
TrF3Ha34	:	-----		-----		-----	:
TrF3Ha35	:	-----		-----		-----	:
TrF3Ha36	:	-----		-----		-----	:
TrF3Ha37	:	-----		-----		-----	:
TrF3Ha38	:	-----		-----		-----	:
TrF3Ha39	:	-----		-----		-----	:
TrF3Ha40	:	-----		-----		-----	:
TrF3Ha41	:	-----		-----		-----	:
TAAATTAGTCTTAATTTAAATAATTAAATAAATTTTAGACTTAAATTTACATAATAATTT							:578

FIGURE 75 (cont)

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```

TrF3Ha1  : - : -
TrF3Ha2  : - : -
TrF3Ha3  : - : -
TrF3Ha4  : - : -
TrF3Ha5  : - : -
TrF3Ha6  : - : -
TrF3Ha7  : - : -
TrF3Ha8  : - : -
TrF3Ha9  : - : -
TrF3Ha10 : - : -
TrF3Ha11 : - : -
TrF3Ha12 : - : -
TrF3Ha13 : - : -
TrF3Ha14 : - : -
TrF3Ha15 : - : -
TrF3Ha16 : - : -
TrF3Ha17 : - : -
TrF3Ha18 : - : -
TrF3Ha19 : - : -
TrF3Ha20 : - : -
TrF3Ha21 : - : -
TrF3Ha22 : - : -
TrF3Ha23 : - : -
TrF3Ha24 : - : -
TrF3Ha25 : - : -
TrF3Ha26 : - : -
TrF3Ha27 : - : -
TrF3Ha28 : - : -
TrF3Ha29 : - : -
TrF3Ha30 : - : -
TrF3Ha31 : - : -
TrF3Ha32 : - : -
TrF3Ha33 : - : -
TrF3Ha34 : - : -
TrF3Ha35 : - : -
TrF3Ha36 : - : -
TrF3Ha37 : - : -
TrF3Ha38 : - : -
TrF3Ha39 : - : -
TrF3Ha40 : - : -
TrF3Ha41 : 579

```

FIGURE 75 (cont)

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TrF3Hb : * 20 * 40 * 60
 : GNAGCATAAACATAAAACCTGTNCCCGATTNATGTAACACAACTCTCCCCTTTTCTTATTAC : 60

TrF3Hb : * 80 * 100 * 120
 : AAGTAAATACCATTAACACAAATAATATGAATACCATAATCTTGAATCATACAAACAACCT : 120

TrF3Hb : * 140 * 160 * 180
 : TGGATCAAACAAAACAACCATGGTTGATCTAGAAACAGAACCAAGTTCACCATTTAT : 180

TrF3Hb : * 200 * 220 * 240
 : TCAATCCCCAGAACACAGACCAAAATCCTCAATAATCATTTGCTGAAGGTATCCCTCTAAT : 240

TrF3Hb : * 260 * 280 * 300
 : TGATCTCACTCCTATAAACTACAAAGATGAAATCATCACCAACCCACTTTCCATTGAAGA : 300

TrF3Hb : * 320 * 340 * 360
 : CTTAGTCAAAGAAATAGGCAAAGCATGTAAAGAATGGGGTTTCTTTCAAGTGATTAAATCA : 360

TrF3Hb : * 380 * 400 * 420
 : CAAAGTTCTCTTTGGATAACGTGAAAGGATGAAGAATCTTCAAAGAAGTTTGTGAACT : 420

TrF3Hb : * 440 * 460 * 480
 : TAGTTTGAGAGAAAACTTAAGGTGAGAAAGAGATGAAGTTAATTTGCTTGGTTATTTTGA : 480

TrF3Hb : * 500 * 520 * 540
 : AGCTGAGCATACAAAAAATGTTAGGGACTGGAAGGAAATTTATGATTTTAATGTGCAACA : 540

TrF3Hb : * 560 * 580 * 600
 : ACCAACTTTTATACCACCTTCGGATGACCAAAATTTTCAGTTTCAATGGGAAAAATCGATG : 600

TrF3Hb : G : 601

FIGURE 76

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TrF3Hb : MNTIILNHTNNLGSNKTTTMVDLETPSPFFIQSPPEHRPKSSIIIAEGIPLIDLTPINVK : 60

TrF3Hb : DEIIITNPLSIEDLVKEIGKACKEWGFFQVINHKVPLDKRERIESSKKPFELSLEEKLV : 120

TrF3Hb : RRDEVNLLGYFEAEHTKNVRDWNKEIYDFNVQQPTFIPPSDDQSFOFQWENRW : 172

FIGURE 77

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```

      *           20           *           40           *           60
TrF3Hc : TTACCCAACAAATNATGTGTGACTGATGTTAGTGTACCAGGAAAGATGGGAGAGGTGGATC : 60

      *           80           *           100          *           120
TrF3Hc : CAGCCTTTCTTCAAATCCAGAAAATAGGCCAAAACCTTCCATAATCCAAGCTGAAGGAATT : 120

      *           140          *           160          *           180
TrF3Hc : CCTGTAATCAATCTCTCCCCATTAATTACCACACAGTTCAAGACTCCTCTGCCATTGAA : 180

      *           200          *           220          *           240
TrF3Hc : AGCTTAGTCAAAGAAATAGGAAATGCTTGCAAGGAATGGGGTTTCTCCAAGTAACAAAC : 240

      *           260          *           280          *           300
TrF3Hc : CATGGTGTCCCTCTAAATCTAAGGCTCAGACTCGAGGAAGCTACCAAGTTTCTTTGCA : 300

      *           320          *           340          *           360
TrF3Hc : CAGAGTTTGGAGGAGAAGAGGAAGCTTACCGTAGATGATAACAGTTTGCCTGGTTATCAT : 360

      *           380          *           400          *           420
TrF3Hc : GATACAGAGCACACCAAGAATGTGCAGAGACTGGRAAGAGTGTGTGATTTTATCCAAA : 420

      *           440          *           460          *           480
TrF3Hc : GACCCCACTTTGATTCCCTCTGAATTCTGATGAACATGATGATCGAGTCACTCAATGGACT : 480

      *           500          *           520          *           540
TrF3Hc : AATCCATCCCTCAATATCCTCCAAACTTCAAAGTTATTTTGGGAAGATATATTAAAGAG : 540

      *           560          *           580
TrF3Hc : ATGGAAGAGCTAGGCTTTAAGTTGCTAGAGCTTATAGCTTTGAGC : 585

```

FIGURE 78

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```

      *      20      *      40      *      60
TrF3Hc : MLVYQERWERWQLSSNPENRPKLSITQAEGIPVINLSPLIHHTVQDSSAIESLVKEIGN : 60

      *      80      *      100     *      120
TrF3Hc : ACKEWGFFQVTNHGVPLNLRRLRLLEEATKVFFAQSLSEKRKLTVDDNSLPGYHDTHTKNV : 120

      *      140     *      160     *      180
TrF3Hc : RDMKEVFDFLSKDPTLILPLNSDEHDDRVTQWTNPSPQYPPNFKVILEEYIKEMENLGFKL : 180

TrF3Hc : LEDIALS : 187

```

FIGURE 79

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```

      *           20           *           40           *           60
TrF3'Ha : GGGAAATGGTGGAGGCGAATGTGACCCTAGGGCTGATGAATTAGTAATGGTAGTTGAGCTT : 60

      *           80           *           100          *           120
TrF3'Ha : ATGSGCGTTAGCTGGAGTTTTCAATATTGGTGATTTTGTTCCTGCCTTGGAAATGGTTAGAT :120

      *           140          *           160           *           180
TrF3'Ha : ATTC AAGGTGTACAAGGAAAAATGAAGAAATTACATAAAAGATTGTATGCATTTTTAACT :180

      *           200          *           220           *           240
TrF3'Ha : AGCATTATTGAAGATCAGATGATTTCCAAGAGTGAGAGCATATATGACTTATTGAGTACG :240

      *           260          *           280           *           300
TrF3'Ha : TTGTTATCACTAAAAGAAAAAGTTGATGAGGATGGTGACAACTTAATGATACTGAGATC :300

      *           320          *           340           *           360
TrF3'Ha : AAAGCATTACTCTTGAACATGTTCCACAGCTGGAACAGACACATCATCAAGCACAAACAGAG :360

      *           380          *           400           *           420
TrF3'Ha : TGGGCTATTGCTGAACTAATAAAAAATCCAAACTAATGATTCGTGTCAAAATGAGTTG :420

      *           440          *           460           *           480
TrF3'Ha : GACACTGTTGTGGGCCGAGACAAGCTTGTAAGTGAACAAGACTTGGCCCATCTTCTCTTAC :480

      *           500          *           520           *           540
TrF3'Ha : TTAGAGGCTGTAATAAAGGAGACATTTTCGTCTCCATCCATCAACCCCTGTTTCTCTCCCA :540

      *           560          *           580           *           600
TrF3'Ha : CGTGTGCAACAAATAGTTGTGAAATCCTCGACTATCAGATTCCCAAGGTGCAACTCTC :600

TrF3'Ha : TTGG : 604

```

FIGURE 80

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```

      *           20           *           40           *           60
TrF3'Ha : GNGGGECDPRADELVMVVELMALAGVFNIGDFVPALEWLDIQGVQGMKKLHKRFDAFLT : 60

      *           80           *           100          *           120
TrF3'Ha : SIIEDHMISKSEKHNDLLSTLLSLKEKVDGDKLNDTEIKALLNMPTAGTDTSSSTE :120

      *           140          *           160          *           180
TrF3'Ha : WAIAELIKNPKLMIRVQNELDTVVGRDKLVTEQDLAHLPLYEAVIKETFRLHPSTPLSLP :180

      *           200
TrF3'Ha : RVATNSCEILDYHIPKGATLL :201

```

FIGURE 81

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```

      *           20           *           40           *           60
TrF3'Ha1 : EGGAATGGTGGAGGCGAATGTGACCCTAGGGCTGATGAA'TTTAAGTAATGGTACTTGAGC : 60
TrF3'Ha2 : ---AATGGTGGAGCGCAATGTGACCCTAGGGCTGATGAA'TTTAAGTAATGGTACTTGAGC : 57

      *           80           *           100          *           120
TrF3'Ha1 : TTATGGCGTTAGCTGGAGTTTTC AATAT TGGTGAT'TTIG'TCCTGCTTTGGAATGGTTAG :120
TrF3'Ha2 : TTATGGCGTTAGCTGGAGTTTTC AATAT TGGTGAT'TTIG'TCCTGCTTTGGAATGGTTAG :117

      *           140          *           160           *           180
TrF3'Ha1 : ATATTCAAGGTGTACAAGGAAAAATGAAGAAATACATAAAAGATTTGATGCATTTTAA :180
TrF3'Ha2 : ATATTCAAGGTGTACAAGGAAAAATGAAGAAATACATAAAAGATTTGATGCATTTTAA :177

      *           200          *           220           *           240
TrF3'Ha1 : CTAGCATTATTGAAGATCACATGATTTCCAAGAGTGAGAAGCATAATGACTTATTGAGT :240
TrF3'Ha2 : CTAGCATTATTGAAGATCACATGATTTCCAAGAGTGAGAAGCATAATGACTTATTGAGT :237

      *           260          *           280           *           300
TrF3'Ha1 : CGTTGTTTACACTAAAGAAAAAGTTGATGAGGATGGTGACAAACTTAATGATACTGAG :300
TrF3'Ha2 : CGTTGTTTACACTAAAGAAAAAGTTGATGAGGATGGTGACAAACTTAATGATACTGAG :297

      *           320          *           340           *           360
TrF3'Ha1 : TCAAAGCATTACTCTTGAACATGTTACAGCTGGAACAGACACATCATCAAGCACAAAG :360
TrF3'Ha2 : TCAAAGCATTACTCTTGAACATGTTACAGCTGGAACAGACACATCATCAAGCACAAAG :357

      *           380          *           400           *           420
TrF3'Ha1 : AGTGGGCTATTGCTGAACATAATAAAAAATCCAAAACTAATGATTCGTGTTCAAATGACT :420
TrF3'Ha2 : AGTGGGCTATTGCTGAACATAATAAAAAATCCAAAACTAATGATTCGTGTTCAAATGACT :417

      *           440          *           460           *           480
TrF3'Ha1 : TGGACACTGTTGTGGGCCCGAGACAAGCTTTGTAAC TGAACAAGACTTTGGCCCATCTTCCTT :480
TrF3'Ha2 : TGGACACTGTTGTGGGCCCGAGACAAGCTTTGTAAC TGAACAAGACTTTGGCCCATCTTCCTT :477

      *           500          *           520           *           540
TrF3'Ha1 : ACTTAGAGGCTGTAATAAAGGAGACATTTGCTCTCCATCCATCAACCCCTCTTTCTCTCC :540
TrF3'Ha2 : ACTTAGAGGCTGTAATAAAGGAGACATTTGCTCTCCATCCATCAACCCCTCTTTCTCTCC :537

      *           560          *           580           *           600
TrF3'Ha1 : CACGTGTTGCAACAAATAGTTGTGAAATCCTCGACTATCAC :581
TrF3'Ha2 : CACGTGTTGCAACAAATAGTTGTGAAATCCTCGACTATCAC :597

TrF3'Ha1 : ----- : -
TrF3'Ha2 : ACTTGG : 603

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FIGURE 82

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      *           20           *           40           *           60
TrPALa : GNAGGAAATTTCAACTAAATATGCCTTTAATTCTTTNINATANATNTTTGAATTTTCNTT : 60

      *           80           *           100          *           120
TrPALa : CTCCTAAAAATTCTATAGCTACCACATCANCACACATAACANNAATTAGAATATATTN : 120

      *           140          *           160          *           180
TrPALa : TATNTACTATTTTAAGATATGGAAGTAGTAGCAGCAGCAATCACAAAAACAATGGCAAG : 180

      *           200          *           220          *           240
TrPALa : ATTGATTCATTTTGCTTGAATCATGCTAATGCTAATAACATGAAAGTGAATGGTGTGAT : 240

      *           260          *           280          *           300
TrPALa : CCTTTGAATTGGGGTGTGGCTGCTGAGGCAATGAAGGGAAGTCACTTGGATGAGGTGAAG : 300

      *           320          *           340          *           360
TrPALa : CGTATGGTGGAGGAATACCGGAAACCGGTTGTCCGTCTTGGTGGCGAGACACTGACGATT : 360

      *           380          *           400          *           420
TrPALa : TCTCAGGTGGCTGCCATTGCTGCACACGATGGTGCAACGGTGGAGCTATCGGAATCTGCT : 420

      *           440          *           460          *           480
TrPALa : AGAGCCGCGCTTTAAGGCGAGCAGTGACTGGGTTATGGAGAGTATGAACAAAGGTACAGAC : 480

      *           500          *           520          *           540
TrPALa : AGTTATGGTGTCACTACAGGGTTCGGCGCTACCTCGCACC GCCGAACCAACAAAGGTGGT : 540

      *           560          *           580          *           600
TrPALa : GCTTTGCAGAAAGAGCTCATAAGGTTNTTTTGAATGCAGGAATATTTGGAATGGAACNTG : 600

      *           620
TrPALa : AGACAAAGCCACACACTACCC : 621

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FIGURE 83

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      *           20           *           40           *           60
TrPALa : MEVVAAAITKNNKGKIDSPCLNHANANNMKVNGADPLNWGVAAEAMKGSHLDEVKRMVEEY : 60

      *           80           *           100          *           120
TrPALa : RKPVVRLGGETLTISQVAAIAAHGATVELSESARAGVKASSDWVMESMNMKGTDSYGVTT : 120

      *           140          *
TrPALa : GFGATSHRRTKQGGALQKELIRFECRNIWKWNRQSHTLP : 159

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FIGURE 84

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      *           20           *           40           *           60
TrPALa1:  GNNCGGAAATTCCAACTAAATATGGCTTTAAATCTTTNTNATANATNTTTGAATTTCCCTT : 60
TrPALa2:  CGAGGAAATTCCAACTAAATATTCCTTTAAATCTTTTATNATANATNTTTGAATTTCTT : 60
TrPALa3:  -----TCAAGAAATACACCTTTNNNTCTTTNTTATNTNTTTTATTTCCTT : 50

      *           80           *           100          *           120
TrPALa1:  CTCCTCAAAAATTCCTATAGCTACCAACATCANCACAACATAACANNAATTAAGAAAATATTN :120
TrPALa2:  CTCCTCAAAAATTCCTATAGCTACCAACATCANCACAACATAACANNAATTAAGAAAATATTN :120
TrPALa3:  CTCCTCTNGAAATTCCTATAGCTACCAACATCACAAGTAAACATTTATTACTAGGTATTA :110

      *           140          *           160          *           180
TrPALa1:  TATNTACTATTTTAAAGATATGGAAGTAGTAGCANACAGCAATCACAAAAACAATGGCAAG :180
TrPALa2:  TATNTACTATTTTAAAGATATGGAAGTAGTAGCAGCAGCAATCACAAAAACAATGGCAAG :180
TrPALa3:  TATNTACTATTTTAAAGATATGGAAGTAGTAGCAGCAGCAATCACAAAAACAATGGCAAG :170

      *           200          *           220          *           240
TrPALa1:  ATTGATTCATTTTGCTTGAATCATGCTAATGCTAATAACATGAAAGTGAATGGTCTGAT :240
TrPALa2:  ATTGATTCATTTTGCTTGAATCATGCTAATGCTAATAACATGAAAGTGAATGGTCTGAT :240
TrPALa3:  ATTGATTCATTTTGCTTGAATCATGCTAATGCTAATAACATGAAAGTGAATGGTCTGAT :230

      *           260          *           280          *           300
TrPALa1:  CCTTTGAATTTGGGGTGTGGCTGCTGAGGCAATGAAGGGAAGTCACTTGGATGAGGTGAAG :300
TrPALa2:  CCTTTGAATTTGGGGTGTGGCTGCTGAGGCAATGAAGGGAAGTCACTTGGATGAGGTGAAG :300
TrPALa3:  CCTTTGAATTTGGGGTGTGGCTGCTGAGGCAATGAAGGGAAGTCACTTGGATGAGGTGAAG :290

      *           320          *           340          *           360
TrPALa1:  CGTATGGTGGAGGAATACCGGAAACCGGTGTGTCGCTCTTGGTGGCGAGACGCTGACGATT :360
TrPALa2:  CGTATGGTGGAGGAATACCGGAAACCGGTGTGTCGCTCTTGGTGGCGAGACGCTGACGATT :360
TrPALa3:  CGTATGGTGGAGGAATACCGGAAACCGGTGTGTCGCTCTTGGTGGCGAGACGCTGACGATT :350

      *           380          *           400          *           420
TrPALa1:  TCTCAGGTGGCTGCCATTGCTGCACACGATGGTGCAACGGTGGTCTATCGGAATCTGCT :420
TrPALa2:  TCTCAGGTGGCTGCCATTGCTGCACACGATGGTGCAACGGTGGAGCTATCGGAATCTGCT :420
TrPALa3:  TCTCAGGTGGCTGCCATTGCTGCACACGATGGTGCAACGGTGGAGCTATCGGAATCTGCT :410

      *           440          *           460          *           480
TrPALa1:  AGAGCCGGCGTTAAGGCGAGCAGTGACTGGGTTATGGAGACTATGAACAAAGGTACAGAC :480
TrPALa2:  AGAGCCGGCGTTAAGGCGAGCAGTGACTGGGTTATGGAGACTATGAACAAAGGTACAGAC :480
TrPALa3:  AGAGCCGGCGTTAAGGCGAGCAGTGACTGGGTTATGGAGACTATGAACAAAGGTACAGAC :470

      *           500          *           520          *           540
TrPALa1:  AGTTATGGTGTCACTACGGGTTTCGGCGCTACCTCTCCACCCCGCAACCAACAAAGGTGGT :540
TrPALa2:  AGTTATGGTGTCACTACGGGTTTCGGCGCTACCTCTCCACCCCGCAACCAACAAAGGTGGT :540
TrPALa3:  AGTTATGGTGTCACTACGGGTTTCGGCGCTACCTCTCCACCCCGCAACCAACAAAGGTGGT :530

      *           560          *           580          *           600
TrPALa1:  GCTTTGCAGAAAGAGCTCATAAGGTTTATTGCTTCTGCTGAAT :582
TrPALa2:  GCTTTGCAGAAAGAGCTCATAAGGTTTATTGGAAGCTTGAATTTTGGAAATGGAACATG :600
TrPALa3:  GCTTTGCAGAAAGAGCTCATAAGGTTTATTGGAATGCAGAAATTTTGGAAATGGAACATG :590

      *           620
TrPALa1:  ----- : -
TrPALa2:  AGCTCAAGCCACACACTACCC :621
TrPALa3:  AATCAAAATCC----- :600

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FIGURE 85

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TrPALb : GNAGGAAANAATTNTATTGTTATTATTTCCCCCACACACGGAANAATTNTATTGTTN : 60

TrPALb : CTTATTTCCTCCACACACATAACNAATACATTWICCTCTCCTCTCATCACAATTATTA : 120

TrPALb : CTTTCTACACACCCCCCTCAACTATTATTAACTAACATAATGGAGGGAATTACCAATG : 180

TrPALb : GCCATGCTGAGCAACTTTTTCGTGACCAAAAGTGTGTGGTGATCCACTCAACTGGGGTG : 240

TrPALb : CAGCGCGGGAGTCGTTGATGGGGAGTCATTTGGATGAGGTGAAGCGTATSGTGGAGGAAT : 300

TrPALb : ACCGTAATCCATTGGTTAAATTTGGCGGCGAGACGCTTACCATTGCTCAGGTGGCTGGAA : 360

TrPALb : TTGCTTCTCATGATAGTGGTGTGAGGGTGGAGCTGTCTGASTCCGCCAGGGCCGGCGCTTA : 420

TrPALb : AGGCGAGTACTGATGGGTGATGGACAGCATGAACAATGGGACTGATAGTTATGGTGTTA : 480

TrPALb : CCACCGGTTTCGGCGCCACCTCTCACCGGAGAACCAAGCAGGTGGTGCTTGCAAGAGG : 540

TrPALb : AGCTAATTAGGTTTTTGAATGCTGGAATATTTGGCAATGGTACAGAATCTAACTGTACAC : 600

TrPALb : TACCACACACAGCAACCAGAGCTGCAATGCTTGTGAGAATCAACACTCTTCTCAAGAGG : 660

TrPALb : AATATTCTTGAAATGGCCTTTGTAAATTTTGG : 693

FIGURE 86

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TrPALb : MEGITNGHAEATPCVTKSVGDP LNWGAAAE SLMGSHLDEVKRMVEEYRNPLVKIGGETLT : 60

TrPALb : IAQVAGIASHD SGVRVELSE SARAGVKASSDWVMD SMNNGTDSYGVTGFGATSHRRTKQ : 120

TrPALb : GGALQKELIRFLNAGIFGNGTESNCTLPHTATRAAMLVRINTLLQEEYFLNGLCKFL : 177

FIGURE 87

[illegible]

FIGURE 88

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TrPALb1 : TGGCTTCTCATGATAGTGGTGTGAGGGTGGACGCTGCGAGCTCCGACAGGCCGGCGGCGTT : 420
TrPALb2 : TTGCTTCTCATGATAGTGGTGTGAGGGTGGACGCTGCTGAGTCCCGAGGCCGGCGGCGTT : 381
TrPALb3 : TTGCTTCTCATGATAGTGGTGTGAGGGTGGACGCTGCTGAGTCCCGAGGCCGGCGGCGTT : 379
TrPALb4 : TTGCTTCTCATGATAGTGGTGTGAGGGTGGACGCTGCTGAGTCCCGAGGCCGGCGGCGTT : 379
TrPALb5 : TTGCTTCTCATGATAGTGGTGTGAGGGTGGACGCTGCTGAGTCCCGAGGCCGGCGGCGTT : 379
TrPALb6 : TTGCTTCTCATGATAGTGGTGTGAGGGTGGACGCTGCTGAGTCCCGAGGCCGGCGGCGTT : 378
TrPALb7 : TTGCTTCTCATGATAGTGGTGTGAGGGTGGACGCTGCTGAGTCCCGAGGCCGGCGGCGTT : 378
TrPALb8 : TTGCTTCTCATGATAGTGGTGTGAGGGTGGACGCTGCTGAGTCCCGAGGCCGGCGGCGTT : 342

TrPALb1 : AGGCGAGTAGTGA*TTGGGTGATGGAAGCATGAACAAATGGGACTGATAGT*TAGCGTGT : 480
TrPALb2 : AGGCGAGTAGTGA*TTGGGTGATGGAAGCATGAACAAATGGGACTGATAGT*TAGCGTGT : 441
TrPALb3 : AGGCGAGTAGTGA*TTGGGTGATGGAAGCATGAACAAATGGGACTGATAGT*TAGCGTGT : 441
TrPALb4 : AGGCGAGTAGTGA*TTGGGTGATGGAAGCATGAACAAATGGGACTGATAGT*TAGCGTGT : 439
TrPALb5 : AGGCGAGTAGTGA*TTGGGTGATGGAAGCATGAACAAATGGGACTGATAGT*TAGCGTGT : 439
TrPALb6 : AGGCGAGTAGTGA*TTGGGTGATGGAAGCATGAACAAATGGGACTGATAGT*TAGCGTGT : 438
TrPALb7 : AGGCGAGTAGTGA*TTGGGTGATGGAAGCATGAACAAATGGGACTGATAGT*TAGCGTGT : 438
TrPALb8 : AGGCGAGTAGTGA*TTGGGTGATGGAAGCATGAACAAATGGGACTGATAGT*TAGCGTGT : 402

TrPALb1 : CCACCGGTT*TTGGGCCACCCTCTACCCGAGAACCAAGCAGGGTGGTGCCTTGCAGAAAG : 540
TrPALb2 : CCACCGGTT*TTGGGCCACCCTCTACCCGAGAACCAAGCAGGGTGGTGCCTTGCAGAAAG : 501
TrPALb3 : CCACCGGTT*TTGGGCCACCCTCTACCCGAGAACCAAGCAGGGTGGTGCCTTGCAGAAAG : 501
TrPALb4 : CCACCGGTT*TTGGGCCACCCTCTACCCGAGAACCAAGCAGGGTGGTGCCTTGCAGAAAG : 499
TrPALb5 : CCACCGGTT*TTGGGCCACCCTCTACCCGAGAACCAAGCAGGGTGGTGCCTTGCAGAAAG : 499
TrPALb6 : CCACCGGTT*TTGGGCCACCCTCTACCCGAGAACCAAGCAGGGTGGTGCCTTGCAGAAAG : 441
TrPALb7 : CCACCGGTT*TTGGGCCACCCTCTACCCGAGAACCAAGCAGGGTGGTGCCTTGCAGAAAG : 498
TrPALb8 : CCACCGGTT*TTGGGCCACCCTCTACCCGAGAACCAAGCAGGGTGGTGCCTTGCAGAAAG : 462

TrPALb1 : AGCTAAATTAGGTT*TTTGAATGCTGGAATATT*TTGCCAATGGTACAGAAATCT* : 592
TrPALb2 : AGCTAAATTAGGTT*TTTGAATGCTGGAATATT*TTGCCAATGGTACAGAAATCT*TAACGTACAC : 561
TrPALb3 : AGCTAAATTAGGTT*TTTGAATGCTGGAATATT*TTGCCAATGGTACAGAAATCT*TAACGTACAC : 561
TrPALb4 : AGCTAAATTAGGTT*TTTGAATGCTGGAATATT*TTGCCAATGGTACAGAAATCT*TAACGTACAC : 559
TrPALb5 : AGCTAAATTAGGTT*TTTGAATGCTGGAATATT*TTGCCAATGGTACAGAAATCT*TAACGTACAC : 559
TrPALb6 : AGCTAAATTAGGTT*TTTGAATGCTGGAATATT*TTGCCAATGGTACAGAAATCT*TAACGTACAC : 559
TrPALb7 : AGCTAAATTAGGTT*TTTGAATGCTGGAATATT*TTGCCAATGGTACAGAAATCT*TAACGTACAC : 558
TrPALb8 : AGCTAAATTAGGTT*TTTGAATGCTGGAATATT*TTGCCAATGGTACAGAAATCT*TAACGTACAC : 522

TrPALb1 : TACCACACACAGCAACGAGAGCTGCAATGCT*TTGTGAGAATCAACACTCTTCTTCAAG : 618
TrPALb2 : TACCACACACAGCAACGAGAGCTGCAATGCT*TTGTGAGAATCAACACTCTTCTTCAAG : 621
TrPALb3 : TACCACACACAGCAACGAGAGCTGCAATGCT*TTGTGAGAATCAACACTCTTCTTCAAG : 621
TrPALb4 : TACCACACACAGCAACGAGAGCTGCAATGCT*TTGTGAGAATCAACACTCTTCTTCAAG : 590
TrPALb5 : TACCACACACAGCAACGAGAGCTGCAATGCT*TTGTGAGAATCAACACTCTTCTTCAAG : 616
TrPALb6 : TACCACACACAGCAACGAGAGCTGCAATGCT*TTGTGAGAATCAACACTCTTCTTCAAG : 616
TrPALb7 : TACCACACACAGCAACGAGAGCTGCAATGCT*TTGTGAGAATCAACACTCTTCTTCAAG : 567
TrPALb8 : TACCACACACAGCAACGAGAGCTGCAATGCT*TTGTGAGAATCAACACTCTTCTTCAAG : 532

TrPALb1 : AATATTCTCTGAAAGGCGTT*TTGTAATTTTTCG : 654
TrPALb2 : AATATTCTCTGAAAGGCGTT*TTGTAATTTTTCG : 654
TrPALb3 : AATATTCTCTGAAAGGCGTT*TTGTAATTTTTCG : 654
TrPALb4 : AATATTCTCTGAAAGGCGTT*TTGTAATTTTTCG : 654
TrPALb5 : AATATTCTCTGAAAGGCGTT*TTGTAATTTTTCG : 654
TrPALb6 : AATATTCTCTGAAAGGCGTT*TTGTAATTTTTCG : 654
TrPALb7 : AATATTCTCTGAAAGGCGTT*TTGTAATTTTTCG : 654
TrPALb8 : AATATTCTCTGAAAGGCGTT*TTGTAATTTTTCG : 654

FIGURE 88 (cont)

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TrPALC : AACAAAGATCGTTATGCCTTAGAACTTCACCTCAATGGCTTGGTCCTTTGATTGAAGTGAT : 60

TrPALC : AAGATTTTCAACCAATCAATTGAAGAGAGAAATTAACTCGGTCAACGACAAACCTTTGAT : 120

TrPALC : CGATGTTTCAAGGAACAAGGCCATTTCATGGTGGTAACTTTCAAGGAACACCTATTGGAGT : 180

TrPALC : TTCAATGGATAACACACGTTTAGCTCTTGCTTCAATTGGTAAACTCATGTTTGCTCAATT : 240

TrPALC : CTCTGAAC TTGTTAATGATTTTACAAACCGGGTTCGCTTCGAATCTTACTGCTAGTAG : 300

TrPALC : GAACCCGAGCTTGGACTATGGTTTCAAGGGATCGGAAATTGCCATGGCTTCGTATTGTTTC : 360

TrPALC : CGAGTTACAATATCTTTGCTAATCCTGTCAACCCCATGTCCAAAGTGCCGAGCAACACAA : 420

TrPALC : CCAAGATGTTAACTCTTTGGGTTTGATTTCATCTAGAAAAACAATGAAGCTATTGAGAT : 480

TrPALC : TCTCAAGCTCATGTCTTCCACTTCTTTGATTGCATTATGTCAAGCAATCGACTTAAGGCA : 540

TrPALC : CTTGGAGGAAAATCTCAGGAACACCGTCAAGAACACGGT : 579

FIGURE 89

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      *           20           *           40           *           60
TrPALc : TRSLCLRTSPQWLGPLIEVIRFSTKSIEREINSVNDNPLIDVSRNKAIHGGNFQGTPIGV : 60

      *           80           *           100          *           120
TrPALc : SMDNTRLALASIGKLMFAQFSELVNDFYNNGLPSNLTASRNPSLDYGFGKSEIAMASYCS : 120

      *           140          *           160          *           180
TrPALc : ELQYLANPVTTHVQSABEQHNQDVNSLGLISSRKTNEAIEILKMSSTFLIALCQAIDLRH : 180

      *
TrPALc : LEENLRNTVKNT : 192

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FIGURE 90

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TrPALd :   *           20           *           40           *           60
          : GGTC AATNCAGCTTNGGAGATCTAGTCCCCCTTTCTTACTNTGCTGGTTTACTAACTGGA : 60

TrPALd :   *           80           *           100          *           120
          : AGACCNAATTCTAAAGCTCATGGGCCTACAGGAGAAGTACTTAATGCAAAAGAAGCTTTT : 120

TrPALd :   *           140          *           160          *           180
          : CAATTGGCTGGAATCAATACCGAGTTCTTTGAATTACAACCAAAAAGGCTCTTGCACTT : 180

TrPALd :   *           200          *           220          *           240
          : GTTAATGGAAGCTGCTGTGGTTCTGGTTTAGCTTCTATTGTTCTTTTGAGGCTAACATA : 240

TrPALd :   *           260          *           280          *           300
          : TTGGCGGTGTTGTCTGAAGTTCTATCGGCAATTTTCGCTGAAGTTATGCAAGGGGAAGCCC : 300

TrPALd :   *           320          *           340          *           360
          : GAATTTACTGATCATTTGACACATAAGTTGAAGCACCACCTGGTCAAATTGAGGCTGCT : 360

TrPALd :   *           380          *           400          *           420
          : GCTATTATGGAACACATTTTGGATGGGAGTGCTTATGTTAAAGACGCGAAGAAGTTGCAT : 420

TrPALd :   *           440          *           460          *           480
          : GAGATGGACCCCTTTACAGAAGCCAAAGCAAGATAGATATGCACTTAGAACTTCACCACAA : 480

TrPALd :   *           500          *           520          *           540
          : TGGCTTGGTCTCTTGATTGAAGTGATTAGATTTTCAACCAAGTCAATTGAGAGAGAGATC : 540

TrPALd :   *           560          *           580          *
          : AACTCTGTCAATGACAACCCCTTTGATTGATGTTTCGAGAAACAAGGCTTTG : 591

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FIGURE 91

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      *           20           *           40           *           60
TrPALd : GQXSXGDLVPLSYXAGLLTGRXNSKAHGPTGEVLNAKEAFQLAGINTEFFELQPKEGLAL : 60

      *           80           *           100          *           120
TrPALd : VNGTAVGSGLASIVLFEANILAVLSEVLSAIFAEVMQKPEFTDHLTHKLKHHHPGQIEAA : 120

      *           140          *           160          *           180
TrPALd : AIMEHILDGSAYVKDAKKLHEMDPLQKPKQDRYALRTSPQWLGPLIEVIRFSTKSIEREI : 180

      *
TrPALd : NSVNDNPLIDVSRNKAL : 197

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FIGURE 92

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      *           20           *           40           *           60
TrPAle : GNINGGAAATTNCAACTCNATTNTTCTTTNTATAATNTTGAATTCCTTCTCTCTCAAA : 60

      *           80           *           100          *           120
TrPAle : TTCTATAGCTACTCTACCACATCACACAACATAACAAAATTAGAAATATTTCATTACTATA : 120

      *           140          *           160          *           180
TrPAle : CTATTAAGATATGGAAGTAGTAGCAGCAGCAATCACAAAAACAACGGCAAGATTGATTC : 180

      *           200          *           220          *           240
TrPAle : ATTTTGCTTGAATCATGCTAATGCTAATAACATGAAAGTGAATGATGCTGATCCTTTGAA : 240

      *           260          *           280          *           300
TrPAle : TTGGGGTGTGGCTGCTGAGGCAATGAAGGGAAGTCACTTGGATGAGGTGAAACGTATGGT : 300

      *           320          *           340          *           360
TrPAle : GGAGGAGTACCGGAAGCCGATTGTCCCTCTTGGTGGCGAGACGCTGACGATTCTCAGST : 360

      *           380          *           400          *           420
TrPAle : GGCTGCCATTGCTGCACACGATGGTGCATGGTTGAGCTGTGCGGAATCTGCTAGAGCCGG : 420

      *           440          *           460          *           480
TrPAle : CGTTAAGGCAAGCAGTGATTGGGTTATGGAGAGTATGAACAAAGGTACTGACAGTTATGG : 480

      *           500          *           520          *           540
TrPAle : TGTCAACACAGGGTTCGGCGCTACCTCNCACCGCCGAACCAACAAGGTGGTGCTTTACA : 540

      *           560          *           580          *
TrPAle : GAAAGGGCTCATAAGGTTTGTGAATGCTGGAATATTGNAATGNAACTGAN : 592

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FIGURE 93

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TrPAle : MEVVAAAITKNNNGKIDSFCLNHANANNMKVNDADPLNHWGVAAEAMKGSHLDEVKRMVEEY : 60

TrPAle : RKPIVRLGGETLTISQVAAIAAHDGAMVELSESARAGVKASSDW/MESMKNKGTDSYGVTT : 120

TrPAle : GFGATXHRRTKQGGALQKGLIRFLNAGIFXNXTX : 154

FIGURE 94

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      *           20           *           40           *           60
TrPALf : CNATTGTTAGTNGTTTCNCCCAOCCACATAACAATAATCTCTCTCTGATCAC : 60

      *           80           *           100          *           120
TrPALf : AATTATTACTTTACTACACCCCTCCTCTCAACTATTATTAACTAGCATAATGGAGGGAATT : 120

      *           140          *           160           *           180
TrPALf : ACCAATGGCCATGCTGAAACAACCTTTTAGCGTGACCAAAAGTGNNNGNGATCCACTCAAC : 180

      *           200          *           220           *           240
TrPALf : TGGCGNGCAGCGCGGAGTCGTCGACGGGGAGTCATTTGGATGAGGTGAAGCGTATGGNG : 240

      *           260          *           280           *           300
TrPALf : GAGGAGTACCGTAATCCGNTGGTTAAARTTGGCGGCAGAGCGCTTACCATTGCTNNGGTA : 300

      *           320          *           340           *           360
TrPALf : NCTGGAATTGCTTCTCATGATAGTGAGTGAGGGTGAGCTGTCCGAGTTCGCAAGGGCC : 360

      *           380          *           400           *           420
TrPALf : GCGCTTAAGGCGAGTAGTGATTGNGTGATGGATAGCATGAACAATGGGACTGATAGTTAC : 420

      *           440          *           460           *           480
TrPALf : GGTGTTACCACCGCNTTTGGTGCCACCTGTCAOCCGAGAACCAGCCANGGTGGTGCCCTT : 480

      *           500          *           520           *           540
TrPALf : GCAGAAGGAGCTAAATTNNGGTGTTTTGAANGCTGGNAATANTTTGGC NNTGGTTCAGAA : 540

      *           560
TrPALf : ATCTNAACTTGTNCACTTACCACACC : 566

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FIGURE 95

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      *           20           *           40           *           60
TrPALf : MEGITNGHAETTFVTKSXXDPLNWXAAAESSTGSHLDEVKRMXBEYRNPXVKIGGETLT : 60

      *           80           *           100          *           120
TrPALf : IAXVXGIAHDSGVRVELSEFARAGVKASSDXVMDSMNNGTDSYGVTTXFGATCHRRTKP : 120

      *           140          *
TrPALf : XWCLAEGAKXXCFEXWXXFGXGSRIXTCXLTT : 152

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FIGURE 96

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      *           20           *           40           *           60
TrPALf1 : C N A T T G T T A G T N G T T C C N C C C A C C N A C A T A A C N A A T A C N T A N T T C T C T C C T C T G A T C A C : 60
TrPALf2 : ----- C C A T A A C A A A T A C A T T A T T C T C T C C T C T G A T C A C : 35

      *           80           *           100          *           120
TrPALf1 : A A T T A T T A C T T T N C T A C A C C C T C C T C T C A A C T A T T A T T A A C T A G C A T A A T G G A G G G A A T T : 120
TrPALf2 : A A T T A T T A C T T T A C T A C A C C C T C C T C T C A A C T A T T A T T A A C T A G C A T A A T G G A G G G A A T T : 95

      *           140          *           160          *           180
TrPALf1 : A C C A A T G G C C A T G C T G A A A C A A C T T T T T C C G T G A C C A A A A G T G N G G N G A T N N A N T G N N C : 180
TrPALf2 : A C C A A T G G C C A T G C T G A A A C A A C T T T T A T C G T G A C C A A A A G T G N T G G T G A T C C A C T C A A C : 155

      *           200          *           220          *           240
TrPALf1 : T C C G C N C M ----- : 188
TrPALf2 : T G G C C T G C A G C C C G G A G T C G T C G A C G G G A G T C A T T T G G A T G A G G T G A A G C G T A T G G N C : 215

      *           260          *           280          *           300
TrPALf1 : ----- : -
TrPALf2 : G A G G A T A C C G T A A T C C G N T G G T T A A A A T T G G C G G C G A G A C G C T T A C C A T T G C T N N G G T A : 275

      *           320          *           340          *           360
TrPALf1 : ----- : -
TrPALf2 : N C T G G A A T T G C T T T C T C A T G A T A G T G G A G T G A G G G T G G A G C T G T C C G A G T T C C A A G G G C C : 335

      *           380          *           400          *           420
TrPALf1 : ----- : -
TrPALf2 : G S C G T T A A G G C G A G T A G T G A T T G N G T G A T G G A T A G C A T G A A C A A T G G G A C T G A T A G T T A C : 395

      *           440          *           460          *           480
TrPALf1 : ----- : -
TrPALf2 : E G T G T T A C C A C C G N T T T G G T G C C A C C T G T C A C C G G A G A A C A A G C C A N G G T G G T G C C T T : 455

      *           500          *           520          *           540
TrPALf1 : ----- : -
TrPALf2 : G C A G A A G G A G C T A A A T T T N N G G T G T T T T G A A N G C T G G N A A T A N T T T G G C N T G G T T C A G T A : 515

      *           560
TrPALf1 : ----- : -
TrPALf2 : A T C T N A A C T T G T N C A C T T A C C A C A C C : 541

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FIGURE 97

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TrVRa : * 20 * 40 * 60
 : GTAAGAGTTGAGAAAAANACCAATAAAGTAAACNCTATNTAGAAAGAGAGTCAAAAARTG : 60

TrVRa : * 80 * 100 * 120
 : GCTGAAGGAAAAGGAAGGGTTTGTGTTACTGGAGGAACAGGTTTCTTGGTTTCATGGATC : 120

TrVRa : * 140 * 160 * 180
 : ATCAAGAGTCTTCTTGAATAATGGATCTCTGTTAATACCACTATTAGAGCTGATCCAGAA : 180

TrVRa : * 200 * 220 * 240
 : CGTAAGAGGGATGTAAGCTTCTTAACAAATCTACCCGGCGCATCCGAAAGGCTACATTTC : 240

TrVRa : * 260 * 280 * 300
 : TTCAACGCCGATCTAGACGACCCAGAGAGTTTCAACGAAGCAATTGAAGGTTGTGTCGGG : 300

TrVRa : * 320 * 340 * 360
 : ATATTCCACACCGCTTCACCAATCGATTTCGCCGTGAGTGAGCAGAGAAATAGTGACA : 360

TrVRa : * 380 * 400 * 420
 : AAAAGAACAGTGGATGGAGCATTAGGAATTTTAAAGCATGTGTGAATTCAAAGACAGTG : 420

TrVRa : * 440 * 460 * 480
 : AAGAGATTATTATTACACTTCRAAGNGGTTCTGCTGTTTCATTCAATGGAAAAACAAGAT : 480

TrVRa : * 500 * 520 * 540
 : GNNNTGGATGAGAGTATTGGAGTGATGTTGATTGCTTAGAAGTGTAAACCATTTGGT : 540

TrVRa : * 560 * 580 * 600
 : TGGAGTTATGGNGTGTCAAGACTTTGGCTGAGAAAGCAGTGCTTGAATTTGGTCNACAA : 600

TrVRa : * 620 * 640 * 660
 : AATGGGATTGATGTTGTTACTTTGATTCTTCTCTTTTATTGTTGGAGGTTTGTGTTGCC : 660

TrVRa : * 680 * 700 * 720
 : AAGCTTCTCTGATTCTGTTGAGAAAGCTCTTGTGTTGGTACTAGGCAAAAAGGAACAART : 720

TrVRa : * 740 * 760 * 780
 : GGTATTATAAGTTTCCACATGGTACATGTAGATGATGTGGCTAGAGCACATATCTATCTA : 780

TrVRa : * 800 * 820 * 840
 : CTTGAGAATCTCTGTTCCAGGAGGTAGATATAATTGTTCCACATTCTTTGTATCTATTGAA : 840

TrVRa : * 860 * 880 * 900
 : GAAATGTCACAGCTTCTCTCAGCCAAATATCCAGATATCAAATACTATCAGTAGATGAG : 900

TrVRa : * 920 * 940 * 960
 : TTGAAGGAATTAAGGGGCAAGATTGCCAGATTGAACTCGAAGAAGCTCGTGGACGCT : 960

TrVRa : * 980 * 1000 * 1020
 : GGTTTTGAGTTTAAAGTATAGTGTGATGATATGTTGATGATGCGATTCAATGCTGCAAG : 1020

TrVRa : * 1040 * 1060 * 1080
 : GAAAAAGGCTATCTCTAAGCATGTATTGAAAAATCCATGAAGTTGAGAAAAACAATAATG : 1080

TrVRa : * 1100 * 1120 * 1140
 : TCCCTAAATCAATGATGGCTAATGAGATGTACAAGTTTATGCAATTAAGTTATTGTGAT : 1140

TrVRa : * 1160 * 1180
 : CAATCAAAATAATGAATAATCTGTTCATTTTCCGAAAAA : 1185

FIGURE 98

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      *           20           *           40           *           60
TrVRa : MAEGKGRVCVTGGTGPLGSWIIKSLLENGYSVNTTIRADPERKRDVSFLTNLPGASERLH : 60

      *           80           *           100          *           120
TrVRa : PFNADLDDPESFNEALEGCVGIFHTASPIDFAVSEPEEIVTKRTVDGALGILKACVNSKT : 120

      *           140          *           160          *           180
TrVRa : VRFIIYTSXGSAVSPNGKNKDXDESDSDVDLLRSVKPFQWSYXVFKTLAEKAVLEFGX : 180

      *           200          *           220          *           240
TrVRa : QNGIDVVTLILPPIVGGFVCPKLPDSVEKALVVLGKKBEQIGIISFHMVHVDDVARAHY : 240

      *           260          *           280          *           300
TrVRa : LLENPVPGGRYNCSPFFVSIEMSQLLSAKYPEYQILSVDELKEIKGARLPDLNSKKLVD : 300

      *           320
TrVRa : AGFEFKYSVDDMFDDAIQCCKEKGYL : 326

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FIGURE 99

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TrVRa1 :	GTAGTAGTTGAGAAAAAATACNAATAAAGTAAACNCTATNTAGAAAGAGAGTCAAAAATG	60
TrVRa2 :	---AGAGTTGAGAAAAAANNCCAATAAAGTAAACNCTATNTAGAAAGAGAGCTNNAAAATG	57
TrVRa3 :	-----	-
TrVRa4 :	-----	-
TrVRa5 :	-----	-
TrVRa6 :	-----	-
TrVRa1 :	GCTGAAGGAAAAGGAAGGGTTTGTGTTACTGGAGGAACAGGTTTTCTTGGTTCATGGATC	120
TrVRa2 :	GCTGAAGGAAAAGGAAGGGTTTGTGTTACTGGAGGAACAGGTTTTCTTGGTTCATGGATC	117
TrVRa3 :	-----	-
TrVRa4 :	-----	-
TrVRa5 :	-----	-
TrVRa6 :	-----	-
TrVRa1 :	ATCAAGAGTCTTCTTGAAAAATGGATACCTCTGTTAATACCACTATTAGAGCTGATCCAGAA	180
TrVRa2 :	ATCAAGAGTCTTCTTGAAAAATGGATACCTCTGTTAATACCACTATTAGAGCTGATCCAGAA	177
TrVRa3 :	-----	-
TrVRa4 :	-----	-
TrVRa5 :	-----	-
TrVRa6 :	-----	-
TrVRa1 :	CGTAAGAGGGATGTAAGCTTCCTAACAAATCTACCCGGCGCATCCGAAAGGCTACATTTC	240
TrVRa2 :	CGTAAGAGGGATGTAAGCTTCCTAACAAATCTACCCGGCGCATCCGAAAGGCTACATTTC	237
TrVRa3 :	-----	-
TrVRa4 :	-----	-
TrVRa5 :	-----	-
TrVRa6 :	-----	-
TrVRa1 :	TTCAACGCCGATCTAGACGACCCAGAGAGTTTCAACGAAGCAATTGAAGGTTGGTCCGG	300
TrVRa2 :	TTCAACGCCGATCTAGACGACCCAGAGAGTTTCAACGAAGCAATTGAAGGTTGGTCCGG	297
TrVRa3 :	-----	-
TrVRa4 :	-----	-
TrVRa5 :	-----	-
TrVRa6 :	-----	-
TrVRa1 :	ATATTCACACCGCTTCACCAATCGATTTCGCCGTGAGTGAGCCAGAAGAAATAGTGAC	360
TrVRa2 :	ATATTCACACCGCTTCACCAATCGATTTCGCCGTGAGTGAGCCAGAAGAAATAGTGAC	357
TrVRa3 :	-----	-
TrVRa4 :	-----	-
TrVRa5 :	-----	-
TrVRa6 :	-----	-
TrVRa1 :	AAAGAACAGTGGATCGAGCATTAGGAATTTTAAAGCATGTGTGAATTCAAAGACAGTG	420
TrVRa2 :	AAAGAACAGTGGATCGAGCATTAGGAATTTTAAAGCATGTGTGAATTCAAAGACAGTG	417
TrVRa3 :	-----	-
TrVRa4 :	-----	-
TrVRa5 :	-----	-
TrVRa6 :	-----	-

FIGURE 100

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TrVRa1 :	AAGAGATTTATTACACTTCAAGNGGTTCTGCTGTTTCATTCAATG	AAAAAACAAAGAT	:	480				
TrVRa2 :	AAGAGATTTATTACACTTCAAGTGGTCTGCTGTTTCATTCAATG	AAAAAACAAAGAT	:	477				
TrVRa3 :	-----	-----	:	-				
TrVRa4 :	-----	-----	:	-				
TrVRa5 :	-----	-----	:	-				
TrVRa6 :	-----	-----	:	-				
		*	500	*	520	*	540	
TrVRa1 :	GNNNNNNATGANA	-----	:	493				
TrVRa2 :	CTTTGGCATGACAGTGATGGAGTGGATGATTTGCAATTTGCTTAGAAGTGTAAACCAATTTGGG	-----	:	537				
TrVRa3 :	-----	-----	:	-				
TrVRa4 :	-----	-----	:	-				
TrVRa5 :	-----	-----	:	-				
TrVRa6 :	-----	-----	:	-				
		*	560	*	580	*	600	
TrVRa1 :	-----	-----	:	-				
TrVRa2 :	TGGAGTTATGCGTCTTCAAGACTTTGGCTGAGAAAGCAGTGCCTTGAATTGGTCTTC	CAAA	:	597				
TrVRa3 :	-----	-----	:	50				
TrVRa4 :	-----	-----	:	41				
TrVRa5 :	-----	-----	:	19				
TrVRa6 :	-----	-----	:	19				
		*	620	*	640	*	660	
TrVRa1 :	-----	-----	:	-				
TrVRa2 :	AAATG	-----	:	601				
TrVRa3 :	AAATGGGATTGATGTGTGTACTTTGATTCCTCCCTTTTATTTGTTGGAGGTTTGT	TTGTGTC	:	110				
TrVRa4 :	AAATGGGATTGATGTGTGTACTTTGATTCCTCCCTTTTATTTGTTGGAGGTTTGT	TTGTGTC	:	101				
TrVRa5 :	AAATGGGATTGATGTGTGTACTTTGATTCCTCCCTTTTATTTGTTGGAGGTTTGT	TTGTGTC	:	79				
TrVRa6 :	AAATGGGATTGATGTGTGTACTTTGATTCCTCCCTTTTATTTGTTGGAGGTTTGT	TTGTGTC	:	79				
		*	680	*	700	*	720	
TrVRa1 :	-----	-----	:	-				
TrVRa2 :	-----	-----	:	-				
TrVRa3 :	AAAGCTTCCTGATTCGTGTGAGAAAGCTCTTGT	TTTGGTACTAGGCAAAAGGAACAAAT	:	170				
TrVRa4 :	AAAGCTTCCTGATTCGTGTGAGAAAGCTCTTGT	TTTGGTACTAGGCAAAAGGAACAAAT	:	161				
TrVRa5 :	AAAGCTTCCTGATTCGTGTGAGAAAGCTCTTGT	TTTGGTACTAGGCAAAAGGAACAAAT	:	139				
TrVRa6 :	AAAGCTTCCTGATTCGTGTGAGAAAGCTCTTGT	TTTGGTACTAGGCAAAAGGAACAAAT	:	139				
		*	740	*	760	*	780	
TrVRa1 :	-----	-----	:	-				
TrVRa2 :	-----	-----	:	-				
TrVRa3 :	GGTATTATAAGTTTCCACATGGTACATGTGATGATGTGGCTAGAGCACATATCTATCTA	-----	:	230				
TrVRa4 :	GGTATTATAAGTTTCCACATGGTACATGTGATGATGTGGCTAGAGCACATATCTATCTA	-----	:	221				
TrVRa5 :	GGTATTATAAGTTTCCACATGGTACATGTGATGATGTGGCTAGAGCACATATCTATCTA	-----	:	199				
TrVRa6 :	GGTATTATAAGTTTCCACATGGTACATGTGATGATGTGGCTAGAGCACATATCTATCTA	-----	:	199				
		*	800	*	820	*	840	
TrVRa1 :	-----	-----	:	-				
TrVRa2 :	-----	-----	:	-				
TrVRa3 :	CTTGAGAATCCTGTTCCAGGAGGTAGATATAAATTTGTTCCACATTCCTTTGTATCTATTGAA	-----	:	290				
TrVRa4 :	CTTGAGAATCCTGTTCCAGGAGGTAGATATAAATTTGTTCCACATTCCTTTGTATCTATTGAA	-----	:	281				
TrVRa5 :	CTTGAGAATCCTGTTCCAGGAGGTAGATATAAATTTGTTCCACATTCCTTTGTATCTATTGAA	-----	:	259				
TrVRa6 :	CTTGAGAATCCTGTTCCAGGAGGTAGATATAAATTTGTTCCACATTCCTTTGTATCTATTGAA	-----	:	259				

FIGURE 100 (cont)

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		*	860	*	880	*	900	
TrVRa1 :	-----							-
TrVRa2 :	-----							-
TrVRa3 :	GAATGTCAACAGCTTCCTTCAGCCAAATATCCAGAATATCAAATACTATCTGTAGATGAG							350
TrVRa4 :	GAATGTCAACAGCTTCCTTCAGCCAAATATCCAGAATATCAAATACTATCTGTAGATGAG							341
TrVRa5 :	GAATGTCAACAGCTTCCTTCAGCCAAATATCCAGAATATCAAATACTATCAGTAGATGAG							319
TrVRa6 :	GAATGTCAACAGCTTCCTTCAGCCAAATATCCAGAATATCAAATACTATCAGTAGATGAG							319
		*	920	*	940	*	960	
TrVRa1 :	-----							-
TrVRa2 :	-----							-
TrVRa3 :	TTGAAGGAAATTAAAGGGGCAAGCTTCCAGATTTCGAACTCGAAGAAGCTCGTGGACGGT							410
TrVRa4 :	TTGAAGGAAATTAAAGGGGCAAGCTTCCAGATTTCGAACTCGAAGAAGCTCGTGGACGGT							401
TrVRa5 :	TTGAAGGAAATTAAAGGGCAAGATTCCAGATTTCGAACTCGAAGAAGCTCGTGGACGGT							379
TrVRa6 :	TTGAAGGAAATTAAAGGGCAAGATTCCAGATTTCGAACTCGAAGAAGCTCGTGGACGGT							379
		*	980	*	1000	*	1020	
TrVRa1 :	-----							-
TrVRa2 :	-----							-
TrVRa3 :	GGTTTTGAGTTTAAGTATAGTGTGATGATATGTTGATGATGCGGATTCGAATGCTCCAACT							470
TrVRa4 :	GGTTTTGAGTTTAAGTATAGTGTGATGATATGTTGATGATGCGGATTCGAATGCTCCAACT							461
TrVRa5 :	GGTTTTGAGTTTAAGTATAGTGTGATGATATGTTGATGATGCGGATTCGAATGCTCCAACT							439
TrVRa6 :	GGTTTTGAGTTTAAGTATAGTGTGATGATATGTTGATGATGCGGATTCGAATGCTCCAACT							439
		*	1040	*	1060	*	1080	
TrVRa1 :	-----							-
TrVRa2 :	-----							-
TrVRa3 :	GAATAAGGCTATCTCTAAGCATGTGTTTGAAAATTCCATGAAGTTGAGAAAACAATAATCTC							530
TrVRa4 :	GAATAAGGCTATCTCTAAGCATGTGTTTGAAAATTCCATGAAGTTGAGAAAACAATAATCTC							521
TrVRa5 :	GAATAAGGCTATCTCTAAGCATGTATTGTGAAAATTCCATGAAGTTGAGAAAACAATAATCTC							499
TrVRa6 :	GAATAAGGCTATCTCTAAGCATGTATTGTGAAAATTCCATGAAGTTGAGAAAACAATAATCTC							499
		*	1100	*	1120	*	1140	
TrVRa1 :	-----							-
TrVRa2 :	-----							-
TrVRa3 :	TGCCTAAAATCAATGATGGCTAAATGAGATGTACAAGTTTAAAGCATTAAGTTATTGTGAT							590
TrVRa4 :	TGCCTAAAATCAATGATGGCTAAATGAGATGTACAAGTTTAAAGCATTAAGTTATTGTGAT							581
TrVRa5 :	TGCCTAAAATCAATGATGGCTAAATGAGATGTACAAGTTTAAAGCATTAAGTTATTGTGAT							559
TrVRa6 :	TGCCTAAAATCAATGATGGCTAAATGAGATGTACAAGTTTAAAGCATTAAGTTATTGTGAT							559
		*	1160	*	1180			
TrVRa1 :	-----							-
TrVRa2 :	-----							-
TrVRa3 :	CAATCAAATAATGAAAATAATCTC							613
TrVRa4 :	CAATCAAATAATGAAAATAATCTC							602
TrVRa5 :	CAATCAAATAATGAAAATAATCTC							575
TrVRa6 :	CAATCAAATAATGAAAATAATCTC							604

FIGURE 100 (cont)

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LpDFra : * 20 * 40 * 60
 : GTSYWTTCGAGTTTGAGAGAAATGGCTTCCAGGGCAAGGTGTGTGTACTGGGGCCTCTGG : 60

LpDFra : * 80 * 100 * 120
 : CTTTGTTCGCTTCTGGCTTGTCAAAAGACTACTCGAGTCCGTTATAATGTTCAGGGAC : 120

LpDFra : * 140 * 160 * 180
 : AGTCAGAGACCCAGGCAATCAGAAGAAGGTAGCACACCTCTGGAACCTAGCAGGGGCCAA : 180

LpDFra : * 200 * 220 * 240
 : GGAAAGGTTGGAGCTTGTCAAAGCTGACCTCTTGGAAAGAAGGGAGCTTCGATGATGCTGT : 240

LpDFra : * 260 * 280 * 300
 : GATGGCCTGTGAGGGGTGCTTCCACACTGCATCACCTATCATCACCAAATCTGATACCAA : 300

LpDFra : * 320 * 340 * 360
 : GGAAGAAATGCTTGATTCTGCAATTAACGGCACTCTAAACGTGCTGAGATCGTGCAAGAA : 360

LpDFra : * 380 * 400 * 420
 : GAATCCTTTTCTCAAAAGGGTTGTTCTCACGTCATCATCGTCAACCGTGAGGCTGAGGGA : 420

LpDFra : * 440 * 460 * 480
 : TGAAGCTGAATCCCAACCAACGTGTGCTGGATGAAACATCATGGAGCTCCGTGGAGTT : 480

LpDFra : * 500 * 520 * 540
 : CTGTGAAAGTATCCAGGTATGGTATGGTGTGCGCAAGATCCTTGCTGAGAAATCAGCTTG : 540

LpDFra : * 560 * 580 * 600
 : GGAGTTCGCCAAGGAGAACAACATCGACCTAGTGGCTGTTCTTCCAACGTCGTGATTGG : 600

LpDFra : * 620 * 640 * 660
 : ACCTAATCTCTCGTCTGAATTAGGACCCACTGTTTATAGATGTCCTTGGCTTATTATAAAG : 660

LpDFra : * 680 *
 : AGAGACAGAGAAAGTTCAACCATGTTTKGGAAGGATG : 695

FIGURE 101

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      *           20           *           40           *           60
LpDFra : VFSSLREWLPGQVCVTGASCFVASWLVKRLLESGYNVLGTVRDPGNQKKVAHLWNLGAK : 60

      *           80           *           100          *           120
LpDFra : ERLELVKADLLEEGSFDDAVMACEGVFHTASPIITKSDTKKEMLDSAINGTLNVLRSCCK : 120

      *           140          *           160          *           180
LpDFra : NPFLKRVVLTSSSSTVRLRDEAEFPPNVLLDETSSWSSVEFCESIQVWYGVAKILAESA : 180

      *           200          *           220          *
LpDFra : EFAKENNIDLVAVLPTFVIGPNLSSELGPTVLDVLGLFKGETEKFMTMGKD : 231

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FIGURE 102

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      *           20           *           40           *           60
LpDFRa1 : -----GTTGAGAGAATGGCTTCNAGGGCAGGTGTGTGTACTGGGGCCTCTGGC : 50
LpDFRa2 : -----TCGAGTTTGAGAGAATGGCTTCNAGGGCAGGTGTGTGTACTGGGGCCTCTGGC : 54
LpDFRa3 : -----GTNGGCTTCCAGGGCAGGTGTGTGTACTGGGGCCTCTGGC : 41
LpDFRa4 : -----GCATTCGAGTTTGAGAGAATGGCTTCNAGGGCAGGTGTGTGTACTGGGGCCTCTGGC : 58
LpDFRa5 : GCTCTTTCGAGTTTGAGAGAATGGCTTCNAGGGCAGGTGTGTGTACTGGGGCCTCTGGC : 60

      *           80           *           100          *           120
LpDFRa1 : TTTCGTTGCTTCTCTGGCTTGTCAAAGACTACTCGAGTCGGGTATAATGTTCTAGGAC : 110
LpDFRa2 : TTTCGTTGCTTCTCTGGCTTGTCAAAGACTACTCGAGTCGGGTATAATGTTCTAGGAC : 114
LpDFRa3 : TTTCGTTGCTTCTCTGGCTTGTCAAAGACTACTCGAGTCGGGTATAATGTTCTAGGAC : 100
LpDFRa4 : TTTCGTTGCTTCTCTGGCTTGTCAAAGACTACTCGAGTCGGGTATAATGTTCTAGGAC : 113
LpDFRa5 : TTTCGTTGCTTCTCTGGCTTGTCAAAGACTACTCGAGTCGGGTATAATGTTCTAGGAC : 120

      *           140          *           160          *           180
LpDFRa1 : GTCAGAGACCCAGGCAATCAGAAGAAGGTAGCACACCTCTGGAACCTAGCAGGGGCCAAG : 170
LpDFRa2 : GTCAGAGACCCAGGCAATCAGAAGAAGGTAGCACACCTCTGGAACCTAGCAGGGGCCAAG : 174
LpDFRa3 : GTCAGAGACCCAGGCAATCAGAAGAAGGTAGCACACCTCTGGAACCTAGCAGGGGCCAAG : 160
LpDFRa4 : GTCAGAGACCCAGGCAATCAGAAGAAGGTAGCACACCTCTGGAACCTAGCAGGGGCCAAG : 178
LpDFRa5 : GTCAGAGACCCAGGCAATCAGAAGAAGGTAGCACACCTCTGGAACCTAGCAGGGGCCAAG : 180

      *           200          *           220          *           240
LpDFRa1 : GAAAGGTTGGAGCTTGTCAAAGCTGACCTCTTGGAAAGAGGGAGCTTCGATGATGCTGAG : 230
LpDFRa2 : GAAAGGTTGGAGCTTGTCAAAGCTGACCTCTTGGAAAGAGGGAGCTTCGATGATGCTGAG : 234
LpDFRa3 : GAAAGGTTGGAGCTTGTCAAAGCTGACCTCTTGGAAAGAGGGAGCTTCGATGATGCTGAG : 220
LpDFRa4 : GAAAGGTTGGAGCTTGTCAAAGCTGACCTCTTGGAAAGAGGGAGCTTCGATGATGCTGAG : 238
LpDFRa5 : GAAAGGTTGGAGCTTGTCAAAGCTGACCTCTTGGAAAGAGGGAGCTTCGATGATGCTGAG : 240

      *           260          *           280          *           300
LpDFRa1 : ATGGGCTGTGAGGGTGTCTTCCACACTGCATCACCTATCATCACCAAATCTGATACCAAG : 290
LpDFRa2 : ATGGGCTGTGAGGGTGTCTTCCACACTGCATCACCTATCATCACCAAATCTGATACCAAG : 294
LpDFRa3 : ATGGGCTGTGAGGGTGTCTTCCACACTGCATCACCTATCATCACCAAATCTGATACCAAG : 280
LpDFRa4 : ATGGGCTGTGAGGGTGTCTTCCACACTGCATCACCTATCATCACCAAATCTGATACCAAG : 298
LpDFRa5 : ATGGGCTGTGAGGGTGTCTTCCACACTGCATCACCTATCATCACCAAATCTGATACCAAG : 300

      *           320          *           340          *           360
LpDFRa1 : GAAGAAATGCTTGATTCTGCAATTAAACGGCACTCTAAACGTGCTGAGATCGTCAAGAAG : 350
LpDFRa2 : GAAGAAATGCTTGATTCTGCAATTAAACGGCACTCTAAACGTGCTGAGATCGTCAAGAAG : 354
LpDFRa3 : GAAGAAATGCTTGATTCTGCAATTAAACGGCACTCTAAACGTGCTGAGATCGTCAAGAAG : 340
LpDFRa4 : GAAGAAATGCTTGATTCTGCAATTAAACGGCACTCTAAACGTGCTGAGATCGTCAAGAAG : 358
LpDFRa5 : GAAGAAATGCTTGATTCTGCAATTAAACGGCACTCTAAACGTGCTGAGATCGTCAAGAAG : 360

      *           380          *           400          *           420
LpDFRa1 : AATCCTTTTCTCAAAGGGTTGTCTCAOGTCATCATCGCAACCGTGAGGCTGAGGGAT : 410
LpDFRa2 : AATCCTTTTCTCAAAGGGTTGTCTCAOGTCATCATCGCAACCGTGAGGCTGAGGGAT : 414
LpDFRa3 : AATCCTTTTCTCAAAGGGTTGTCTCAOGTCATCATCGCAACCGTGAGGCTGAGGGAT : 400
LpDFRa4 : AATCCTTTTCTCAAAGGGTTGTCTCAOGTCATCATCGCAACCGTGAGGCTGAGGGAT : 418
LpDFRa5 : AATCCTTTTCTCAAAGGGTTGTCTCAOGTCATCATCGCAACCGTGAGGCTGAGGGAT : 365

      *           440          *           460          *           480
LpDFRa1 : GAAGCTGAATTCGCCACCCCAACGTTGTCTGGATGAAACATCATGGAGCTCCGTTGAGTTG : 470
LpDFRa2 : GAAGCTGAATTCGCCACCCCAACGTTGTCTGGATGAAACATCATGGAGCTCCGTTGAGTTG : 474
LpDFRa3 : GAAGCTGAATTCGCCACCCCAACGTTGTCTGGATGAAACATCATGGAGCTCCGTTGAGTTG : 425
LpDFRa4 : GAAGCTGAATTCGCCACCCCAACGTTGTCTGGATGAAACATCATGGAGCTCCGTTGAGTTG : 478
LpDFRa5 : ----- : -

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FIGURE 103

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      *           500           *           520           *           540
LpDFRa1 : TGTGAAAGTATCCAGGTATGGTATGGTGTTCGCGAAGATCCTTGGCTGAGAAATCAGCTTGG :530
LpDFRa2 : TGTGAAAGTATCCAGGTATGGTATGGTGTTCGCGAAGATCCTTGGCTGAGAAATCAGCTTGG :534
LpDFRa3 : ----- : -
LpDFRa4 : TGTGAAAGTATCCAGGTATGGTACGGTGTTCGCAAGATCCTTGGCGAGAAATCAGCTTGG :538
LpDFRa5 : ----- : -

      *           560           *           580           *           600
LpDFRa1 : GAGTTCGCCAAGGAGAACAAATCGACCTAGTGGCTGTCTTCCAAAGCTTCGTGATTGG :590
LpDFRa2 : GAGTTCGCCAAGGAGAACAAATCGACCTAGTGGCTGTCTTCCAAAGCTTCGTGATTGG :594
LpDFRa3 : ----- : -
LpDFRa4 : GAGTTCGCCAAGGAGAACAAATCGACCTAGTGGCTGTCTTCCAAAGCTTCGTGATTGG :598
LpDFRa5 : ----- : -

      *           620           *           640           *           660
LpDFRa1 : CCTAATCTCTCGTCTGAATTAGGACCCACTGTTTATAGATGCTCTTGGCTTATTTAAAGGA :650
LpDFRa2 : CCTAATCTCTCGTCTGAATTAGGACCCACTGTTTATAGATGCTCTTGGCTTATTTAAAGGA :654
LpDFRa3 : ----- : -
LpDFRa4 : CCTAATCTCTCGTCTGAATTAGGACCCACTGTTTATAGATGCTCTTGGCTTATTTAAAGGA :658
LpDFRa5 : ----- : -

      *           680           *
LpDFRa1 : GACACAGAGAAGTTCAC----- : 667
LpDFRa2 : GACACAGAGAAGTTCACCATGTTTGGGAAGGATG : 688
LpDFRa3 : ----- : -
LpDFRa4 : GACACAGAGAAGTTCACCATGTTTGGGAAGGAN- : 691
LpDFRa5 : ----- : -

```

FIGURE 103 (cont)

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```

LpDfRb :      *           20           *           40           *           60
          : GTCTTCGCCTACGAGCGCCCGACGCCCGCGCCGCTACCTCTGCATCGGGGCGGTGCTG : 60

LpDfRb :      *           80           *           100          *           120
          : CACCGCGCGCACTTCTTAAAGCTTCTCAAGGACCTCTTCCCGCAGTACTCTTCAACGCC : 120

LpDfRb :      *           140          *           160          *           180
          : AAGTGCGAAGACGACGCGCAAGCCCATGGCGAAGCGGTACAAGTTCTCCNACCAGAGGCTC : 180

LpDfRb :      *           200          *           220          *           240
          : AGGGACCTGGGATTAAAAATTCACCTCCGCTGGCGGAAAGTTTGACGAGACCGTGACGTGC : 240

LpDfRb :      *           260          *           280          *           300
          : CTGCAAAAAAATGGCCACCTGCTCTGCCCCGTCCCATGGCGCAAGCGTGCATACCTA : 300

LpDfRb :      *           320          *           340          *           360
          : TAATACTACAAGACACGCGCGGGATCGACAAGCCAAGAAACAGAGGATTCTCCGAGGT : 360

LpDfRb :      *           380          *           400          *           420
          : TCACCATGGAATTGTGTATTTACAAAGTTTGAATCTTATTTTTTTTATTATGAAGAAA : 420

LpDfRb :      *           440          *           460          *           480
          : TACGGAAAACCAATACTGTATACCAGAGGCAAGTGTAAATAGTAAATAGTCGTGTAAAT : 480

LpDfRb :      *           500          *           520
          : CTGTTCAGAATGAATGATAAAGTATTTTTTGCAAAAAAAAAA : 524

```

FIGURE 104

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 * 20 * 40 * 60
LpDfRb : VLAYERPDARGRYLCIGAVLHRAHFLKLLKDLFPQYSFTAKCEDDGKPMAPYKFSXQRL : 60

 * 80 * 100
LpDfRb : RDLGLKFTPLAESLYETVTCQLQKNGHLPLPAPMAPKRAYL : 100

FIGURE 105

LpDfRb1: **GTCTCTCGGCTACGAGCGGCCCGAGCGCCGCGGCCCTACCTTCGATCGGGCGCGTCTC** : 60
 LpDfRb2: ----- :
 LpDfRb3: ----- :

LpDfRb1: **CACCGCGCGCAC/TCTCTAAAGCTCTCAAGGACCTCTCTCCCGAGTACCTCCATCACCGCG** : 120
 LpDfRb2: ----- :
 LpDfRb3: ----- :

LpDfRb1: **AAGTGCGAAGACGACGCGCAAGCCCATGGCGAAGCCGTACAAGTCTCTCCAGCAGGCTC** : 180
 LpDfRb2: ----- **AAGCGGTACAAGTCTCCNACCAGNNGCTC** : 30
 LpDfRb3: ----- **CTTCTCNACCAGAGGCTC** : 19

LpDfRb1: **AGGGACCTGGGATTTAAATTTCACTCCGCTGGCGGAAGTTGTGTACGAGACCGTGACGTGC** : 240
 LpDfRb2: **AGGGACCTGGGATTTAAATTTCACTCCGCTGGCGGAAGTTGTGTACGAGACCGTGACGTGC** : 90
 LpDfRb3: **AGGGACCTGGGATTTAAATTTCACTCCGCTGGCGGAAGTTGTGTACGAGACCGTGACGTGC** : 79

LpDfRb1: **CTGCAAAAAAATGGCCACCTGCCCTCTGCCCGCTCCCATGGCGCCAAGCGTGCTACCTTT** : 300
 LpDfRb2: **CTGCAAAAAAATGGCCACCTGCCCTCTGCCCGCTCCCATGGCGCCAAGCGTGCTACCTTT** : 150
 LpDfRb3: **CTGCAAAAAAATGGCCACCTGCCCTCTGCCCGCTCCCATGGCGCCAAGCGTGCTACCTTT** : 139

LpDfRb1: **TAATATTACAAAGACACGCGCGGGATCGACAAGCCAAGAAACAGAGGATTTCTCCCGAGGT** : 360
 LpDfRb2: **TAATATTACAAAGACACGCGCGGGATCGACAAGCCAAGAAACAGAGGATTTCTCCCGAGGT** : 210
 LpDfRb3: **TAATATTACAAAGACACGCGCGGGATCGACAAGCCAAGAAACAGAGGATTTCTCCCGAGGT** : 199

LpDfRb1: **TCACCATGGAATTGTGTATTCTCTCAAAAGTTTGAAATCTTATTTTTTATTATGAAGGAA** : 420
 LpDfRb2: **TCACCATGGAATTGTGTATTCTCAAAAGTTTGAAATCTTATTTTTTATTATGAAGGAA** : 270
 LpDfRb3: **TCACCATGGAATTGTGTATTCTCAAAAGTTTGAAATCTTATTTTTTATTATGAAGGAA** : 259

LpDfRb1: **TACCGTAACCAATACTCTGTATACCAGAGGCAAGCTTAAGAATCTAAATAGTCGTGTAAAT** : 480
 LpDfRb2: **TACCGTAACCAATACTCTGTATACCAGAGGCAAGCTTAAGAATCTAAATAGTCGTGTAAAT** : 330
 LpDfRb3: **TACCGTAACCAATACTCTGTATACCAGAGGCAAGCTTAAGAATCTAAATAGTCGTGTAAAT** : 319

LpDfRb1: **CTGTGTCAAGAAATGAATGATAAAGTATTTTTTTCGCAAAAAA** : 524
 LpDfRb2: **CTGTGTCAAGAAATGAATGATAAAGTATTTTTTTCGCAAAAAA** : 374
 LpDfRb3: **CTGTGTCAAGAAATGAATGATAAAGTATTTTTTTCGCAAAAAA** : 363

FIGURE 106

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LpF3Ha : TCTCNAGACACACTGTGTAACACGGTAGCGAGTGGCAAGACTAGCAGAAAGTACGGACA : 60
 * 20 * 40 * 60
 LpF3Ha : TCAGCTAACCATTCCTCAACTAGAATAAGCATGGCTCCGGCGATGTCCAACCCCTCCTCTC : 120
 * 80 * 100 * 120
 LpF3Ha : AGTGATCGGGTGGCAGCTCCAAAGAAAGTCCCATCTAGCCACGTTAGAGCCGTTGGGAGAC : 180
 * 140 * 160 * 180
 LpF3Ha : CGCCCAGACCTCGCCAATGTCGACACAGAGTCCGGCGGGGCATTCGGCTCATCGACCTG : 240
 * 200 * 220 * 240
 LpF3Ha : AAGCAGCTCGAAGGTCCAGGGCGCGCAGGTCGTCGAGGCCATCGGCTCCGCGTCGCAG : 300
 * 260 * 280 * 300
 LpF3Ha : AACGATGGGTTTTTCATGGTGACGAATCATGGCATCCAGAGGCGGTCGTGGAGGGGATG : 360
 * 320 * 340 * 360
 LpF3Ha : CTGAGCGTGGCGAGGGAGTTCTTCCACCTGCCGAGTCGGAGCGGCTCAAGTGTACTCTC : 420
 * 380 * 400 * 420
 LpF3Ha : GACGACCCCAAGAAAGCGGTCGGGCTGTGACGAGCTTCAACGTGCGCAGCGAGAAGGTG : 480
 * 440 * 460 * 480
 LpF3Ha : AGCAACTGCGCGACTTCTCCGGCTGCATTGCTACCTCTTTGAGAGCTTCGTGCGACCA : 540
 * 500 * 520 * 540
 LpF3Ha : TGGCCGTGCAACCCCGCCCTTCAGGCAAGTCGTCGGCACCTACTCGACGGAAGCGAGA : 600
 * 560 * 580 * 600
 LpF3Ha : GCGCTGGCGCTGAGGCTCCTGGAGGCGATATCGGAGAGCCTAGGGCTGGAGAGAGGCCAC : 660
 * 620 * 640 * 660
 LpF3Ha : ATGGTGAAAGGCCATGGGGCGGCACGCGCAGCACATGGCGGTGAATCTACTACCCGCCGTGC : 720
 * 680 * 700 * 720
 LpF3Ha : CCGCAGCCGGAGCTCACCTACGCTCTGCCAGGGCACACGGACCCCAACGCCCTCACCATC : 780
 * 740 * 760 * 780
 LpF3Ha : CTCCTCATGGATCCCAGCTCTCCGGCCTCAGGTCTCAGGGACGGCGCCAAAGTGGATC : 840
 * 800 * 820 * 840
 LpF3Ha : GCCGTCCACCCACGCCCAACGCCCTGGTCATCAACCTAGGCGACAGCTACAGGCGCTG : 900
 * 860 * 880 * 900
 LpF3Ha : AGCAACGCGCGGTACAAGAGCGTGTGGCACC GGCGAGTGAACGGGAGCAGAGCGT : 960
 * 920 * 940 * 960
 LpF3Ha : CTGTGCGTGGCATCTTTCTGTGCCCGTCAACAGCGCGGTATCTGCCCGCGCGCGAGG : 1020
 * 980 * 1000 * 1020
 LpF3Ha : CTCGTCGGCGACGGGGAGGACCCCGTCTACCGGAGCTACACCTACGACGAGTACTACAAG : 1080
 * 1040 * 1060 * 1080
 LpF3Ha : AGGTTTGTGGAGCAGGAACCTGGATCAGGAGCACTGCCTCGAGCTCTTCAGGAGTCAAGC : 1140
 * 1100 * 1120 * 1140

FIGURE 107

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```

          *           1160           *           1180           *           1200
LpF3Ha : TGATGCTTGAACCTTGAGTTACTAGCTAGCTCCTTAACAGTGCAAATCCATGGCCCCAA :1200

          *           1220           *           1240           *           1260
LpF3Ha : GAGGGCCCCGATTGCATGGTTACTTATGTTGTTTGAAGTGGTATTGCTTAAGTGCCTAAT :1260

          *           1280           *           1300           *           1320
LpF3Ha : AACATTGCTACATTTCTACTNCTATCTTGTCGGTTTAAATTTATAAGATGGCCTAACCTTT :1320

          *           1340           *           1360           *           1380
LpF3Ha : TTCTTAATTGTATGCATNCTGAACATATTTAAGTGTGTGTGTTTCAGACAGTTTAGTCTGC :1380

LpF3Ha : A :1381

```

FIGURE 107 (cont)

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      *           20           *           40           *           60
LpF3Ha : MSNPLLSDRVARSKKVPSSHVRVAVGDRPDLANVDHESGAGIPLIDLKQLEGPGRRRVVERA : 60

      *           80           *           100          *           120
LpF3Ha : IGSACENDGFFMV/TNHGIPEAVVEGMLSVAEFFHLPBSERLKCYSDDPKKAURLSTSFN : 120

      *           140          *           160          *           180
LpF3Ha : VRTEKVSINWRDPLRLHCYPLESFVDQWPSNPPAFRQVVGTYSTEARALALRLLEAISESL : 180

      *           200          *           220          *           240
LpF3Ha : GLERGHMV/KAMGRHAQHMAVNYYPPCPQPELTYGLPGHTDPNALTILLMDPHVSGLQVLR : 240

      *           260          *           280          *           300
LpF3Ha : DGAKWIAVHPRPNALVINLGDQLQALSNGAYKSVNHRAVVNAEQERLSVASFLCPCMSAV : 300

      *           320          *           340
LpF3Ha : ICPAPRLVGDEDPVYRSYTYDEYYKRFWSRNLDQEHCLFLFRSQH : 346

```

FIGURE 108

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LpF3Ha1 :	TC	20	*	40	*	60	
LpF3Ha2 :	TC	20	*	40	*	60	: 60
LpF3Ha3 :	TC	20	*	40	*	60	: -
LpF3Ha1 :	TC	80	*	100	*	120	: 120
LpF3Ha2 :	TC	80	*	100	*	120	: 118
LpF3Ha3 :	TC	80	*	100	*	120	: -
LpF3Ha1 :	TC	140	*	160	*	180	: 180
LpF3Ha2 :	TC	140	*	160	*	180	: 178
LpF3Ha3 :	TC	140	*	160	*	180	: -
LpF3Ha1 :	TC	200	*	220	*	240	: 240
LpF3Ha2 :	TC	200	*	220	*	240	: 238
LpF3Ha3 :	TC	200	*	220	*	240	: -
LpF3Ha1 :	TC	260	*	280	*	300	: 300
LpF3Ha2 :	TC	260	*	280	*	300	: 298
LpF3Ha3 :	TC	260	*	280	*	300	: -
LpF3Ha1 :	TC	320	*	340	*	360	: 360
LpF3Ha2 :	TC	320	*	340	*	360	: 358
LpF3Ha3 :	TC	320	*	340	*	360	: -
LpF3Ha1 :	TC	380	*	400	*	420	: 420
LpF3Ha2 :	TC	380	*	400	*	420	: 418
LpF3Ha3 :	TC	380	*	400	*	420	: -
LpF3Ha1 :	TC	440	*	460	*	480	: 480
LpF3Ha2 :	TC	440	*	460	*	480	: 478
LpF3Ha3 :	TC	440	*	460	*	480	: -
LpF3Ha1 :	TC	500	*	520	*	540	: 540
LpF3Ha2 :	TC	500	*	520	*	540	: 538
LpF3Ha3 :	TC	500	*	520	*	540	: -
LpF3Ha1 :	TC	560	*	580	*	600	: 600
LpF3Ha2 :	TC	560	*	580	*	600	: 598
LpF3Ha3 :	TC	560	*	580	*	600	: 12
LpF3Ha1 :	TC	620	*	640	*	660	: 660
LpF3Ha2 :	TC	620	*	640	*	660	: 658
LpF3Ha3 :	TC	620	*	640	*	660	: 72
LpF3Ha1 :	TC	680	*	700	*	720	: 720
LpF3Ha2 :	TC	680	*	700	*	720	: 718
LpF3Ha3 :	TC	680	*	700	*	720	: 132

FIGURE 109

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```

      *           740           *           760           *           780
LpF3Ha1 : CCGCAGCCGGAGCTCACCTACGGTCTGCCAGGGCA :755
LpF3Ha2 : CCGCAGCCGGAGCTCACCTACGGTCTGCCAGGGCACACGGACCCCAATGCCCTCACCATN :778
LpF3Ha3 : CCGCAGCCGGAGCTCACCTACGGTCTGCCAAGCACACGGACCCCAACGCCCTCACCATC :192

      *           800           *           820           *           840
LpF3Ha1 : ----- : -
LpF3Ha2 : CT :780
LpF3Ha3 : CTCTCATGGATCCCCACGCTCTCCGGCTTCCAGGTCTCTCAGGGACGGGCGCAAGTGGATC :252

      *           860           *           880           *           900
LpF3Ha1 : ----- : -
LpF3Ha2 : ----- : -
LpF3Ha3 : GCGCTCCACCCACGCCCCAACGCCCTGCTCATCAACCTAGGCGGACGAGCTACAGGCGCTC :312

      *           920           *           940           *           960
LpF3Ha1 : ----- : -
LpF3Ha2 : ----- : -
LpF3Ha3 : AGCAACGGCGCGGTACAAGAGCGTGTGGCACCAGGAGTGGTGAACCGCGAGCAGGAGCGG :372

      *           980           *           1000          *           1020
LpF3Ha1 : ----- : -
LpF3Ha2 : ----- : -
LpF3Ha3 : CTGTCCGTGGCATCTTTCCTGTGCCCGTGCAACAGCGCGGTATCTTGCCCGCGCCGAGG :432

      *           1040          *           1060          *           1080
LpF3Ha1 : ----- : -
LpF3Ha2 : ----- : -
LpF3Ha3 : CTCGTCCGCGACGGGGAGSACCCCGTCTACCGGAGCTACACCTACGACGAGTACTACAA :492

      *           1100          *           1120          *           1140
LpF3Ha1 : ----- : -
LpF3Ha2 : ----- : -
LpF3Ha3 : AGGTTTITGGAGCAGGAACCTGGATCAGGAGCACTGCCCTCGAGCTCTTCAGGAGTCAGCAC :552

      *           1160          *           1180          *           1200
LpF3Ha1 : ----- : -
LpF3Ha2 : ----- : -
LpF3Ha3 : TGAATGCTTGAACTTGAGTTACTAGCTAGCTCTCCTTAACAGTGCAAATCCATGGCCCA :612

      *           1220          *           1240          *           1260
LpF3Ha1 : ----- : -
LpF3Ha2 : ----- : -
LpF3Ha3 : GAGGCCCCCGATTGCATGGTFACTTATGTGTGTGTGAACGGTATTGCTTAAGTGCCCTAAT :672

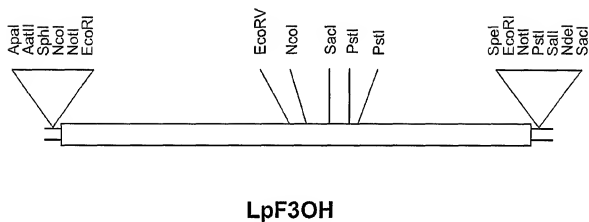
      *           1280          *           1300          *           1320
LpF3Ha1 : ----- : -
LpF3Ha2 : ----- : -
LpF3Ha3 : AACATGGCTACATCTCTACTNCTATCTTGTCGGTTTAAAAATTATAAGATGGCCTAACCTTT :732

      *           1340          *           1360          *           1380
LpF3Ha1 : ----- : -
LpF3Ha2 : ----- : -
LpF3Ha3 : TTCTTAATGTGATGCATNCTGAACATATTTAAGTGTGNGTGTTCAGACAGTTTATGCTCTG :792

LpF3Ha1 : - : -
LpF3Ha2 : - : -
LpF3Ha3 : A : 793

```

FIGURE 109 (cont)

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```

1  GAATTTCGATT AAGCAGTGGT AACAAACGCAG AGTACGCGGG GACTCTCAGA
51 ACACACTGTG TAACCACGGT AGCGAGTGGC AAGACTAGCA GAAAGTACGG
101 ACATCAGCTA ACCATTCCCTC AACTAGAAATA AGCATGGCTC CGGCGATGTC
151 CAACCCCTCTC CTCAGTGATC GGGTGGCAGC CTCCAAGAAA GTCCCATCTA
201 GCCACGTTAG AGCGGTGGGA GACCGCCAG ACCTCGCCAA TGTGCACCAC
251 GAGTCCGGCG CGGGCATTCC GCTCATCGAC CTGAAGCAGC TCGAAGGTCC
301 AGGGCGCCGC AGGGTCGTCG AGGCCATCGG CTCGCGCTGC GAGAACGATG
351 GGTTTTTCAT GGTGACGAAT CATGGCATCC CAGAGGCGGT CGTGAGGGGG
401 ATGCTGAGCG TGGCGAGGGA GTTCTTCCAC CTGCCGGAGT CGGAGCGGCT
451 CAAGTGCTAC TCCGACGACC CCAAGAAGGC GGTCCGGCTG TCGACGAGCT
501 TCAACGTGCG CACGGAGAAG GTGAGCAACT GGC CGCACTT CCTCCGGCTG
551 CATTGCTACC CTCTTGAGAG CTTCGTCGAC CAGTGGCCGT CGAACC CGCC
601 CGCCTTCAGG CAAGTCGTCG GCACCTACTC GACGGAAGCG AGAGCGCTGG
651 CGCTGAGGCT CCTGGAGGCG ATATCGGAGA GCCTAGGGCT GGAGAGAGGC
701 CACATGGTGA AGGCCATGGG GCGGCACGCG CAGCACATGG CGGTGAACTA
751 CTACCCGCGG TGCCCGCAGC CGGAGCTCAC CTACGGTCTG CCAGGGCACA
801 AGGACCCCAA TGCCATCAGC CTCCTCCTGC AGGACGGCGT CTCGGCGCTG
851 CAGGTCCAGC GCGACGCGCG GTGGTGGGCC GTC AACCCGG TGCCCAACGC
901 CCTCGTCATC AACATCGGCG ATCAGTTACA GGCGCTGAGC AACGACCGAT
951 ACAAGAGCGT GAACCA CAGA GTGATCGTCA ACAGCGCGAG CGAGAGGATT
1001 TCGGTGCCGA CGTTCTACTG CCCGTCGCGG GACACGGTGG TCGCGCGCGC
1051 CGACGCGCTG GTGGACGAGC CCCACCCCTG GGCCTACCAG CCCTTCACGT
1101 ACCAGGAGTA CTACGAGGAG TTCTGGAAGA TGGGCCTTCA GTCAGCAAGT
1151 TGCCCTCGACA GGTTCGAGC GATCGAGTGA TGGACAAGAC GTGGGCCGTT
1201 GTTATCTCCT GGGCCATGAG CGTTGCCGCA GCCGATGTGT CGCCATATGG
1251 TGGAGACGTT TCCTCCCTCC GGA AAAAGAAA AATAAAACAG AGTGGAGACC
1301 ACTAGAACCG TCAGATAGCA TCCCAAAAAA AAAAAAAA AAAAAAAAAA
1351 AAAAGTACTC TCGTGTGTTA CCACTGCTTA ATCACTAGTG AATTCT

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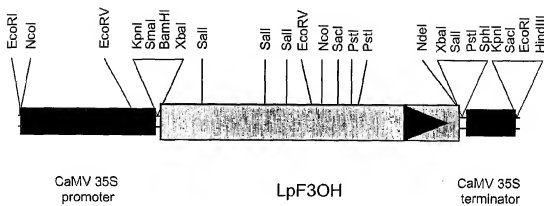
FIGURE 111

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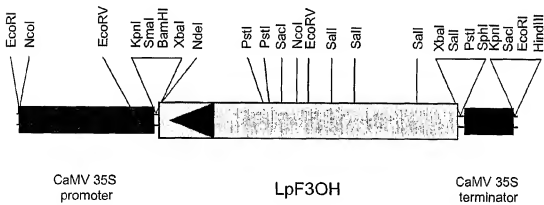
1 MAPAMSNPLL SDRVARSKKV PSSHVRAVGD RPDLANVDHE SGAGIPLIDL
51 KQLEGPGRRR VVEAIGSACE NDGFFMVTNH GIPEAVVEGM LSVAREFFHL
101 PESERLKCYS DDPKKAVRLS TSFNV RTEKV SNWRDFLR LH CYPLESFVDQ
151 WPSNPPAFRQ VVGTYSTEAR ALALRLLEAI SESLGLERGH MVKAMGRHAQ
201 HMAVNYPPC PQPELTYGLP GHKDPNAITL LLQDGVSGLQ VQRDGRWVAV
251 NPVPNALVIN IGDQLQALSN DRYKSVNHRV IVNSASERIS VPTFYCPSFD
301 TVVAPADALV DDAHPRAYQP FTYQEYEEF WKMGLQSASC LDRFRRIE

FIGURE 112

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pDH51LpF3OH sense



pDH51LpF3OH anti

FIGURE 113

The diagram shows a linear representation of the pLpF3OH plasmid construct. It starts with a Tc resistance gene, followed by a 35S terminator, the *ascC1* gene, a 35S promoter, another 35S promoter, the *LpF3OH* gene, a 35S promoter, the *rbcS* terminator, and ends with a Tt resistance gene. Various restriction sites are marked with arrows above the construct: Bcl, EcoRV, NcoI, EcoRV, EcoRI, SmaI, NcoI, EcoRV, HindIII, BamHI, XbaI, PstI, XbaI, SalI, XbaI, SalI, EcoRV, XbaI, NcoI, PstI, XbaI, SalI, XbaI, HindIII, and SphI.

[illegible]

pPZP221:35S²LpF3OH anti

FIGURE 114

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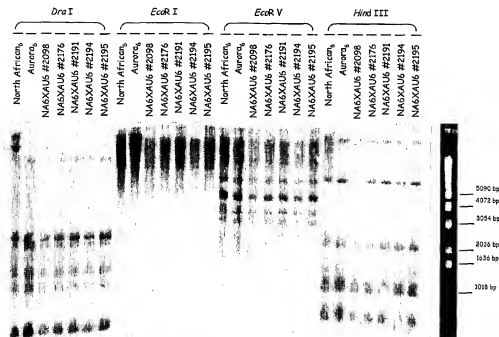
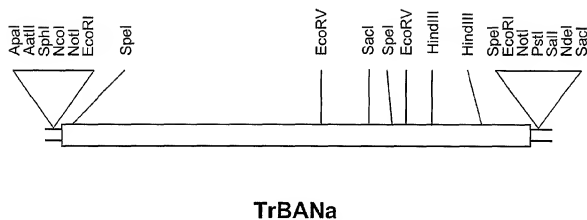


FIGURE 115

189/271**FIGURE 116**

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```

1  GAATTCGATT AAGCAGTGGT AACAAACGCAG AGTACGCGGG ATAAAAACTG
51  CACTAGTGTG TATAAGTTTC TTGGTGAAAA AAGAGTTTGT AAATTAACAT
101 CATGGCTAGT ATCAAACAAA TTGGAACAA GAAAGCATGT GTGATTGGTG
151 GCACTGGTTT TGTTCATCT ATGTTGATCA AGCAGTTACT TGAAAAGGGT
201 TATGCTGTTA ATACTACCGT TAGAGACCCA GATAGCCCTA AGAAAAATATC
251 TCACCTAGTG GCACTGCAAA GTTTGGGGGA ACTGAATCTA TTTAGAGCAG
301 ACTTAACAGT TGAAGAAGAT TTTGATGCTC CTATAGCAGG ATGTGAACTT
351 GTTTTTC AAC TTGCTACACC TGTGAAC TTT GCTTCTCAAG ATCCTGAGAA
401 TGACATGATA AAGCCAGCAA TCAAAGGTGT GTTGAATGTG TTGAAAGCAA
451 TTGCAAGAGC AAAAGAAGTT AAAAGAGTTA TCTTAACATC TTCGGCAGCC
501 GCGGTGACTA TAAATGAACT CAAAGGGACA GGTCAATGTTA TGGATGAAAC
551 CAACTGGTCT GATGTTGAAT TTCTCAACAC TGCAAAACCA CCCACTTGGG
601 GTTATCCTGC CTCAAAAATG CTAGCTGAAA AGGCTGCATG GAAATTTGCT
651 GAAGAAAATG ACATTGATCT AATCACTGTG ATACCTAGTT TAACAACTGG
701 TCCTTCTCTC ACACCAGATA TCCCATCTAG TGTGGCTTG GCAATGTCTC
751 TAATAACAGG CAATGATTTT CTCATAAATG CTTTGAAAGG AATGCACTTT
801 CTGTCGGGTT CGTTATCCAT CACTCATGTT GAGGATATTT GCCGAGCTCA
851 TATATTTCTT GCAGAGAAAG AATCAGCTTC TGGTAGATAC ATTTGCTGTG
901 CTCACAATAC TAGTGTTCCT GAGCTTGCAA AGTTTCTCAA CAAACGATAT
951 CCTCAGTATA AAGTTCCAAC TGAATTTGAT GATTGCCCCA GCRAAGCAAA
1001 GTTGATAATC TCTTCTGAAA AGCTTATCAA AGAAGGGTTC AGTTTCAAGC
1051 ATGGTATTGC CGAAACTTTC GACCAGACTG TCGAGTATTT TAAGACTAAG
1101 GGGGCACTGA AGAATTAGAT TTTGATATTT CTAATTCAAT AGCAAAC TCT
1151 AAGCTTGTTA TGTGTTTGTG AAGTTCAGAG TGAATATCA AATGAATAAG
1201 TGGAGAGAGC ACAA TAAGAG GAGAGCACA TAATTTTGGG AAAAAAAAAA
1251 AAAAAAAAAA AAAAAAAGT ACTCTGCGTT GTTACCACTG CTTAATCACT
1301 AGTGAATTC

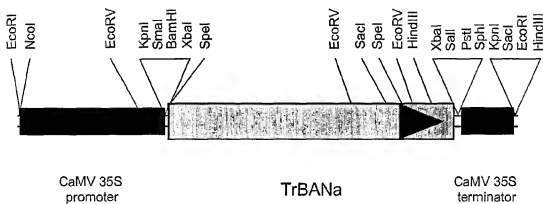
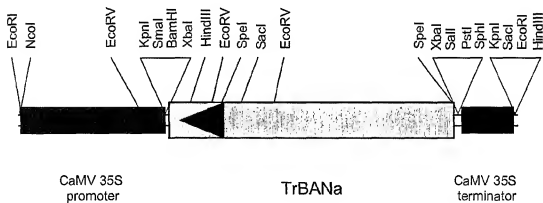
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FIGURE 117

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1 MASIKQIGNK KACVIGGTGF VASMLIKQLL EKGAVNTTV RDPDSPKKIS
51 HLVALQSLGE LNLFRADLTV EEDFDAPIAG CELVFQLATP VNFASQDPEN
101 DMIKPAIKGV LNVLKAIARA KEVKRVILTS SAAAVTINEL KGTGHVMDDET
151 NWSDEVFLNT AKPPTWGYP A SKMLAEKAAW KFAEENDIDL ITVIPSLTTG
201 PSLTPDIPSS VGLAMSLITG NDFLINALKG MQFLSGSLSI THVEDICRAH
251 IFLAEKESAS GRYICCAHNT SVPELAKFLN KRYPQYKVPT EFDDCPSKAK
301 LIISSEKLIK EGFSFKHGIA ETFDQTVEYF KTKGALKN

FIGURE 118

192/271**pDH51TrBANa sense****pDH51TrBANa anti****FIGURE 119**

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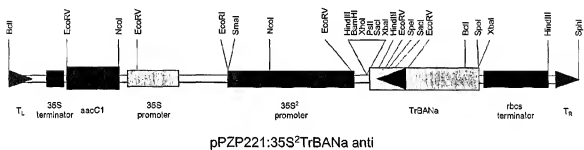
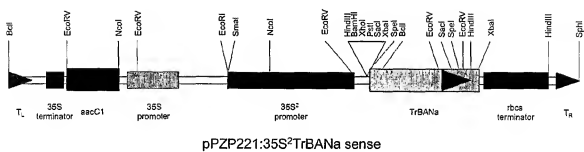
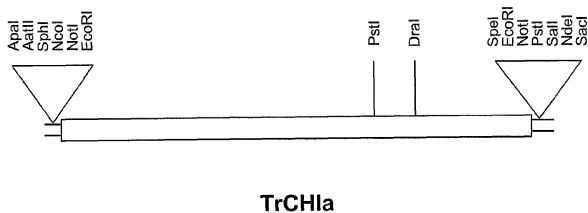


FIGURE 120

194/271**FIGURE 121**

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```

1  GAATTCGATT AAGCAGTGGT AACACGCAG AGTACGCGGG GACTTAAACA
51  TTGACACAAG TCCCAATAAA AAAAGATCTG AAACAACATA GTCAACCCAT
101 TTTTAAACAT TAAACTAAAA ATATGTCGGC CATCACCSCA ATCCAAGTCG
151 AGAACCTTGA ATTTCCGGCT GTGGTTACTT CTCGGGCCAC CGGTAAGTCA
201 TATTTTCTTG GTGGTGCAGG GGAGAGAGGT TTGACTATTG AAGGAAACTT
251 CATCAAGTTC ACTGCCATAG GAGTATATTT GGAAGATGTA GCAGTGGCTT
301 CACTTGCCAC TAAATGGAAG GGTAATCCT CTGAGGAGTT GCTTGAGACT
351 CTTGACTTCT ATAGAGACAT CATTTTCAGGA CCCTTTGAAA AGTTGATTCG
401 AGGATCGAAG ATTAGGGAAT TGAGTGGTCC TGAGTACTCA AGGAAGGTTA
451 ATGAAAACTG CGTGGCACAC TTAAAATCTG TTGGGACTTA TGGAGATGCT
501 GAAGCTGAAG CTATGCAAAA ATTTGTTGAA GCCTTCRAGC CTATTAATTT
551 TCCACCTGGT GCCTCTGTTT TTTACAGGCA ATCACCTGAT GGAATATTAG
601 GGCTTAGTTT CTCTCAAGAT GCAAGTATAC CAGAAAAGGA GGCTGCAGTA
651 ATAGAGAACA AGGCAGCTTC ATCGGCAGTG TTAGAAACTA TGATTGGTGA
701 ACATGCTGTT TCTCTGATT TAAAGCGTTG TTTGGCTGCA AGATTACCTG
751 CCTTGTGTAA CGAGGGTACT TTCAAGATTG AATGAAAAC TATTATTATT
801 ATCTCCAAAA GCATTGCAGC ACAAGATTGA GTCATTTATG AGCATGGACA
851 TTTTATGTGC CACACATGTT TAACTTTTGT ATCTCTCTTT AGATTCTCAT
901 CAATATCAAT AATACTAATA TGAAACGAAG TCAAAAAAAA AAAAAAAA
951 AAAAAAAA AAAAGTACTC TGC GTTGTTA CCACTGCTTA ATCACTAGT
1001 AATTC

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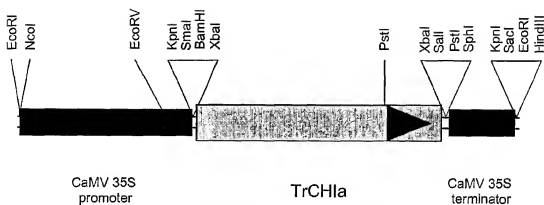
FIGURE 122

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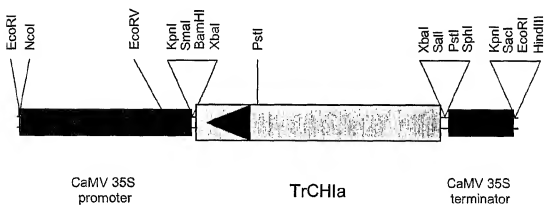
1 MSAITAIQVE NLEFPAVVTs PATGKSYFLG GAGERGLTIE GNFIKFTAIG
51 VYLEDVAVAS LATKWKGKSS EELLETLDFY RDIISGPFEK LIRGSKIREL
101 SGPEYSRKVN ENCV AHLKSV GTYGDAEAEA MQKFVEAFKP INFPPGASVF
151 YRQSPDGILG LSFsqDASIP EKEAAVIENK AASSAVLETM IGEHAVSPDL
201 KRCLAAARLPA LLNEGTFKIE

FIGURE 123

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pDH51TrCHla sense



pDH51TrCHla anti

FIGURE 124

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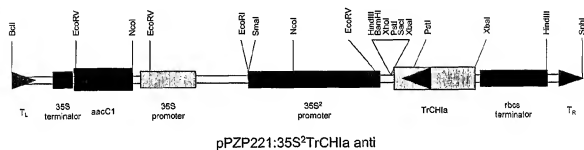
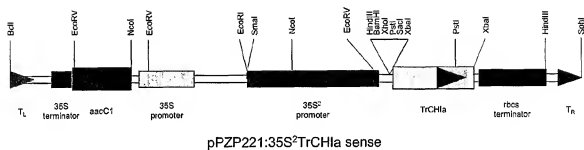
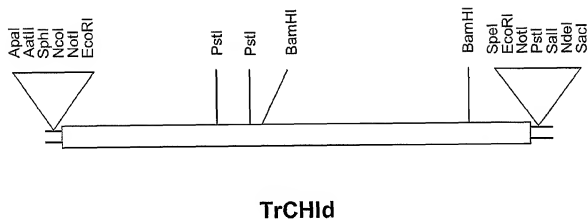


FIGURE 125

199/271**FIGURE 126**

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```

1  GAATTCACCTA GTGATTAAGC AGTGGTAACA ACGCAGAGTA CGCGGGGACA
51 TTACAACCTCA CAACACCTTC TCCATTACCA TCTATCTTCT ACTAAGTTCA
101 ACGAGATCAA TGGCACTTCC TTCGTGCACC GCTTTGAATA TCGAGAACAA
151 TCTATPCCCT CCTACCGTCA CACCACCGGG ATCCACCAAC AATTTCTTCC
201 TCGGCGGTGC AGGAGAGCGG GGTCTTCAAA TTCAAGACAA ATTTGTCAAA
251 TTCACCGCTA TTGGTGTTTA TCTACAGGAC ATTGCTGTTC CTTACCTCGC
301 CACTAAATGG AAGGGTAAGA CTGCTCAAGA GCTAACGGAA ACTGTTCCCTT
351 TCTTCAGGGA CATCGTTACA GGTCCATTTC AGAAATTAT GCAGGTGACA
401 ATGATCTTGC CATTGACTGG GCAACAATAC TCAGAGAAAG TGTGAGAAAA
451 TTGTGTAGCT ATTTGGAAGT CTCCTGGGAT TTATACCGAC GAAGAAGCCA
501 AAGCAATTGA GAAGTTTGTT TCTGTCTTCA AAGATGAAAC ATTCCCACCA
551 GGCTCCTCTA TCCTTTTTCAC AGTATTACCC AAAGGATTAG GATCACTAAC
601 GATAAGTTTC TCTAAAGATG GATCCATTCC AGAGACCGAG TCTGCAGTTA
651 TAGAGAATAA GCTACTCTCA CAAGCTGTGC TTGAGTCGAT GATAGGGGCG
701 CACGGTGTCT CCCCTGCAGC AAAACAGAGT TTGGCCACCA GGTATATCCGA
751 GTTATTCAAC GAGGTTGGTG ATGCTAGCAA CTGATTATAT CAACAAAACG
801 AAAATGAAAG TCCTTCTGTC AATAAAGACC AAGCGGAAAT TTTATTTTAG
851 GTGCACTTTG AAATGACCTC TTTGGCGACT TTTTCTTGTA CTAATAATAA
901 AGAGTGTGTT TGTATCATGT TGTAATTTTA TTTTAGAAAA AGTGAGGTAA
951 GAAAGGAGTC CTTATGTTTA TTTCAATTAT TGAAAAATTA TTTGCATGTA
1001 TAATTGATTT CAACTGATGT TATTTAATCA CGTTTTTCTT AAAAAAATAA
1051 AAAAAAATAA AAAAAAATAA GTACTCTGCG TTGTTACCAC TGCTTAATCG
1101 AATTC

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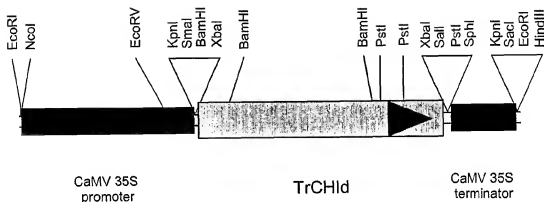
FIGURE 127

201/271

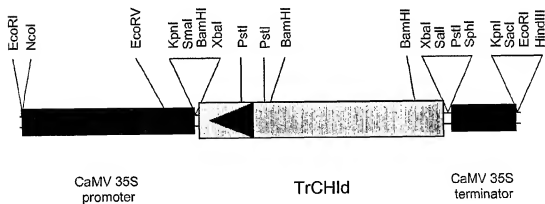
1 MALPSVTALN IENNLFPPTV TPPGSTNNFF LGGAGERGLQ IQDKFVKFTA
51 IGVYLQDIAV PYLATKWKKG TAQELTETVP FFRDIVTGPF EKFMQVTMIL
101 PLTGQQYSEK VSENCVAIWK SLGIYTDEEA KAIEKFVSVF KDETFFPPGSS
151 ILFTVLPGKL GSLTISFSKD GSIPETESAV IENKLLSQAV LESMIGAHGV
201 SPAAKQSLAT RLSELFNEVG DASN

FIGURE 128

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pDH51TrCHld sense



pDH51TrCHld anti

FIGURE 129

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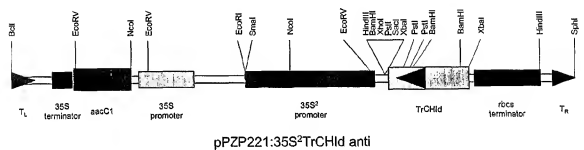
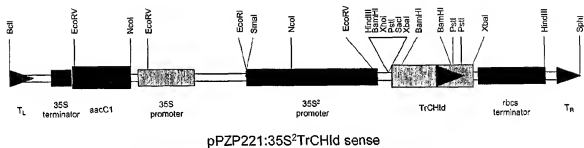


FIGURE 130

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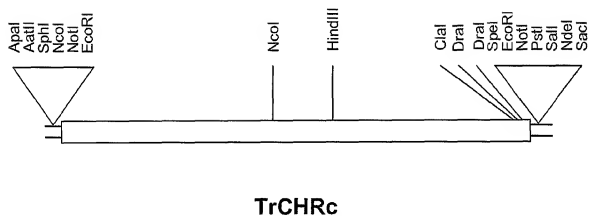


FIGURE 131

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```

1  GAATTCGATT AAGCAGTGGT AACACGCAG AGTACGCGGG GATTCAAACA
51 TAGCTCAAAG TGTGTAACAA ATTTCCTTAAC TTAAACACATT TTCAACCCAA
101 CAAAAAAAAA CAAAGACAAA AACATGGGTA GTGTTGAAAT TCCAACAAAG
151 GTTCTTACTA ACAGTTCCTAG TCAAGTGAAA ATGCCTGTGG TTGGAATGGG
201 ATCAGCACCT GATTTACAT GTAAGAAAGA CACAAAAGAT GCAATCATTTG
251 AAGCCATCAA ACAGGGTTAT AGACACTTTG ATACTGCTGC TGCTTATGGC
301 TCAGAACAAAG CTCTTGGTGA AGGTTTGAAA GAAGCAATTG AACTTGGTCT
351 TGCTACTAGA GAAGACCTTT TTGTTACTTC TAAACTTTGG GTCAGTAAA
401 ATCATCCTCA TCTTGTGTGT CCTGCTCTTC AAAATCTCT CAAGACTCTT
451 CAATTGGAGT ACTTGGACTT GTATTGATC CATTGGCCAC TTAGTTCTCA
501 GCCTGGAAAG TTTTCATTTT CAATTGATGT GGCAGATCTC TTGCCATTTG
551 ATGTGAAGGG TGTTTGGGAA TCCATGGAAG AAGGCTTGAA ACTTGGACTC
601 ACTAAAGCTA TTGGTGTTAG TAACTTCTCT GTCAAGAAAC TTCAAAATCT
651 TGTCTCAGTT GCCACTGTTC TTCCTGCTGT CAATCAAGTG GAGATGAACC
701 TTGCATGGCA ACAAAGAAG CTTAGAGAAT TTTGCAATGC AAATGGAATA
751 GTGTTAACTG CATTTCACCC ATTGAGAAAA GGTGCAAGCA GGGGACCAAA
801 TGAAGTTATG GAAAAATGATA TGCTTAAAGA GATTGCAGAT GCTCATGGAA
851 AGTCTGTGTC ACAAATTTCA TTGAGATGGT TATATGAACA AGGAGTCACT
901 TTTGTTCCCA AGAGCTATGA TAAGGAAAGA ATGGGTCAAA ATTTGGGTAT
951 CTTTGATTGG ACATTGGCAA AAGAAGATCA TGAGAAAATT GATCAAAATTA
1001 AGCAGAACCG TTTGATCCCT GGACCAACCA AGCCAGGACT CAGTGACCTA
1051 TGGGATGATG AAATATAAAG TGGAAGATGT TAAAAGTCCC TTAAGCTCAC
1101 TCAATATCTA TCTATTGTGT ACTTTTGTGA TTTGGGGTTT GAAATTGAGT
1151 CACCCCTGTT TCTGTATCGA TTTAAATTTT AAATAATCAA TTTTTCATTA
1201 CAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AGTACTCTGC GTTGTTACCA
1251 CTGCTTAATC ACTAGTGAAT TC

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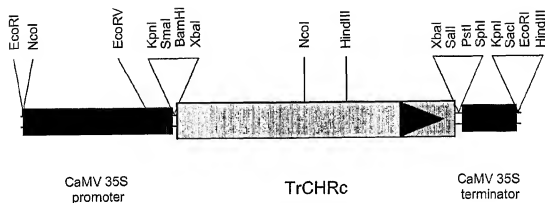
FIGURE 132

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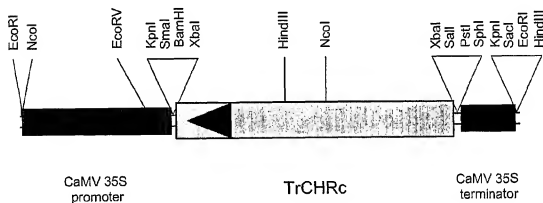
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51 HFDTAAAYGS EQALGEGLEKE AIELGLVTRE DLFVTSKLWV TENHPHLVVP
101 ALQKSLKTLQ LEYLDLYLIH WPLSSQPGKF SFPIDVADLL PFDVKGVWES
151 MEEGLKLGLT KAIGVSNFSV KKLQNLVSVV TVLPAVNQVE MNLAWQQKKL
201 REFCNANGIV LTAFSPLRKG ASRGPNEVME NDMLKEIADA HGKSVAQISL
251 RWLYEQGVTF VPKSYDKERM GQNLAIFDWT LAKEDHEKID QIKQNRILIP
301 PTKPGLSDLW DDEI

FIGURE 133

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pDH51TrCHRC sense



pDH51TrCHRC anti

FIGURE 134

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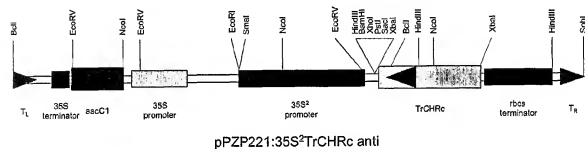
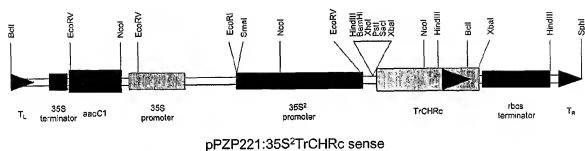


FIGURE 135

209/271**TrCHSa1****FIGURE 136**

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```

1  GAATTCGATT  AAGCAGTGGT  ATCAACGCAG  AGTACGCGGG  GACAACAAC
51  ATAACCTCCT  GTTATTAACC  AATTGAGTTC  AAATTACATA  CATAGCAGGA
101 ACTATACTAA  AGATATCAAC  ATGGTTAGTG  TTTCTGAAT  TCGCAAGGCT
151 CAAAGGGCTG  AAGGCCCTGC  AACTATTTTG  GCCATTGGTA  CTGCAAAATCC
201 AGCAAAATCGT  GTTGACCGA  GTACATATCC  TGATTTCTAC  TTCAAAATCA
251 CTACAGTGA  GCATAAGGTT  GAGCTTAAAG  AGAAATTTCA  GCGCATGTGT
301 GATAAATCTA  TGATCAAGAG  CAGATACATG  TATCTAACAG  AAGAGATTTT
351 GAAAGAAAAAT  CCTAGTCTTT  GTGAATACAT  GGCACCTTCA  TTGGATGCTA
401 GGCAAGACAT  GGTGGTGGTT  GAGGTACCTA  GACTTGGGAA  GGAGGCTGCA
451 GTGAAAAGCTA  TCAAAGAATG  GGGTCAACCA  AAGTCAAAGA  TTACTCACTT
501 AATCTTTTGC  ACCACAAGTG  GTGTTGACAT  GCCTGGTGCC  GATTACCAAC
551 TCACAAAAC  CTTAGGTCTT  CGCCCATATG  TGAAGAGGTA  CATGATGTAT
601 CAACAAGGGT  GCTTTGCAGG  TGGGACGGTT  CTTCGTTTGG  CCAAGGATTT
651 GGCCGAGAAC  AACAAAGGTG  CTCGTGTGTT  GGTGTTTGC  TCTGAAGTAA
701 CCGCAGTCAC  ATTCCGCGGC  CCCAGTGACA  CTCATTTTGA  CAGTCTTGTT
751 GGACAAGCAC  TATTCGGAGA  TGGAGCTGCT  GCACCTCATG  TTGGCTCAGA
801 CCCAGTACCA  GAAATTGAGA  AGCCAATATT  TGAGATGGTT  TGGACCGCAC
851 AGACAATTGC  TCCAGATAGT  GAAGGTGCCA  TTGATGGTCA  TCTTCGTGAA
901 GCTGGACTAA  CATTTTCATCT  TCTTAAAGAT  GTTCCTGGGA  TTGCTCAAA
951 GAACATTGAT  AAGGCATTGG  TTGAGGCATT  CCAACCATTA  AACATCTCTG
1001 ATTACAATTC  AATCTTTTGG  ATTGCTCATC  CAGGTGGTCC  TGCAATTCTA
1051 GACCAAGTTG  AGATAAAGTT  GGGCTTAAAA  CCTGAAAAAA  TGAAGGCCAC
1101 CAGAGATGTA  CTTAGTGAAT  ATGGTAACAT  GTCAAAGTGA  TGTGTATTGT
1151 TCATCTTAGA  TGAGATGAGA  AAGAAATCGG  CTGAAAAATG  ACTTAAACC
1201 ACAGGAGAAG  GACTTGACTG  GGGTGTGTTG  TTTGGATTTG  GGCCCGGACT
1251 TACCATTGAA  ACTGTTGTTT  TACATAGTGT  GGCTATATGA  GAATGAGAGA
1301 CTTGATTGTT  TTTTATTGTA  TTGTATTGTA  TTACTTTTAA  TCTTGGTTGA
1351 ACCTCCATTT  TAAGAATAAA  TATGGAGTTC  AATATGGACC  ATCCTGTTAA
1401 AATAATATAT  CGTTAATAGC  TATTATTTTA  GTGCTGTGTT  CTTTTTACTA
1451 AACTATTTTA  TTTTAGTATT  TGTTTTGTAC  CAAAAAATAA  AAAAAAATAA
1501 AAAAAAGTA  CTCTGCGTTG  TTACCACTGC  TTAATCACTA  GTGAATTC

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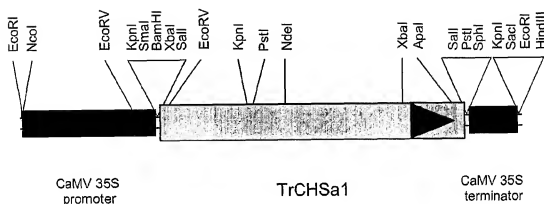
FIGURE 137

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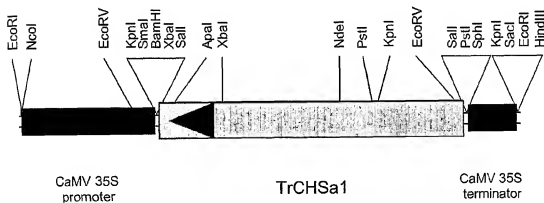
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51 ELKEKFQRMK DKSMIKSRYM YLTBEILKEN PSLCEYMAPS LDARQDMVVV
101 EVPRLGKEAA VKAIKEWGQP KSKITHLIFC TTSGVDMPGA DYQLTKLLGL
151 RPYVKRYMMY QQGCFAGGTV LRLAKDLAEN NKGARVLVVC SEVTAVTFRG
201 PSDTHLDSL VQALFGDGAA ALIVGSDEVP EIEKPIFEMV WTAQTIAPDS
251 EGAIDGHLRE AGLTFHLLKD VPGIVSKNID KALVEAFQPL NISDYNSIFW
301 IAHPGGPAIL DQVEIKLGLK PEKMKATRDV LSEYGNMSSA CVLFILDEMR
351 KKSANGLKT TGEGLDWGVL FGFPGGLTIE TVVLHSAI

FIGURE 138

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pDH51TrCHSa1 sense



pDH51TrCHSa1 anti

FIGURE 139

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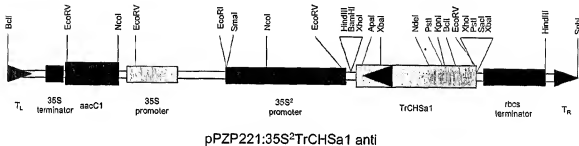
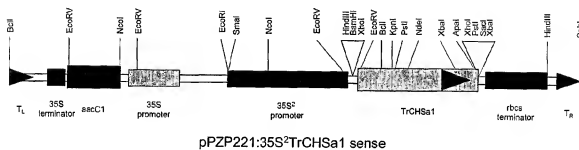
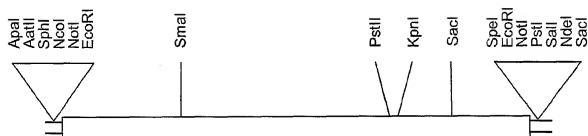


FIGURE 140

214/271**TrCHSa3****FIGURE 141**

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```

1  GAATTCACTA GTGATTAAGC AGTGGTAACA ACGCAGAGTA CGCGGGGAAC
51  AAAAACCAACT ACGCATATTA TATATATATA TATATAGTCT ATAAITGAAA
101  GAAACTGCTA AAGATATTAT TAAGATATGG TGAGTGTAGC TGAAATTCGC
151  AAGGCTCAGA GGGCTGAAGG CCCTGCAACC ATTTTGGCCA TTGGCACTGC
201  AAATCCACCA AACCGTGTGG AGCAGAGCAC TCAAAGAGAA GTTCCAACGC
251  AAATTACAAA CAGTGAGCAC AAGACTGAGC TCAAAGAGAA GTTCCAACGC
301  ATGTGTGACA AATCCATGAT CAAGAGCAGA TACATGTATC TAACAGAAGA
351  GATTTTGAAA GAAAATCCTA GTCCTTGTGA ATACATGGCA CCTTCATTGG
401  ATGCTAGGCA AGACATGGTG GTGGTTGAGG TACCTAGACT TGGGAAGGAG
451  GCTGCAGTCA AGGCCATTAA AGAATGGGGT CAACCAAAGT CAAAGATTAC
501  TCACTTAATC TTTTGCACCA CAAGTGGTGT TGACATGCCT GGTGCTGATT
551  ACCAACTCAC AAAACTCTTA GGTCTTCGCC CATATGTGAA AAGGTATATG
601  ATGTACCAAC AAGGTTGTTT TGCAGGAGGC ACGGTGCTTC GTTTGGCAAA
651  AGATTGGCC GAGAACAAAC AAGGTGCTCG TGTGCTAGTT GTTTGTTCTG
701  AAGTCAACGC AGTCACATTT CGCGGCCCCA GTGATACTCA CTTGGACAGT
751  CTTGTTGGAC AAGCATTGTT TGGAGATGGA GCCGCTGCAC TAATTGTTGG
801  TTCTGATCCA GTGCCGAAA TTGAGAAACC AATATTGAG ATGGTTTGGG
851  CTGCACAAAC AATTGCTCCA GACAGTGAAG GTGCCATTGA TGGTCATCTT
901  CGTGAAGCTG GGCTAACATT TCATCTTCTT AAAGATGTTT CTGGGATTGT
951  ATCAAAGAAC ATTAATAAAG CATTGGTTGA GGCTTTCCAA CCATTAGGAA
1001 TTTCTGACTA CAACTCAATC TTTTGGATTG CACACCCGGG TGGACCTGCA
1051 ATTCTTGATC AAGTAGAACA AAAGCTAGCC TTGAAGCCCG AAAAGATGAG
1101 GGCCACGAGG GAAGTCTTAA GTGAATATGG AAACATGTCA AGCGCATGTG
1151 TATTGTTCAT CTTAGATGAG ATGCGGAAGA AATCGGCTCA AAATGGACTT
1201 AAGACAACTG GAGAAGGACT TGATTGGGGT GTGTTGTTCG GCTTCGGACC
1251 AGGACTTACC ATTGAAACCG TTGTTCTTCG TAGCGTGGCT ATATAAGATG
1301 TGTGATTGTT TTTATTTTAA TGTATTACTT TTAATCTTGC TGCCTTGAAT
1351 TTCGATTTAA GAATAAATAA ATATATCTTT TGATAAAAAA AAAAAAAA
1401 AAAAAAAAAA AAGTACTCTG CGTTGTTACC ACTGCTTAAT CGAATTC

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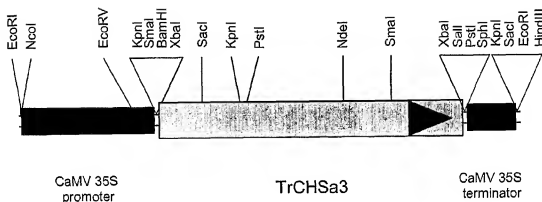
FIGURE 142

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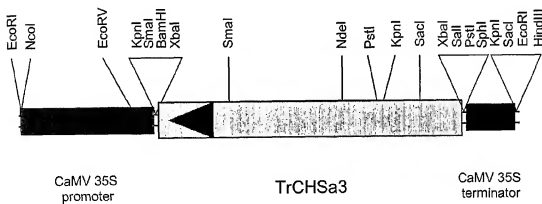
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51 ELKEKFQRMK DKSMIKSRYM YLTEEILKEN PSLCEYMAPS LDARQDMVVV
101 EVPRLGKEAA VKAIKEWGQP KSKITHLIFC TTSGVDMPGA DYQLTKLLGL
151 RPYVKRYMMY QQGCFAGGTV LRLAKDLAEN NKGARVLVVC SEVTAVTFRG
201 PSDTHLDSL VQALFGDGAA ALIVGSDPVP EIEKPIFEMV WTAQTIAPDS
251 EGAIDGHLRE AGLTFHLLKD VPGIVSKNIN KALVEAFQPL GISDYSIFW
301 IAHPPGPAIL DQVEQKLALK PEKMRATREV LSEYGNMSSA CVLFILDEMR
351 KKSQAQNLKT TGEGLDWGVL FGFGPGLTIE TVVLRSAI

FIGURE 143

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pDH51TrCHSa3 sense



pDH51TrCHSa3 anti

FIGURE 144

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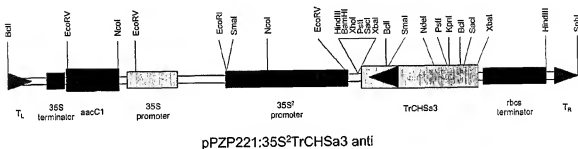
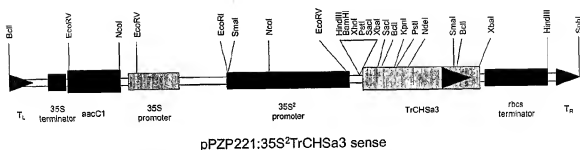
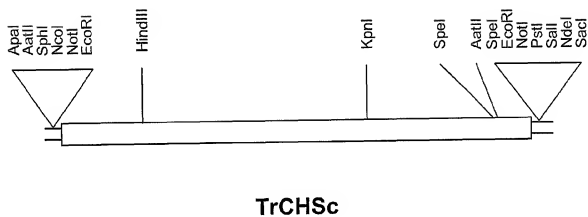


FIGURE 145

219/271**FIGURE 146**

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1	GAATTCGATT	AAGCAGTGGT	AACAACGCAG	AGTACGCGGG	GATTCAATCT
51	GTTGTGCATA	AAATTCATCT	ATTGCATAGA	AAACCATACA	CATTGTGATCT
101	TGCAAAGAAG	AAATATGGGA	GACGAAGGTA	TAGTGAGAGG	TGTCACAAAG
151	CAGACAACCC	CTGGGAAGGC	TACTATATTG	GCTCTTGGCA	AGGCATTCCC
201	TCACCAACTT	GTGATGCAAG	AGTGTTTAGT	TGATGGGTAT	TTTAGGAGACA
251	CTAATTGTGA	CAATCCTGAA	CTTAAGCAGA	AACTTGCATG	ACTTTGTAAG
301	ACAACCACCG	TAAAAACAAG	GTATGTTGTT	ATGAATGAGG	AGATACTAAA
351	GAAATATCCA	GAACTTGTG	TCGAAGGCGC	CTCAACTGTA	AAACAACGTT
401	TAGAGATATG	TAATGAGGCA	GTAACACAAA	TGGCAATTGA	AGCTTCCCAA
451	GTTTGCCATA	AGAATTGGGG	TAGATCCCTTA	TCGGACATAA	CTCATGTGGT
501	TTATGTTTCA	TCTAGTGAAG	CTAGATTACC	CGGTGGTGAC	CTATACTTGT
551	CAAAAGGACT	AGGACTAAAC	CCTAAAAATTC	AAAGAACCAT	GCTCTATTTT
601	TCTGGATGCT	CGGGAGGCGT	AGCCGGCCTT	CGCGTTGCGA	AAGACGTAGC
651	TGAGAACAAC	CCTGGAAGTA	GAGTTTGTCT	TGCTACTTCG	GAAACTACAA
701	TTATTGGATT	CAAGCCACCA	AGTGTTTGATA	GACCTTATGA	TCTTGTGTGT
751	GTGGCATTCT	TTGGAGATGG	TGCTGGTGCA	ATGATAATTG	GCTCAGACCC
801	GGTATTTTGAA	ACTGAGACAC	CATTGTTTGA	GCTGCATACT	TCAGCTCAGG
851	AGTTTATACC	AGACACCGAG	AAGAAAAATTG	ATGGGCGGCT	GACGGAGGAG
901	GGCATAAGTT	TCACACTAGC	AAGGGAACTT	CCGCAGATAA	TCGAAGACAA
951	TGTTGAGGGA	TTCTGTAATA	AACTAATTGA	TGTTGTGTGG	TTGGAGAATA
1001	AGGAGTACAA	TAAGTTGTTT	TGGGCTGTGC	ATCCAGGTGG	GCCTCGCATA
1051	TTGAATCGCG	TGGAGAAGCG	GCTTGAGTTG	TCGCCGCAGA	AGCTGAATAG
1101	TAGTAGAAAA	GCTCTAATGG	ATTATGGAAA	TGCTAGCAGC	AATACTATTG
1151	TTTATGTGCT	GGAATATATG	CTAGAAGAGG	AAAAGAAAGT	TAAAAAGGCG
1201	GGTGGAGGAG	ATTCTGAATG	GGGATTGATA	CTTGCTTTTG	GACCTGGAAT
1251	TACTTTTGAG	GGGATTCTAG	CAAGGAACCT	GTGTGCATGA	AGCTTTATAC
1301	AAATTGTGATG	CATGACTTAT	ACTCTTATTT	CTACTAATTA	TTATATTAAG
1351	CAAAATTCAGA	ACTTTTAAAGT	AATGATTTAA	TGAAGAATAC	TTATAGTATA
1401	TTGACTTTTAT	TCACTTTCAA	AGCAAGTTTA	TGATCCTAAG	ACATGGGTAGA
1451	ACTTGAGCAT	GTGGAATAGT	TGTAACAAAA	ACTCTAAGCA	AATAGAGACT
1501	TTATGTAGTA	TAAAGCATTT	CCAGACATGA	TAAATAATGG	TACCTCAGAA
1551	CATAAAATAT	ATTTAGCTAT	CTTTCATCCC	CAACTTTTACA	CATCCACCAA
1601	GGTACAGAAT	AAGCATATGT	CAACACAAAA	TGTACTCTAA	GTCTAACATG
1651	AGTAACCAAA	CATGATGCCT	GATTAAAGTA	AAAGAAAAAG	AAATCTGAGG
1701	GCAATAGTCT	TCAATCACAC	CACCTCCAGAG	GGAAAGGCGTA	GAAACAAGCTG
1751	TCCGCCGAAA	ACACTGCAAT	TCAATAAATA	TCATTAGGAC	AACAGTGCAG
1801	AGTCATGCGG	GAAATGTCTT	AAGTCACTGT	ACTAAAAATA	TAGGATTATA
1851	TTATGAACTA	TACTAACCTT	TTACATAAAT	AGTAACAGAA	ATCAGCTAAG
1901	ATGAATGTCT	GGACAATTTT	TGAGATAAGA	ACCATGACGG	CCATAAGCCA
1951	TACCCCAAGG	CAACCAATAA	ATGTCCACAG	GTATCTAACA	CGTGTGCAAA
2001	GAAATAGTAA	GTTATTAGGA	GATGTGCGGT	TACGAAATTC	AAGCTACACA
2051	ACAAAAGGAG	GCCAGAACAA	CAGCAATCTT	GTAACCCAGAT	GACACACAATA
2101	AAATGTAAC	TTAAGAGAGC	CGAACACACA	AAACATTGCAA	CTCAGATGGA
2151	ATTGCTGCCA	TGTAACTAGT	AGGAGATTTG	GGACGTCAAA	TCAGTATATT
2201	ATGCAAAATC	AAGGTATGAC	CGCCTTGTCT	ATTGTAGCAT	ACAACAAACG
2251	TACAGTGGGT	TTGTCCCTCT	CAAAAATGGCA	GGATCTTTAC	AGCACAATAT
2301	TTGGTTTTGT	CATACTTATA	CCATAAAAAA	AAAAAAAAAA	AAAAAAAAAA
2351	AAAGTACTCT	CGCTTGTTC	CAGTCTTAA	TCAGTGTGA	ATTC

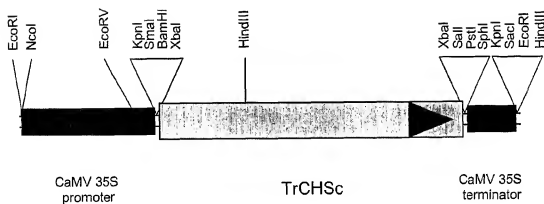
FIGURE 147

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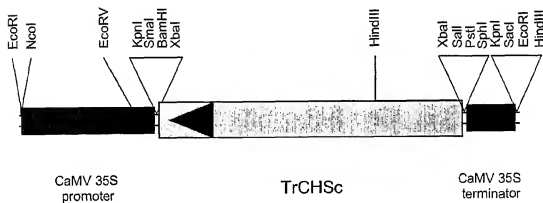
1 MGDEGIVRGV TKQTTPGKAT ILALGKAPPH QLVMQECLVD GYFRDTNCDN
51 PELKQKLARL CKTTTVKTRY VVMNEILKK YPELVVEGAS TVKQRLEICN
101 EAVTQMAIEA SQVCLKNWGR SLSDITHVVY VSSSEARLPG GDLYLSKGLG
151 LNPKIQR TML YFSGCSGGVA GLRVAKDVAE NNPGRSVLLA TSETTIIGFK
201 PPSVDRPYDL VGVALFGDGA GAMIIGSDPV FETETPLFEL HTSAQEFIPD
251 TEKKIDGRLT EEGISFTLAR ELPQIIEDNV EGFCNKLIDV VGLENKEYNK
301 LFWAVHPGGP AILNRVEKRL ELSPQKLNAS RKALMDYGNA SSNTIVYVLE
351 YMLEEEKKIK KAGGGDSEWG LILAFGPGIT FEGILARNLC A

FIGURE 148

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pDH51TrCHSc sense



pDH51TrCHSc anti

FIGURE 149

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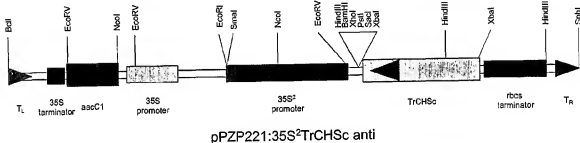
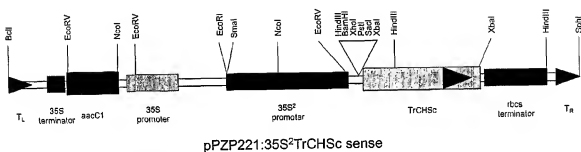
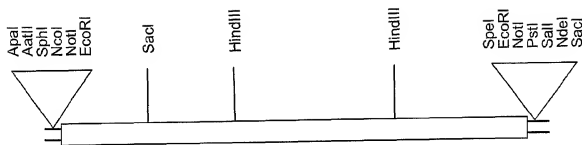


FIGURE 150

224/271**TrCHSd2****FIGURE 151**

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```

1  GAATTCGATT AAGCAGTGGT AACAAACGCAG AGTACGCGGG GATAGCAACA
51 CACACTTTGA TTTCTTTTGG AGTCCTTGCT ACGTGGCTTT ACCAAAAAAC
101 GTTGCTAAGT CATCAACCAT TCCAATTCC TTAATAAACC TATCAGTACT
151 CACCATCTTT TCTTCCCTCC TGCTAACTTT AGACTCAGAG AAGATGGTGA
201 ATGTTAATGA GATCCGCCAG GCACAGAGAG CTGAAGGCC TGCCACCGTG
251 TTGGCAATCG GCACTGCAAC TCCTCCAAAC TGTGTCGATC AGAGTACATA
301 CCCAGACTAC TACTTCCGCA TCACAAACAG TGAGCACAAG ACAGAGCTCA
351 AAGAAAAAAT CCAGCGCATG TGTGACAAAT CTATGATTAA GAAGAGATAC
401 ATGCATTTGA CAGAAGAGAT TTTGAAGGAG AATCCAAGTT TATGTGAGTA
451 CATGGCACCT TCATTGGATG CAAGACAAGA CATGGTGGTT GTGGAAGTAC
501 CAAGGCTAGG AAAAGAGGCT GCAACAAAGG CTATCAAGGA ATGGGGTCAA
551 CCTAAGTCCA AGATTACTCA CCTCATCTTT TGCACCACAA GTGGTGTGGA
601 CATGCCTGGC GCCGACTATC AGCTTACAAA GCTTTTAGGC CTTCGTCCGC
651 ATGTGAAGCG TTATATGATG TACCAACAAG GTTGTTCGCG TGGTGGTACG
701 GTGCTTCGTT TGGCTAAAGA CTTGGCTGAA AACAAACAAAG GTGCCCGTGT
751 GTTGGTGGTT TGTTCAAGAG TCACTGCGGT TACTTTCCGT GGAACCAAGT
801 ACACTCATCT TGATAGCCTT GTGGGGCAAG CATGTGTTTG AGATGGTGCA
851 GCAGCTGTGA TTGTAGGTTT AGACCCATTA CCACAAGTTG AGAAGCCCTT
901 GTTTGAATTG GTATGGACTG CTCAAACAAT CCTTCCAGAC AGTGAAGGAG
951 CCATTGATGG GCACCTTCGT GAAGTGCGGC GAGAAAGCTC TTGTTGAGGC
1001 GATGTTCCCTG GACTCATCTC AAAGAACATT TTCTATATTT TGGATCGCAC
1051 CTTTCAACCT TTAGGTATCT CTGATTACAA TTCTATATTT TGAATCGCAC
1101 ATCCTGGTGG ACCTGCAATT CTGGACCAAG TGGGAAGCCAA ATTAAGCCTTA
1151 AAGCCAGAGA AAATGCAAGC CACCCGGCAT GTGCTTAGCG AGTATGGTAA
1201 CATGTCAAGT GCATGTGTGT TATTTATCTT GGTAGAGATG AGGAGGAAGT
1251 CAAAAGAAAG TGGACTTGCC ACAACAGGCG AGGGGCTGGA ATGGGGTGTA
1301 CTATTGCGTT TTGGACCCGG ACTCACTGTT GAGACTGTAT TGCTCCATAG
1351 TGTGCCACT TAAATGCGCT AGATATGCTA TAACTATATG CTTATTTAAT
1401 TCTTTGTTTC TGGGGGATTT TATCTTCACT TACTTCACTG AGCATTTGAA
1451 TAAAGTTTGT TTTAATTATT CATAATGTAA TATGGTGTG CTTAATGTAC
1501 CCATCCATAT AATATTGTGA ATACATATAT TAATCAACTT GCAATTTCAT
1551 GAAAAA AAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA
1601 AAAAAA AAAAAA AAGTACTCTG CGTTGTTACC ACTGCTTAAT
1651 CACTAGTGAA TTC

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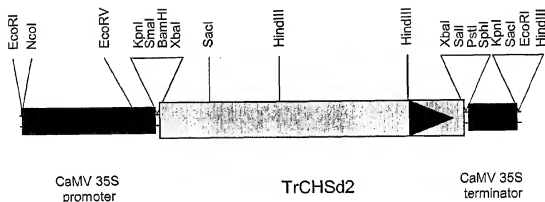
FIGURE 152

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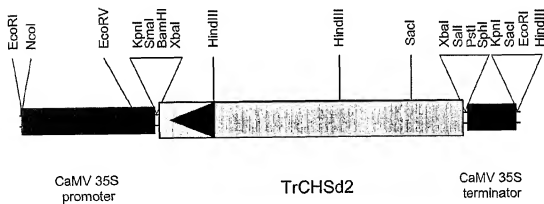
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51 ELKEKFQRC DKSMIKKRYM HLTEBILKEN PSLCEYMAPS LDARQDMVVV
101 EVPRLGKEAA TKAKEWQQP KSKITHLIFC TTSGVDMPGA DYQLTKLLGL
151 RPHVKRYMMY QQGCFAGGTV LRLAKDLAEN NKGARVLVVC SEITAVTFRG
201 PSDTHLDSLV GQALFGDGAA AVIVGSDPLP QVEKPLFELV WTAQTILPDS
251 EGAIDGHLRE VGLTFHLLKD VPGLISKNIE KALVEAFQPL GISDYNISFW
301 IAHFGGPAIL DQVEAKLSLK PEKMQATRHV LSEYGNMSSA CVLFILDEMR
351 RKSKEDGLAT TEGLEWGV LFGFGPGLTVE TVLLHSVAT

FIGURE 153

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pDH51TrCHSd2 sense



pDH51TrCHSd2 anti

FIGURE 154

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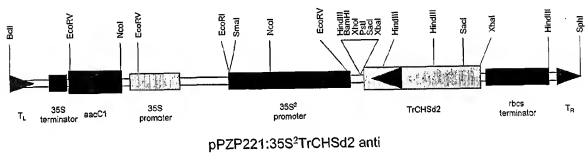
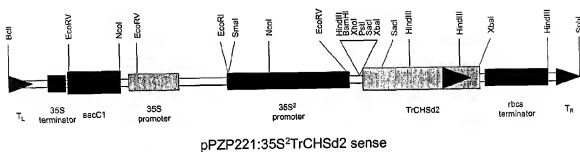
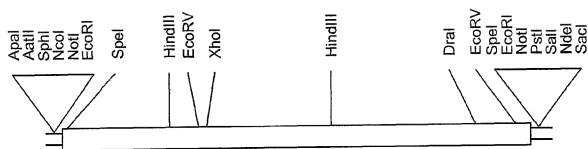


FIGURE 155

229/271**TrCHSf****FIGURE 156**

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1 **GAATTC**GATT AAGCAGTGGT AACAAACGCAG AGTACGCGGG ACTAAGCCTT
 51 GATTTCATTGT TTGTTTCCTCAT AACACAAGAA CTAGTGTTTTG CTTGAATCTTT
 101 AAGAAAAAAT GCCTCAAGGT GATTGTGAATG GAAGTTTCCTC GGTGAATGGA
 151 GCACGTGCTA GACGTGCTCC TACTCAGGGA AAGGCAACGA TACTTGCATT
 201 AGGAAAGGCT TTCCCCGCC AGGTCCCTCCC TCAAGAGTGC TTGGTGGAAG
 251 GATTTCATTCT CGACACTAAG TGTGACGATA CTTATATATAA GGAGAAATTG
 301 GAGCGTCTTT GCAAAAAACAC AACTGTGAAA ACAAGATACA CAGTAATGTC
 351 AAAGGAGATC TTAGACAACCT ATCCAGAGCT AGCCATAGAT GGAACACCAA
 401 CAATAAGGCA AAAGCTTGAA ATAGCAATC CAGCAGTAGT TGAATGGCA
 451 ACAAGAGCAA GCAAGAGATTG CATCAAAGAA TGGGGAAGGT CACCTCAAGA
 501 TATCACACAC ATAGTCTATG TTTCTCTGAG CGAAATTCGT CTACCCGGTG
 551 GTGACCTTTA TCTTGCAAT GAACTCGGCT TAAACAGCGA TGTTAATCGC
 601 GTAATGCTCT ATTTCTCTCG TTGCTACGGC GGTGTCACTG GCTTACGTGT
 651 CGCCAAAGAC ATCGCCGAAA ATAACCTCGG TAGTAGGGTG TTACTCACAA
 701 CATCCGAGAC CACTATTCTC GGTTTTCGAC CACCGAGTAA AGCTAGACCT
 751 TATGACCTCG TTGGCGCTGC ACTTTTCGGT GATGGCGCCG CTGCTGCAAT
 801 AATTGGAACA GACCCATATAT TGAATCAAGA ATCACCTTTC ATGGAATTGA
 851 ACCATGCAGT CCAAAAAATTC TTGCGTGTATA CACAAAATGT GATTGATGGT
 901 AGAATCACTG AAGAGGGTAT TAATTTTAAAG CTTGGAAGAG ACCTTCCTCA
 951 AAAAAATTGA GACAAATATTG AAGAAATTTTG CAAGAAAATT ATGGCTAAAA
 1001 GTGATGTTAA GGAATTTAAT GACTTATTTT GGGCTGTTCA TCCTGGTGGG
 1051 CCAGCTATAC TCAATAAGCT AGAAAATATA CTCAAATTGA AAAGTGATAA
 1101 ATTGGATTGT AGTAGGAAGG CATTAATGGA TTATGGAATG GTTAGTAGCA
 1151 ATACTATATT CTATGTGATG GAGTATATGA GAGATTATTT GAAGGAAGAT
 1201 GGAAGTGAAG AATGGGGATT AGGATTGGCT TTTGGACCAG GGATTACTTT
 1251 TGAAGGGGTT CTCCTCCGTA GCCTTTAATC TTGAAATAAT AATTCATATG
 1301 AAATTACTTG TCTTAAGATT GTGATAGGAA GATGAATATG TATTGGATTA
 1351 ATATTGATAT GGTGTATTTT TAAGTTGATT TTAAGAAAAG TTTTATTAATA
 1401 AAGTATGATG TAACAATTGT TGTTTGAATG TTAAAGGGA AGTATACTAT
 1451 TTTAAGTTCT TGACCATACT GATTTTCTCT TTACACATTT TCATATCTAA
 1501 AATTGTCTTA TGATATCTTC ATTTGTGATA CTGTAATAAT ATAATATCTA
 1551 ATTTGGCTGG CAAAATGAAA GATTTTTCAC CGAAAAAATA AAAAAAATAA
 1601 AAAAAAATAA AAGTACTCTG CGTTGTTACC ACTGCTTAAT CACTAGTGAA
 1651 **TTC**

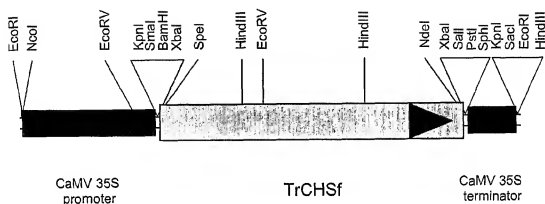
FIGURE 157

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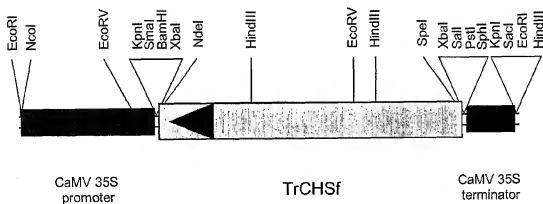
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51 RDTKCDDTYI KEKLERLCKN TTVKTRYTVM SKEILDNYPE LAIDGTPTIR
101 QKLEIANPAV VEMATRASKD CIKEWGRSPQ DITHIVYVSS SEIRLPGGDL
151 YLANELGLNS DVNRVMLYFL GCYGGVTGLR VAKDIAENNP GSRVLLTTSE
201 TTILGFRPPS KAPYDLVGA ALFGDGAAAA IIGTDPILNQ ESPFMELNHA
251 VQKFLPDTQN VIDGRITEEG INFKLGRDLP QKIEDNIEEF CKKIMAKSDV
301 KEFNDLFWAV HPGGPAILNK LENILKLKSD KLDCSRKALM DYGNVSSNTI
351 FYVMEYMRDY LKEDGSEEWG LGLAFGPGIT FEGVLLRSL

FIGURE 158

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pDH51TrCHSf sense



pDH51TrCHSf anti

FIGURE 159

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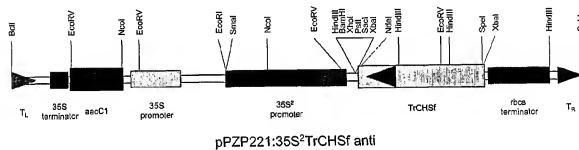
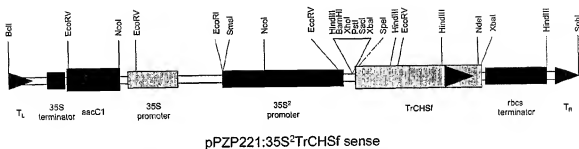
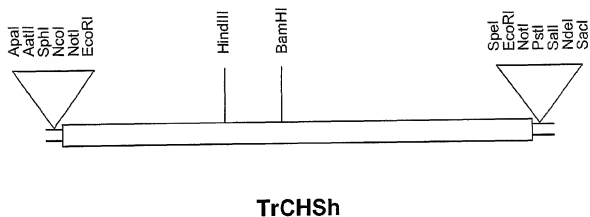


FIGURE 160

234/271**FIGURE 161**

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```

1  GAATTCACCTA GTGATTAAGC AGTGGTAACA ACGCAGAGTA CGCGGGGGGAA
51  TCACCAAAAT CAACACCAAT AATAACCTTC CAAATTCFCG TTACCTCACC
101 AATCTCTATT TTTCATTATA TATCTTGGGT ACATCTTTTG TTACCTCCAA
151 CAAAAAATG GTGACCGTAG AAGAGATTTC TAACGCCCAA CGTTCAAATG
201 GCCCTGCCAC TATCTTAGCT TTGGCACAG CCACTCCTTC TAAGTGTGTC
251 ACTCAAGCTG ATTATCCTGA TTACTACTTT CGTATCACC ACAGCGAACA
301 TATGACTGAT CTTAAGGAAA AATTCAAGCG GATGTGTGAT AGATCAATGA
351 TAAAGAAACG TTACATGCAC CTAACAGAAG ACTTCTTGAA GGAGAATCCA
401 AATATGTGTG AATACATGCG ACCATCACCTA GATGTAAGAC GAGACATAGT
451 GGTGTGTGAA GTACCAAAGC TAGGTAAAGA AGCAGCAAAA AAAGCCATAT
501 GTGAATGGGG ACAACCAAAA TCCAAATCA CACATCTTGT TTTCTGCACC
551 ACTTCCGGTG TTGACATGCC GGGAGCCGAT TACCAACTCA CCAAACCTTTT
601 AGGCCTAAAA CCTTCTGTCA AGCGTCTCAT GATGTATCAA CAAGGTTGTT
651 TCGCTGGCGG CACAGTTCCT CGCTTAGCAA AAGACCTTGT TGAGAAATAC
701 AAAATGCAA GAGTTCCTGT TGTTTGTCTT GAAATTACTG CGGTACTTTT
751 TCGTGGACCA TCGGATACTC ATCTTGATTG GCTCGTGGGA CAGGCGCTTT
801 TTGGTGATGG AGCCGCAGCA ATGATTATTG GTGCGGATCC TGATTTAAAC
851 GTGGAGCGTC CGATTTTCGA GATTGTTTCG GCTGCTCAGA CTATTCTTCC
901 TGATTCTGAT GGCAGCAATT ATGGACATCT TCGTGAAGTG GGGCTCACTT
951 TTCATTTATT GAAAAGATGT CCGGGGATTA TTTCAAAGAA CATTGAAAAA
1001 AGTTTAGTTG AAGCTTTTGC GCCTATTGGG ATTAATGATT GGAACCTAAT
1051 ATTTTGGGTT GCACATCCAG GTGGACCGGC TATTTTAGAC CAGGTTGAAG
1101 AGAAACTCCA TCTTAAAGAG GAGAAACTCC GGTCCACCCG GCATGTGCTT
1151 AGTGAATATG GAAATATGTC AAGTGCAATG GTTTTATTTA TTTTGGATGA
1201 AATGAGAAAA AGGTCATAAG AGGAAGGGAT GATTACAAC TGGTGAAGGGT
1251 TGGAATGGGG TGTGTTGTTT GGGTTTGAC CGGGTTTAA TGTGTAACCC
1301 GTTGTGCTTC ATAGTGTTCC GGTTCAGGGT TGAATTTATT ATACATAGAT
1351 TGAAAAATAA AATTTGCCTG CCGAGAGATG TGAACCTA TTTGTAGGCAA
1401 GCTCAAAATTA AAGTTTGAGA TAATATTGTG CTTTAGTTAT TATGGTATGT
1451 AATGTAATGT TTTTACTTTT TTCGAAATTC ATGTAATTGA ATATGTAAG
1501 TAATATGTTT GGGTTGGAAT ATAATTATTT GTTAACTAAA AAAAAAATAA
1551 AAAAAAATAA AAAAAGTACT CTGCGTTGTT ACCACTGCTT AATCGAATTC

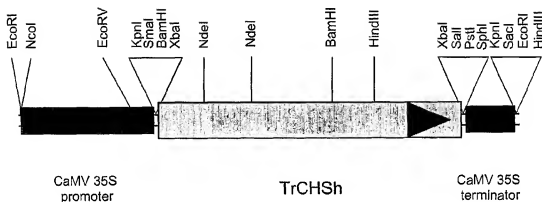
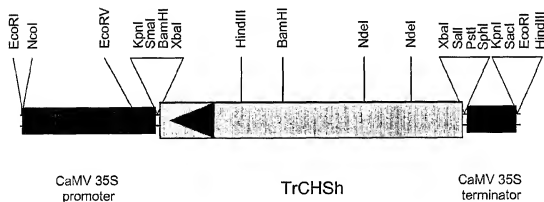
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FIGURE 162

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1 MVTVEEIRNA QRSNGPATIL AFGTATPSNC VTQADYPDYY FRITNSEHMT
51 DLKEKFKRMC DRSMIKKRYM HLTEDFLKEN PNMCEYMAPS LDVRRDIVVV
101 EVPKLGKEAA KKAICEWGQP KSKITHLVFC TTSGVDMPGA DYQLTKLLGL
151 KPSVKRLMMY QQGCFAGGTV LRLAKDLVEN NKNARVLVVC SEITAVTFRG
201 PSDTHLDSLV GQALFGDGAA AMIIGADPDL TVERPIFEIV SAAQTILPDS
251 DGAIDGHLRE VGLTFHLLKD VPGIISKNIE KSLVEAFAPI GINDWNSIFW
301 VAHPGGPAIL DQVEEKLHLK EEKLRSTRHV LSEYGNMSSA CVLFILDEMR
351 KRSKEEGMIT TGEGLEWGV LFGFGPGLTVE TVVLHSPVPQ G

FIGURE 163

237/271**pDH51TrCHSh sense****pDH51TrCHSh anti****FIGURE 164**

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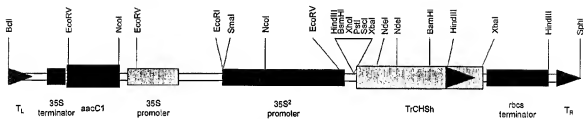
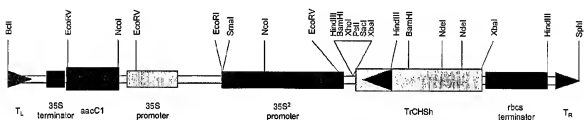
pPZP221:35S²TrCHSh sensepPZP221:35S²TrCHSh anti

FIGURE 165

239/271**TrDFRd****FIGURE 166**

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```

1  GAATTCACTA GTGATTAAGC AGTGGAACA ACGCAGAGTA CGCGGGGGTG
51 ACTTGATCTA GCAGTTATCA AACACAACAG TCCTCCACTT GAGCTCTGTT
101 TCTCCACATG TCGAAGCTAG TTTGCGTCAC CGGCGGCAGC GGATGCATCG
151 GTTCATGGCT AGTCCATCTC CTTCTCCTCC GCGGCTACAC TGTTCACGCC
201 ACCGTCCAAA ATCTCAATGA TGAGAACGAA ACGAAGCATC TAGAAGCTCT
251 CGAAGGAGCA CAAACTAATC TCCGTCTCTT CCAGATCGAT CTCTTAACT
301 ACGACACAAT CCTCGCTGCT GTCCGCGGTT GCGTCGGAAT TTTCCACCTC
351 GCTTCACCTT GCACTGTAGA CAAAGTTCAT GATCCTCAGA AGGAGCTTTT
401 GGATCCTGCA ATTAAGGGA CTTTGAATGT GCTTACTGCA GCTAAGGAAG
451 TAGGGGTGAA GCGTGTGGTT GTTACCTCGT CTGTCTCGGC GATTACTCCT
501 AGTCCTGATT GGCTTCTGA TGTGTTAAA AGAGAGGATT GTTGGACTGA
551 TGTGAATAT TGCAAGAAAA AAGAGTTGTG GTATCCGTTG TCCAAAACAT
601 TGGCTGAGAA AGCTGCGTGG GATTTTTCCTA AAGAAAAATGG TTTGGATGTT
651 GTTGTGGTGA ATCCCGGTAC TGTGATGGGT CCTGTTATTC CACCACGGCA
701 TAATGCAAGC ATGCTCATGC TTGTGAGACT TCTTGAAGGC TGCCTGAAA
751 CATTTGAAGA CTATTTTATG GGATTGGTCC ACTTCAAAGA TGTAGCATTG
801 GCGCATATTT TGGTGATGA GAACAAAGAA GCATCTGGTA GACATGTGTG
851 TGTGAAACT ATCTCTCACT ACGGTGATTT TGTGGCAAAA GTTGTGAAC
901 TTTATCCAGA ATATAGTGTT CCTAGGATGC AGCGAGATAC GCAACCTGGA
951 TTGTTGAGAG CGAATGATGG ATCAAAGAAG CTCATAGATT TGGGTTTGGGA
1001 ATTCAATTCCA ATGGAGCAAA TTATCAAGGA TGCTGTAGAG AGTTTGAAGA
1051 ACAAGGAT CATTCTTGA ATGATGTTAC TGTCTTTTGG AGAACCCTAT
1101 AGTTACCAGA GTATAGACTA AATAATATAT AGGTGATGGG TCAGAGAATG
1151 AGTACTTATG TCATGAGTTG TGTCTGTATA ATATGTTTTC TCAATTCTTA
1201 TATGTTAAAT TGCTAATGTT AACTTCAATA TTTATCAGCC AGTATTGTTT
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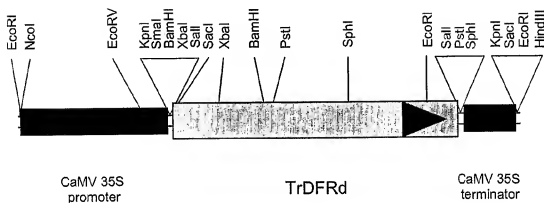
FIGURE 167

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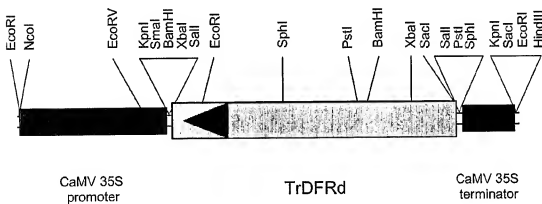
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101 AIKGTNLVLT AAKEVGVKRV VVTSSVSAIT PSPDWPSDVV KREDCWTDVE
151 YCKKKELWYP LSKTLAEKAA WDFSKENGLD VVVVNP GTVM GPVIPPRHNA
201 SMLMLVRLLE GCAETFEDYF MGLVHFKDVA LAHILVYENK EASGRHVCVE
251 TISHYGDFVA KVAELYPEYS VPRMQRDTQP GLLRANDGSK KLIDLGLEFI
301 PMEQIIKDAV ESLKNKGFIS

FIGURE 168

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pDH51TrDFRd sense



pDH51TrDFRd anti

FIGURE 169

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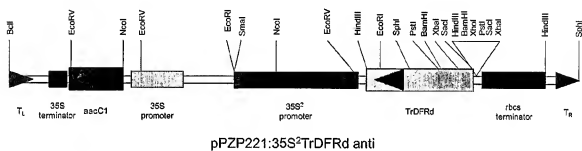
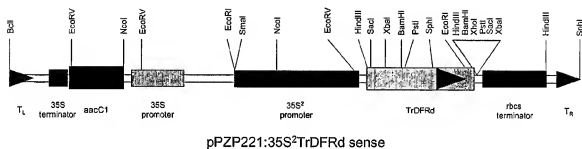
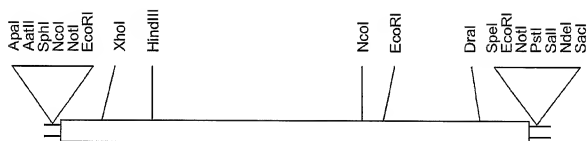


FIGURE 170

244/271**TrF3Ha****FIGURE 171**

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1  GAATTCGATT AAGCAGTGGT AACAAACGCAG AGTACGCGGG GACCACTCTA
51  TTTATTTCCTA CTTAAACCTC ACAAATAATA AACACACAAA CACACAAAACA
101 CCAAAAACAG AGCACCGTTT CCATCATCAA ACAATGGCAC CAGCCAAAAC
151 TCTAAGTTAT CTCTCACAAAC AAAACACTCT CGAGTCAAGT TTCGTTAGGG
201 AAGAAAGATGA GCGTCCAAAA GTTGCCATACA ATAACCTCAG CAACGAGATT
251 CCAATCATT CTCTTGCTGG AATTGATGAG GTTGATGGTC GTAGAACAGA
301 GATATGTAAC AAGATTGTTG AAGCTTGTTGA GAATTGGGGT ATTTTTCAGG
351 TTGTTGATCA TGGTGTGTGAT ACAAACCTTG TTTCTGAGAT GACCCGTTTT
401 GCTAGAGAGT TTTTGTCTTT GCCACCGGAA GAGAAGCTCC GGTTTGACAT
451 GTCCGGTGGT AAAAAGGGTG GTTTCATTGT CTCTAGTCAT CTTCAAGGAG
501 AAGCAGTGAA GGATTGGAGA GAGCTAGTGA CATATTTTTC ATACCCAATT
551 AAACAAAGAG ATTATPCAAG GTGGCCAGAC AAGCCAGAAG GATGGAAAAG
601 GGTAACAGAA AAATACAGTG AAAACCTAAT GAATTTAGCT TGCAAGCTAT
651 TGGAAGTTTT ATCAGAAGCA ATGGGTTTAG AAAAAGAAAGC TCTAACAAAA
701 GCATGTGTTG ATATGGATCA AAAAGTTGTT ATAAATTATT ACCCAAAATG
751 CCTGAACCT GACCTCACAC TTGGCCTTAA ACGTCACACT GACCCGTGGCA
801 CATTACTCT TTTGCTTCAA GATCAAGTTG GTGGTCTTCA AGCTACCAAA
851 GATAATGGTA AGACGTGGAT TACAGTTCAA CCAGTTGAAG GTGCTTTTGT
901 TGTTAATCTT GGAGACCATG GTCATATCT AAGTAATGGA CGGTTCAAAA
951 ATGCTGACCA TCAAGCAGTG GTGAATTGCA ACTACAGCCG TTTATCAATA
1001 GCAACATTTT AAAATCCAGC TCCAGATGCA ACTGTGTACC CTTTGAAGAT
1051 TAGAGATGGT GAAAAATCTG TGTGGAAGA ACCAATCACT TTTGCTGAAA
1101 TGTATAGAAG GAAGATGACC AAAGACCTTG AAATTGCTAG GATGAAGAAG
1151 TTGGCTAAGG AACACAACCT TAGGGACTTG GAGGAGAACA AGACTAAAATA
1201 TGAGGCCAAA CCTTTGAATG AGATCTTTGC TTAATTAATT AGCTTTAATT
1251 TAAATAATAA ATTTTAGACT TAATTTACAT ATAATAATTT TAATTTTTTG
1301 TTCAATTAAT CTATGTTTAA TTTGTCGTTA TTGTCCACGT GTATTAGCT
1351 GCTTGTTGT GTGTGCCTTG GAGAAATATC AATAATATTA CATCTATGTT
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1451 GCTTAATCAC TAGTGAATTC

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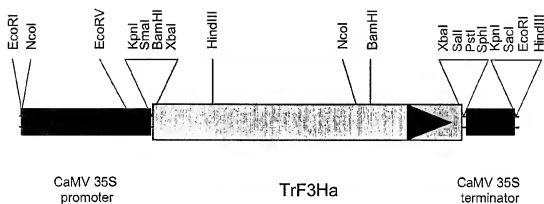
FIGURE 172

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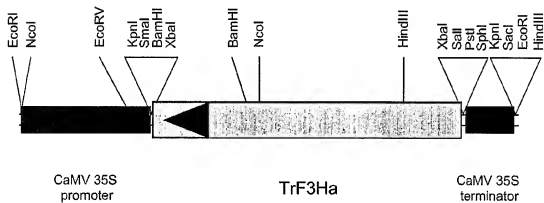
1 MAPAKTLSYL SQQNTLESSF VREEDEREKV AYNNFSNEIP IISLAGIDEV
51 DGRRTTEICNK IVEACENWGI FQVVDHGVDT KLVSEMTRFA REFFALPPEE
101 KLRFDMSGGK KGGFIVSSHL QGEAVKDWRE LVTYFSYPIK QRDYSRWPK
151 PEGWKEVTEK YSENLMLNAC KLEVLSEAM GLEKEALTKA CVDMDQKVVI
201 NYYPKCPEPD LTLGLKRHTD PGTITLLQD QVGGLQATKD NGKTWITVQP
251 VEGAFVVNLG DHGHYLSNGR FKNADHQAVV NSNYSRLSIA TFQNPAPDAT
301 VYPLKIRDGE KSVLEEPITF AEMYRRKMTK DLEIARMKKL AKEQQLRDLE
351 ENKTKYEAKP LNEIFA

FIGURE 173

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pDH51TrF3Ha sense



pDH51TrF3Ha anti

FIGURE 174

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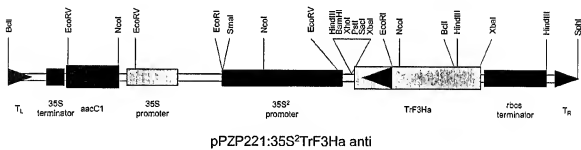
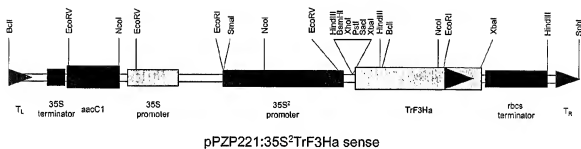
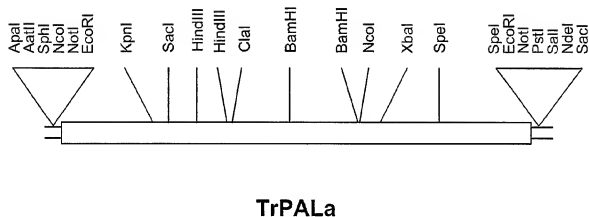


FIGURE 175

249/271**FIGURE 176**

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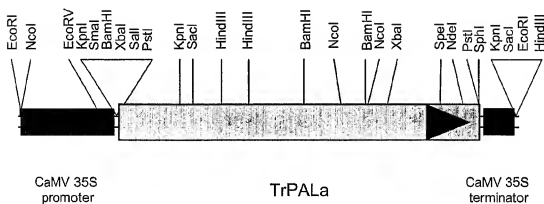
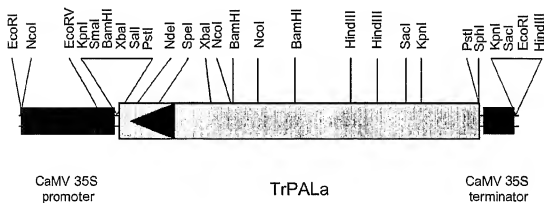
1	GAATTC GATT	AAGCAGTGGT	AACAACGCAG	AGTACGCGGG	GAGGAAATTC
51	ACAACCTCAAA	TATTCCCTTTA	ATTCTTTTCAT	ATAATCATTT	GAATTTCCAT
101	TCTCCCTAAA	AATTCCTATAG	CTACCACATC	ACACAACATA	ACAAATTAAAG
151	AAATATTTTAT	TACTATATTA	AGATATGGAA	GTAGTAGCAG	CAGCAATCAC
201	AAAAAACAAAT	GGCAAGATTG	ATTCATTTTG	CTTGAATCAT	GCTAATGCTA
251	ATAACATGAA	AGTGAATGGT	GCTGATCCTT	TGAATTGGGG	TGTGGCTGGT
301	GAGGCAATGA	AGGGAAGTCA	CTTGGATGAG	GTGAAGCGTA	TGGTGGAGGA
351	ATACCGGAAA	CCGTTTGTCC	GCTCTTGGTG	CGAGACACTA	ACGTTCTCTC
401	AGGTGGCTGTC	CATTGCTGCA	CACGATGGTG	CAACGGTGGA	GCTATCGGAA
451	TCTGCTAGAG	CCGGCGTTAA	GGCAAGCAGT	GACTGGGTTA	TGGAGAGTAT
501	GAACAAAGGT	ACCGACAGCT	ACGGTGTCCC	AACAGGGTTC	GGCGCTACCT
551	CGCACCGCCG	AACCAAAACAA	GGTGGTGCTT	TGCAGAAAGA	GCTCATAAAG
601	TTTTTGAATG	CTGGAATATT	TGGAATTGGG	ACTGAGTCAA	GCCACACACT
651	ACCACACACA	GCCACAAGAG	CTGCCATGCT	AGTGAGAATC	AACACACTTC
701	TCCAAGGGCTA	TTCAGGAATT	AGATTTTGAA	TCTTAGAAGC	TATCACCAGG
751	CTCTTTAACA	ACAATGTCAC	CCCATGTTTA	CCGCTTCGCG	GTACAAATCAC
801	AGCTTCAGGA	GATTTAGTCC	CTCTTTCTTA	CATTGCTGGT	TTACTAACCG
851	GACGACCAAA	TTCCAAGGCT	CATGGACCTT	CTGGAGAAGT	ACTTAAATGCA
901	AAACAAGCTT	TTCAATCAGC	TGGAATCGAT	GCCGAGTTCT	TTGAATTTACA
951	ACCAAAAGGT	GGCCTTGCCC	TTGTTAACGG	AACCGCTGTT	GGTCTCTGGT
1001	TAGCTTCTAT	TGTTCTTTT	GAGGCTAATA	TATTTGGCGGT	GTGTCTGTA
1051	GTCTTATCTG	CAATTTTCGC	TGAAGTTATG	CAAGGGGAAG	CCGAATTTAC
1101	CATTCAATTTG	ACACATAAGT	TGAAACATCA	CCCTGGTCCA	ATTTGAGGCTG
1151	CTGCTTATTAT	GGAAACACAT	TTGGATGGGA	GTGCTTATGT	TAAAGACGTA
1201	AAGAAGTTGC	ATGAGATGGA	TCCTTTACAG	AAGCCAAATC	AAGATAGCAT
1251	TGCACCTTAGG	ACTTCGCCAC	AATGGCTTGG	TCCTTTGATT	GAAGTAGTAT
1301	GATTCTCTAC	CAAGTCAATT	GAGAGAGAGA	TCAACTCTGT	CAATGACAAAT
1351	CCTTTGATTG	ATGTTTCAAG	GAACAAGGCT	TTGCATGGTG	GAATTTTTC
1401	AGGAACACCT	ATCGGAGTAT	CCATGGATAA	TACACGTTTG	GCTCTTGCAAT
1451	CAATTGGCAA	ACTTATGTTT	GCTCAATTCT	CTGAGCTTGT	CAATGATTTT
1501	TACAACAATG	GATTGCCATC	AAATCTCTCT	GCTAGTAGAA	ATCCGAGCTT
1551	GGATTATGGG	TTCAAGGGAT	CCGAAATTGC	CATGGCTTCT	TATTTGTCGG
1601	AGTTGCAAT	TCTTGCAAA	CCGTTTACAA	CTCATGTCCA	AAGTGCAGAA
1651	CAACACAACC	AAGATGTCAA	CTCTTTGGGT	TGTATTTCCT	CTGAAAAAC
1701	TTATGAAGCA	ATTGAGATCC	TTCAATTGAT	GTCTTCCACA	TTCTTGATTG
1751	CACTTTGTCA	AGCAATTGAT	TTAAGACATT	TGGAGGAGAA	TTTGAAAAAC
1801	TCGGTCAAAA	ATACCGTAAG	CCAAGTGGCC	AAAAGACAC	TAACCATAGG
1851	TGTCAATGGA	GAACCTCATC	CTTCAAGATT	TTGTGAAAA	GACTTATTGA
1901	AAGTGGTTGA	TAGGGAACAT	GTCCTTTGCC	ACATTGATGA	TCCTTGATGT
1951	GCTACATACC	CATTGATGCA	AAAACCTCAG	CAAGTACTAG	TGACATATCG
2001	ATTAGTTAAAT	GGAGAAAGTG	AGAAGAAATT	GAACACATCA	ATCTTCCAAA
2051	AGATTGCAAC	TTTTGAGGAA	GAGTTGAAAA	ACCTTTGCCA	AAAAGAGTTG
2101	AAAGTGCAG	GATTGCATAT	GAAAGTGGAA	ATTCAACAAAT	TCCAAACAG
2151	ATCAATGGAT	GCAGATCTTA	TCCACTCTAC	AAATTTTGTA	GAAAGAGATT
2201	GGGAACCTGGT	TTGCTAACTG	GAGAAAAATG	CATTTTCAACG	GGTGAAGAGT
2251	GTGACAAATC	ATTTCACAGCT	ATGTGTCAAG	GAAAAATCAT	TGATCTCTTT
2301	CTTGAATGCT	TGGGAGAGTG	GAACGGTGCT	CCCTTCCAAA	TTTGTTAAC
2351	TTGATTTGTTA	GTTTCATAAA	TGTTTTATTT	GTATTTTATCA	TTTGTATTTA
2401	TGCGAGTGTA	GTAATAATGA	TTAGGTGTTT	TGTGCCCTTTA	ATTGAAAAAA
2451	AAAAAATAAA	AAAAAATAAA	AAAAGTACTC	TGCGTTGTTA	CCACTGCTTA
2501	ATCACCTAGTG	AATTC			

FIGURE 177

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1 MEVVAAAITK NNGKIDSFCL NHANANMMKV NGADPLNWGV AA EAMKGS HL
51 DEVKRMVEEY RKPVVRLGGE TLTISQVA AI AAHDGATVEL SESARAGVKA
101 SSDWVMESMN KGTD SYGVPT GFGATSHRRT KQGGALQKEL IRFLNAGIFG
151 NGTESSHTLP HTATRAAMLV RINTLLQGYS GIRFEILEAI TKLLNNNVTP
201 CLPLRGTTITA SGDLVPLSYI AGLLTGRPNS KAHGPSGEVL NAKQAFQSAG
251 IDAEFFELQP KEGLALVNGT AVGSGLASIV LFEANILAVL SEVLSAIFAE
301 VMQ GKPEFTD HLTHKLKHP GQIEAAAIME HILDGSAYVK DAKK LHEMDP
351 LQKPKQDRYA LRTSPQWLGP LIEVIRFSTK SIEREINSVN DNPLIDVSRN
401 KALHGGNFQG TPIGVSM DNT RLALASIGKL MFAQFSELVN DFYNNGLPSN
451 LSASRNPSLD YGFKGSEIAM ASYCSELQYL ANPVTTHVQS ABQHNQDVNS
501 LGLISSRKY EAIEILQLMS STFLIALCQA IDLRHLEENL KNSVNTVTSQ
551 VAKKTLTIGV NGELHPSRFC EKDLLKVDR EHV FAYIDDP CSATYPLMQK
601 LRQVLVDHAL VNGESEKNLN TSIFQKIATF EEELKNLCQK RLKVQGLHMK
651 VEIQQFQTRS MDADLIHSTI L

FIGURE 178

252/271**pDH51TrPALa sense****pDH51TrPALa anti****FIGURE 179**

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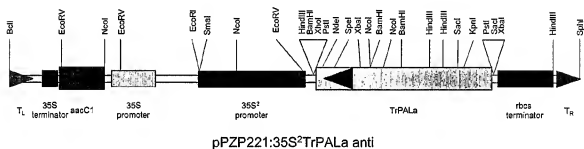
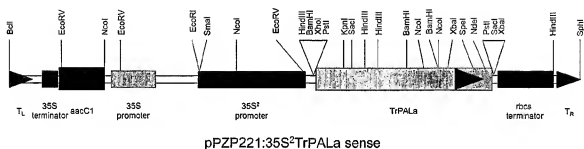
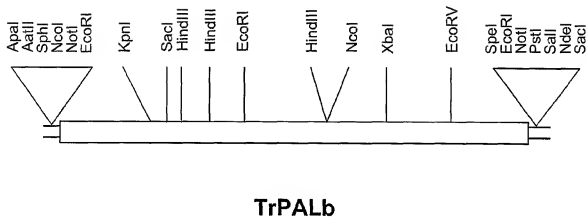


FIGURE 180

254/271**FIGURE 181**

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1	GAATTCG MTT	AAGCAGTGGT	AACAACGCAG	AGTACGCGGG	AGGAAATAAA
51	TTCATCATTTG	TTCCCTTATTT	CCACCCCAAC	ACACATAAAC	AAATACAMTT
101	CCTCTCCTCT	CATCACAATT	ATTACTTTCT	ACACCCCCC	CTCTCAACTT
151	TTATTAACATA	ACATAAATGGA	GGGAATTACT	AATGGCCATG	CTGAAGCAAC
201	TTTTTGGCGTG	ACCAAAAGTG	TTGGTGATCC	ACTCAACTGG	GGTGCAGCCG
251	CGGAGTCGTT	GATGGGGAGT	CATTTGGATG	AGGTGAAGCG	TATGGTGGAG
301	GAATACCGTA	ATCCATTGGT	TAAAAATTGGC	GGCGAGACGC	TTACCATGCG
351	TCAGGTCGGCT	GGAATTGCTT	CTCATGATAG	TGGTGTGAGG	TGGAGCTGTG
401	CTGAGTCCGC	CAGGGCCGGC	GTAAAGGCCA	GTAGTGGTGT	GGTGTATGGAC
451	AGCATGAACA	ATGGGACTGA	TAGTTATGGT	GTATACCACTG	GTTTCGGGCG
501	CACCTCTCAC	CGGAGAACCA	AGCAGGGTGG	TGCCTTGCAG	AAGGAGCTAA
551	TTAGGTTTTTT	GAATGCCGGA	ATATTTGGCA	ATGTTACAGA	ATCTTAAGTG
601	ACACTACCAC	ACACAGCAAC	CAGAGCTGCA	ATGCTTGTGA	GAATCAACAC
651	TCCTCTTCAA	GGATATTCTG	GAATTAGATT	TGAAATTTTG	GAAGCTATCA
701	CAAAGCTTCT	AAACAACAAC	ATTACCCCAT	GTTTACCACT	TCGTGTGTACA
751	ATCCCGGCTT	CCGGTGTATCT	CGTCCCGCTT	TCCTACATTG	CCGGTTTGTG
801	AACCGGTAGA	CCGAACCTCA	AAGCCGTTGG	ACCCTCCGGA	GAAATTTCTCA
851	ATGCAAAAGAA	AGCTTTTCAA	CTTGC CGGCA	TTGGTTCTGA	GTTTTTTGAA
901	TTGCAGCCAA	AAGAAGGTC	TGCTCTTGTT	AATGGTACTG	CTGTGGTTTC
951	TGGTTTAGCT	TCTATTGTTC	TGTTTGAAGC	AAATGTACTA	CGTGTTTTGT
1001	CTGAAGTTAT	GTCCGCCGAT	TTCCGCTGAAG	TATGCAAGG	GAACACAGAA
1051	TTCTACTGATC	ATTTGACTCA	TAAGTTGAAA	CATCACCCTG	GTCAAAATGGA
1101	AGCTCTGTGCA	ATTATGGAAC	ATATTTTGGA	TGGAAAGTGT	TATGTTTAAAG
1151	CAGCTAAGAA	ATTACACGAA	ACCGATCCTT	TACAAAAGCC	GAACCAAGAT
1201	CGTTATGCAC	TTAGAACTTC	ACCTCAATGG	CTTGGTCTCT	TGATTGAAGT
1251	GATAAGATTT	TCAACTAAGT	CAATTGAGAG	AGAAATTAAC	TCGTGTCAATG
1301	ATAACCCCTT	GATTGATGTT	TCAAGGAACA	AGGCCATTCA	CGGTGGTAAT
1351	TTTCAAGGAA	CACCTATTGG	AGTTTCAATG	GATAACACAC	GTTTAGCTCT
1401	TGCTTCAATT	GGTAAACTCA	TGTTTGCTCA	ATTCTCTGAA	CTTGTTAATG
1451	ATTTTTACAA	CAACGGGTTA	CCTTCGAATC	TTACTGCTAG	TAGGAACCCA
1501	AGCTTGGATT	ACGGTTTCAA	GGGATCCGAA	ATTGCCATGG	CTTCTTATTG
1551	TTCTGAGTTA	CAATATCTTG	CTAATCCCTG	CACCAACCAT	GTCCAAAGTG
1601	CGGAGCAACA	CAATCAAGAT	GTAACTCTT	TGGGTTTGAT	TTCTTCAAGA
1651	AAAACAAATG	AAGCTATTGA	GATCCTTAAAG	CTCATGTCTT	CGACATTTCT
1701	GATTGCACTT	TGTCAAAGCA	TTGATTTAAG	GCATTTGGAG	GAAAATCTGA
1751	GGAAACACTGT	CAAGAACACG	GTAAGCCAAAG	TAGCGAAGAG	AACACTCAC
1801	ACCGGTGTTA	ATGGAGAACT	TCATCCTTCT	AGATTTTGTG	AGAAAGATTT
1851	GCTCAAAAGTT	GTGATAGGG	AGTATGTATT	TGCCTATGTC	GACGATCCTT
1901	GTCTAGCTAC	ATACCCCTTG	ATGCAAAAGT	TGAGACAAGT	GCTTGTGGAT
1951	CATGCATTGG	TAAATGCTGA	TGGAGAGAAG	AAATTTGAACA	CATCAATCTT
2001	TCAAAAGATT	GCAACTTTTG	AGGATGAATT	GAAAGCTATC	TTGCCAAAGG
2051	AAAGTTGAAG	TACAAGAAGT	GCATATGAAA	ATGGACAATG	TGGAAATTTCA
2101	AACAAGATTA	AGGAATGCAG	GTCTATATCA	TTGTACAAGT	TTGTTAGAGA
2151	GGAGTTAGGA	ACCGCGTTGC	TAAACCGAGA	AAAAACGATA	TCGCTGGGCG
2201	AAAGGTGTGA	CAAAATGTTC	ACAGCTATGT	GCCAAGGTAA	AAATTTGTAT
2251	CCTCTTTTGG	AATGCCTTGG	AGAGTGGAAAT	GGTGTCTCTC	TACCAATATG
2301	TTAATTAGCA	GAATTAATAT	GTTCCTTTGA	GAAAGTGATT	CTTTATATAT
2351	TGTAGTATA	CTATAGTAGT	TGCATTGAGA	AGCAATTTGT	TTGTCTATAA
2401	GCCTATGGAA	AATGGCAAAA	CAATTTTCTG	CTCAAAGCAT	CGTTTATTAA
2451	GTTTTCCTTA	AAGTGTTAAG	GAACCTTTAA	TTGTTTTTGT	AAATAGAAATG
2501	CATTTGTGTTG	CCACAACCTT	GGGTGCAAAAT	ATCACGTGAT	ACATGTGGTG
2551	TTTGATGTAA	ATGGTGTGTTT	CTCAATTAAT	AAATAGTGTG	TCAGCCATGA
2601	AAAAAATAAA	AAAAAATAAA	AAAAAAGTAC	TCTGCGTTGT	TACCACGTCT
2651	TAATCACTAG	TGAATTC			

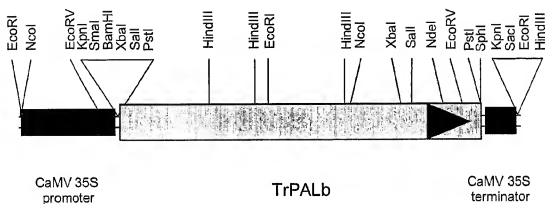
FIGURE 182

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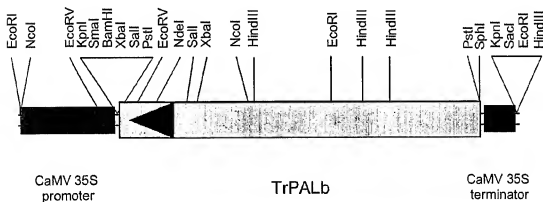
1 MEGITNGHAE ATFCVTKSVG DPLNWGAAAE SLMGSHLDEV KRMVEEYRNP
51 LVKIGGETLT IAQVAGIASH DSGVRVELSE SARAGVKASS GWVMDSMNNG
101 TDSYGVTTGF GATSHRRTKQ GGALQKELIR FLNAGIFGNG TESNCTLPHT
151 ATRAAMLVRI NTLLQGYSGI RFEILEAITK LLNNNITPCL PLRGTTITASG
201 DLVPLSYIAG LLTGRPNska VGPSGEILNA KEAFQLAGIG SEFFELQPKE
251 GLALVNGTAV GSGLASIVLF EANVLAVLSE VMSAIFAEVM QGKPEFTDHL
301 THKLKHHFGQ IEAAAIMEHI LDGSAYVKAA KKLHETDPLQ KPKQDRYALR
351 TSPQWLGPLI EVIRFSTKSI EREINSVNDN PLIDVSRNKA IHGGNFQGTP
401 IGVSMDNTRL ALASIGKLMF AQFSELVNDF YNGLPSNLT ASRNPSLDYG
451 FKGSEIAMAS YCSELQYLAN PVTTHVQSAE QHNQDVNSLG LISSRKTEA
501 IEILKLMSSST FLIALCQAID LRHLEENLRN TVKNTVSQVA KRTLTITGVNG
551 ELHPSRFCEK DLLKVVDREY VFAYVDDPCL ATYPLMQKLR QVLVDHALVN
601 ADGEKNLNTS IFQKIATFED ELKAILPKEV ESTRATAYENG QCGISNKIKE
651 CRSYPLYKFV REELGTALLT GEKTISLGEE CDKLFTAMCQ GKIVDPLEC
701 LGEWNGAPLP IC

FIGURE 183

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pDH51TrPALb sense



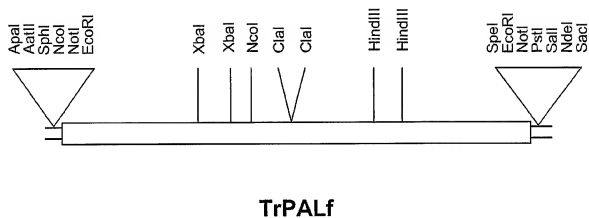
pDH51TrPALb anti

FIGURE 184

The diagram shows a linear map of the *TrpALB* gene construct. It starts with a T_L terminal repeat (black triangle), followed by a 35S promoter (white box), the *secC1* gene (black box), another 35S promoter (white box), the *TrpALB* gene (black box), and an *rbcA* terminator (white box), ending with a T_R terminal repeat (black triangle). Restriction sites are marked above the map: EcoRV, NcoI, EcoRI, SmaI, HindIII, XbaI, SalI, and PstI. The *TrpALB* gene is flanked by *secC1* and *rbcA* genes, which are flanked by T_L and T_R terminal repeats.

pPZP221:35S²TrPALb anti

FIGURE 185

259/271**FIGURE 186**

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```

1  GAATTCACCTA GTGATTAAGC AGTGGTAACA ACGCAGAGTA CGCGGGGAGG
51  AAATAAAATTC ATCATTTGTC ATTTATTTCCC ACCCAACACA ACATAACAAA
101  TACATTATATC TCTCCTCTGA TCACAATTAT TACTTTCTAC ACCCTCCTCT
151  CAACATATTAT TAACTAGCAT AATGGAGGGA ATTACCAATG GCCATGCTGA
201  AACAACTTTT TCGGTGACCA AAGTGTGTGG TGATCCACTC AACTTGGGGTG
251  CAGCCGCGGA GTCGTGTACG GGGAGTCATT TGGATGAGGT GAAGCGTATG
301  GTGGAGGAGT ACCGTAATCC GTTGGCTAAA ATTGCGGGC AGACGCTTAC
351  CATTGCTCAG GTGGCTGGAA TTGCTTCTCA TGATAGTGGT GTAGGGGTGG
401  AGCTGTCCGA GTCCGCAAGG GCCGGCGTTA AGCGAGTAG TGATTGGGGT
451  ATGGATAGCA TGAACAATGG GACTGATAGT TACGGTGTTA CCACCGGTTT
501  TGGTGCCACC TCTCACCAGA GACCAAGCA GGGTGGTGCT TTGCAGAAGG
551  AGCTAATTAG GTTTTGAAT GCTGGAATAT TTGGCAATGG TACAGACTCT
601  AACTGTACAC TACCACACAG AGCAACTAGA GCTGCAATGC TTGTGAGAAT
651  CAACACTCTT CTTCAGGGGT ACTCTGGTAT TAGATTGAA ATTTTGAAG
701  CTATCACAAC GCTTCCAAC AACAACATTA CCCCATGTTT ACCACTTCGT
751  GGTACAATCA CGCGTTCGG TGATCTTGT CCCTTTCCT ACATTGCCGG
801  TTTGTTAACC GGAAGACCCA ACTCCAAGC AGTTGGAAC TCCGGAGAAA
851  TTTTGAATGC TAAAGAAGCT TTTCAACTCG CGCGCAATGG TTTCTGAGTT
901  TTTGAAATGC AACCAAAAGA AGGTCTTGCT CTGTGTAATG GTACTGCTGT
951  TGGCTCTGGT TTAGCTTCTA TTGTTCTGTT TGAAGCAAT GTACTAGCTG
1001 TTTTATCCGA AGTTATGTGC GCGATTTTCG CTGAAGTTAT GCAGGGGAAA
1051 CCGGAATTTA CCGATCAATT GACTCATAAG TTGAAACATC ACCCTGGTCA
1101 AATTGAAGCT GCTGCAATTA TGAACATAT TTTGGATGGA AGTGGTTATG
1151 TTAAGACAGC TAAGAAGTTA CACGAAACCG ATCCTTTACA AAAACCGAAA
1201 CAAGATCGTT ATGCACTTAG AACTTCACCT CAATGGCTTG GTCTTTGAT
1251 TGAAGTGATA AGATTTTCAA CCAATTCGAT TGAAAGAGAA ATTAACTCGG
1301 TCAACGACAA CCCTTTGATC GATGTTTCAA GGAACAAGGC CATTCATGGT
1351 GGTAACTTTC AAGGAACACC TATTGGAGTT TCAATGGATA ACACACGTTT
1401 AGCTCTTGCT TCAATTGGTA AACTCATGTT TGCTCAATTG TCTGAACTTG
1451 TTAATGATTT TTAACAACAC GGGTTGCCTT CGTATCTTAC TGCTAGTAGG
1501 AAAGTGCTCT TGGACTATGG TTTCAAGGGA TCGGAAATGC CCATGGCTCT
1551 GTATTGTPTCC GAGTTACAAT ATCTTGCTAA TCCTGTCAAC ACCCATGTCC
1601 AAAGTGCCGA GCAACACAAC CAAGATGTTA ACTCTTTGGG TTGATTTCTT
1651 TCTAGAAAAA CAAATGAAGC TATTGAGATT CTCACGCTCA TGCTTCTCAC
1701 TTTCTTGATT GCATTATGTC AAGCAATCGA CTTAAGGCAC TTGGAGGAAA
1751 ATCTCAGGAA CACCGTCAAG AACACGGTAA GCCAAGTAGC GAAGAGAACA
1801 CTCACCAACG CCGTCAACCG AGAATTCAT TCTCTAGAT TTTGTGAGAA
1851 AGATTTGCTT AAAGTTGTTG ATAGGGAGTA TGTATTTGCC TATGCCGACG
1901 ATCTCTGTCT AGCTACATAC CCTTTGATGC AAAAGTTGAG ACAAGTGCTT
1951 GTGGATCATG CATTTGGTAA TGTGTATGGA GAGAAGAATT TGAACACATC
2001 AATCTTTCAA AAGATTGCAA CTTTGTAGGA TGAGTTGAAA GCTATTTTGC
2051 CAAAGGAGGT TGAAAGTACA AGAATCGCAT ATGAAAATGG ACAATGTGGA
2101 ATTTCAAACA AGATTAAAGG ATGCAGGTCT TATCCATTGT ACAAGTTTGT
2151 TAGAGGGAG TTAGGAACCG CGTTGCTAAG CGGAGAAAAA ACTATATCGC
2201 CGGGCGAAGA GTGCGATAAA TTGTTTACAG CTATGTGCCA AGGTAAAAAT
2251 GTTGATCCTC TTAGGGAATG CCTCGGAGAG TGGAAATGGT CTCCTCTACC
2301 AATATGTTAA TTAGCATAAT ATGTTTCTCT TGAGAAGTGA TTACTTTTATA
2351 TATTTGTAGT ATACTATAGT AGTTGCAATT AGAAGAAATT GGTTTGTTTAT
2401 TAAGCCTATG GAAATGGGCA AATCAATTTT CTGCTCAAAG CATCGTTTAT
2451 TAAGTTTTCCT TTAAGTGTTT AAGGAACTTT TAATTGTTTT TGTAATAGAA
2501 TTTCAATTGT TTGCCAAC TTTGGGTGCA AATATCACAT GATACATGTG
2551 GTGTTTGATG TAAATGGTGT TTTTCAATA AATAAATAGT GTTTCAACTA
2601 AAAAAAAA AAAAAAAA AAAAAAAG TACTCTGCGT TGTATACCACT
2651 GCTTAATCGA ATTC

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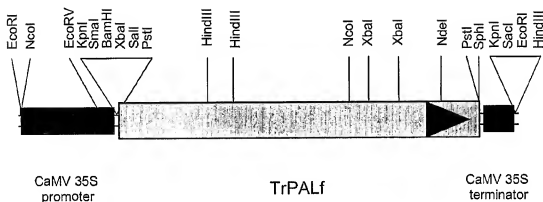
FIGURE 187

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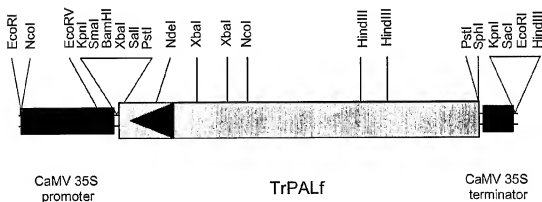
1 MEGITNGHAE TTFCVTKSVG DPLNWGAAAE SLTGSHLDEV KRMVEEYRNP
51 LAKIGGETLT IAQVAGIASH DSGVRVELSE SARAGVKASS DWVMDSMNNG
101 TDSYGVTTGF GATSHRRTKQ GGALQKELIR FLNAGIFGNG TESNCTLPHT
151 ATRAAMLVRI NTLLQGYSIGI RFEILEAITK LPNNNITPCL PLRGTITASG
201 DLVPLSYIAG LLTGRPNska VGPSGEILSA KEAFQLAGIG SEFFELQPKKE
251 GLALVNGTAV GSGLASIVLF EANVLAVLSE VMSAIFAEVM QGKPEPTDHL
301 THKLKHHPGQ IEAAAIMEHI LDGSAYVKAA KKLHETDPLQ KPKQDRYALR
351 TSPQWLGPLI EVIRFSTKSI EREINSVNDN PLIDVSRNKA IHGGNFQGTP
401 IGVSMDNTRL ALASIGKLMF AQFSELVNDF YNNGLPsYLT ASRNPslDYG
451 FKGSEIAMAS YCSELQYLAN PVTTHVQSAE QHNQDVNSLG LISSRKTNEA
501 IEILKLMSST FLIALCQAID LRHLEENLRN TVKNTVSQVA KRTLTTGVNG
551 ELHSSRFCEK DLLKVVDREY VFAYADDPCL ATYPLMQKLR QVLVDHALVN
601 VDGEKNLNTS IFQKIATFED ELKAILPKEV ESTRAYENG QCGISNKIKE
651 CRSYPLYKFV REELGTALLT GEKTISPGEe CDKLFTAMCQ GKIVDPLMEC
701 LGEWNGAPLP IC

FIGURE 188

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pDH51TrPALf sense



pDH51TrPALf anti

FIGURE 189

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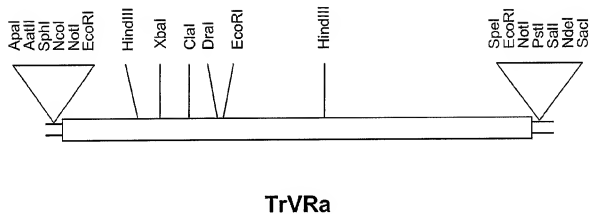


FIGURE 191

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1  GAATTCGATT AAGCAGTGGT AACAAACGCAG AGTACGCGGG ATAGTAGTAG
51  TTGAGAAAAA ATACACA AAT AAAGTAAACA CTATCATAGA AAGAGAGTCA
101 AAAATGGCTG AAGGAAAAGG AAGGGTTTGT GTTACTGGAG GAACAGGTTT
151 TCTTGGTTCA TGGATCATCA AGAGTCTTCT TGAAAATGGA TACTCTGTTA
201 ATACCACTAT TAGAGCTGAT CCAGAACGTA AGAGGGATGT AAGCTTCCTA
251 ACAAATCTAC CCGGCGCATC CGAAAGGCTA CATTTCTTCA ACGCGGATCT
301 AGACGACCCA GAGAGTTTCA ACGAAGCAAT TGAAGGTTGT GTCGGGATAT
351 TCCACACCGC TTCACCAATC GATTTTCGCCG TGAGTGAGCC AGAAGAAAATA
401 GTGACAAAAA GAACAGTGGA TGGAGCATT A GGAATTTTAA AAGCATGTGT
451 GAATTC AAAG ACAGTGAAGA GATTTATTTA CACTTCAAGT GGTTCGCTG
501 TTTCAATTCAA TGAAAAAAC AAAGATGTTT TGGATGAGAG TGATTGGAGT
551 GATGTTGATT TGCTTAGAAG TGTTAAACCA TTTGGTTGGA GTTATGGTGT
601 TTCAAAGACT TTGGCTGAGA AAGCAGTGCT TGAATTTGGT CAACAAAATG
651 GGATTGATGT TGTACTTTG ATCTTCCTT TATTTGTTGG AAGTTTGTG
701 TGTCTTAAGC TTCCTGATC TGTGAGAAA GCTCTTGTGTT TGGTACTAGG
751 CAAAAAGGAA CAAATTGGTA TTATAAGTTT CCACATGGTA CATGTGGATG
801 ATGTGGCTAG AGCACATATT TATCTACTTG AGAATCCTGT TCCAGGAGGT
851 AGATATAATT GTTCACCATT CTTTGTATCT ATTGAAGAAA TGTCACTACT
901 TCTTTCAGCC AAATATCCAG AATATCAAA ACTATCAGTA GATGAGTTGA
951 AGGAAATCAA AGGTGCAAGG TTGCCAGATT TGAACTCGAA AAAGCTCGTG
1001 GACGCTGGTT TTGAGTTTAA GTATAGTGTC GGTGATATGT TCGATGATGC
1051 GATTC AATGC TGCAAGGAAA AAGGCTATCT CTAAGTATGT GTTTGAAAAA
1101 AATTCCATGA AGCTGAGAAA ACAATAATAT GCCTAAAATC AATGATGGCT
1151 AATGAAATGT ACAAGTTTAT GCATAAAGTT ATTTGTGATG AATCAAAATA
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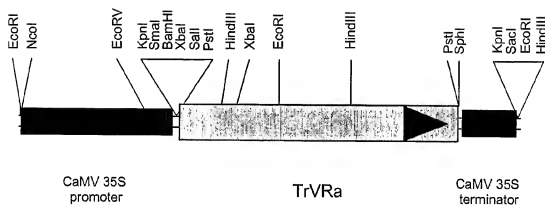
FIGURE 192

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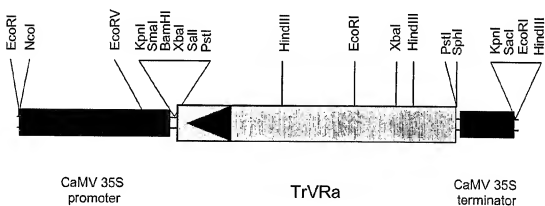
1 MAEGKGRVCV TGGTGFLGSW IIKSLENGY SVNTTIRADP ERKRDVSFLT
51 NLPGASERLH FFNADLDDPE SFNEAIEGCV GIFHTASPID FAVSEPEEIV
101 TKRTVDGALG ILKACVNSKT VKRFIYTSSG SAVSFNGKNK DVLDES DWS
151 VDLRSVKPF GWSYGVSKTL AEKAVLEFGQ QNGIDVVTLI LPFIVGSFVC
201 PKLPDSVEKA LVLVLGKKEQ IGIISFHMVH VDDVARAHY LLENFVPGGR
251 YNCSPFFVSI EEMSQLLSAK YPEYQILSVD ELKEIKGARL PDLNSKKLVD
301 AGFEFKYSVG DMFDDAIQCC KEGGYL

FIGURE 193

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pDH51TrVRa sense



pDH51TrVRa anti

FIGURE 194

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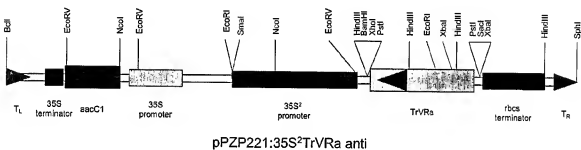
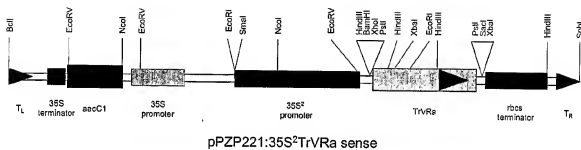


FIGURE 195

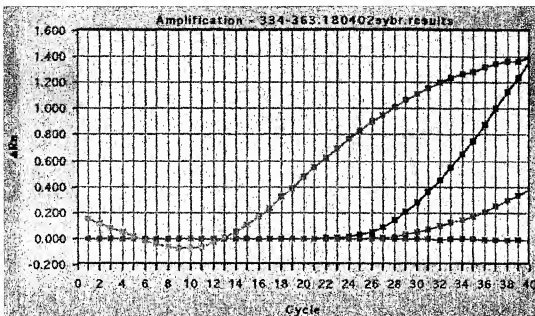
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FIGURE 196

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D



E

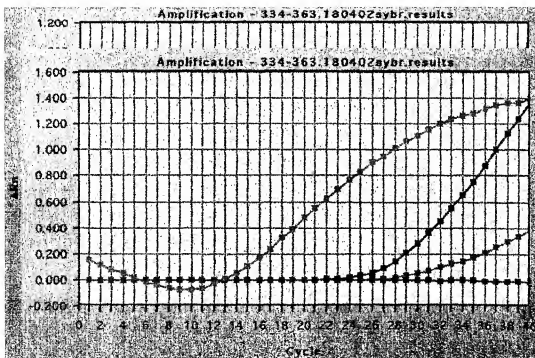
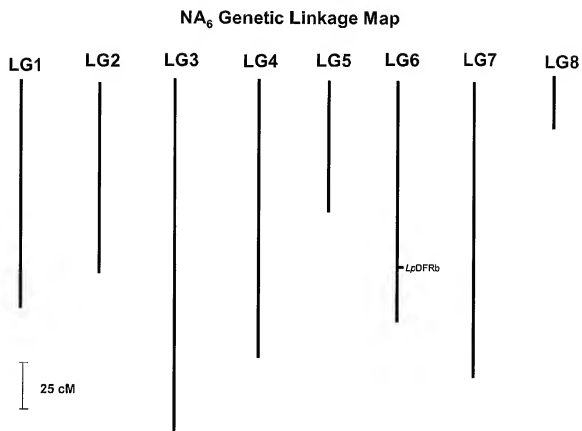


FIGURE 196 (cont)

271/271**FIGURE 197**

SEQUENCE LISTING

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AgResearch Limited

<120> Manipulation of flavonoid biosynthesis in plants

<130> M80393510

<150> PR8113

<151> 2001-10-05

<160> 336

<170> PatentIn version 3.1

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120

tttcggctg tgattacttc tccggccacc ggtaagtc attttcttgg tggtcgaggg
180

gagagaggtt tgactattga aggaaacttc atcaagtcca ctgccatagg agtatatttg
240

gaagatgtag cagtggcttc acttgccact aaatggaagg gcaaatcctc tgaagagttg
300

cttgagacc ttgacttcta cagagatata atttcaggac catttgagaa gttgattcca
360

ggatcgaaga ttagggaatt gagtggctct gagtactcaa ggaagggttaa tgaaaactgt
420

gtggcacact taaaatctgt tgggacttat ggagatgcag aagttgaagc tatgcaaaaa
480

ttgttggaag ccttcaagcc tattaatttt ccacctgggtg cctctgtttt ttacaggcaa
540

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 20 25 30

Gly Glu Arg Gly Leu Thr Ile Glu Gly Asn Phe Ile Lys Phe Thr Ala
 35 40 45

Ile Gly Val Tyr Leu Glu Asp Val Ala Val Ala Ser Leu Ala Thr Lys
 50 55 60

Trp Lys Gly Lys Ser Ser Glu Glu Leu Leu Glu Thr Leu Asp Phe Tyr
 65 70 75 80

Arg Asp Ile Ile Ser Gly Pro Phe Glu Lys Leu Ile Arg Gly Ser Lys
 85 90 95

Ile Arg Glu Leu Ser Gly Pro Glu Tyr Ser Arg Lys Val Asn Glu Asn
 100 105 110

Cys Val Ala His Leu Lys Ser Val Gly Thr Tyr Gly Asp Ala Glu Val
 115 120 125

Glu Ala Met Gln Lys Phe Val Glu Ala Phe Lys Pro Ile Asn Phe Pro
 130 135 140

Pro Gly Ala Ser Val Phe Tyr Arg Gln Ser Pro Asp Gly Ile Leu Gly
 145 150 155 160

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 165 170 175

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120

cgggctgtgg ttactttctcc ggccaccggg aagtcatttt ttcttggtgg tgcagggggag
180

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240

nagn

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120

acttctccgg tcaacggtaa gtcatatttt ctgggtggtg caggggagag aggtttgact
180

attgaaggaa acttcatcaa gttcactgcc ataggagtat atttggaaga tgtagcagtg
240

gcttcacttg ccactaaatg gaagggcaaa tcctctgaag agttgcttga gacccttgac
300

ttctacagag atatcatctt aggaccattt gagaagtgtg ttcgaggatc gaagattagg
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gaattgagtg gtcttgagta ctcaagggaag gttaatgaaa actgtgtggc acacttaaaa
420

ttgttgggga cttacggaga tgcagaagtt gaagctatgc aaaaatttgt tgaagccttc
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aagcctatta attttccacc tgggtgcctct gttttttaca ggcaatcacc tgaagggaata
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aacann

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120

catattttct tgggtgtgca ggggagagag gtttgactat tgaaggaaac ttcatacaagt
180

tcactgccat aggagtatat ttggaagatg tagcagtggc ttcacttgcc actaaatgga
240

agggtaaatc ctctgaggag ttgcttgaga ctcttgactt ctatagagac atcatttcag
300

gaccttttga aaagttgatt cgaggatcga agattagggg attgagtggt cctgagtact
360

caagggaagt taatgaaaac tgcgtggccc acttaaaatc tgttgggact tatggagatg
420

ctgaagctga agctatgcaa aaatttggtg aagccttcaa gcctattaat ttccacctg
480

gtgcctctgt tttttacagg caatcacctg atggaatatt agggcttagt ttctctcaag
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atgcaagtat accagaaaaa gaggctgcag taatagagaa caaggagct tcacggcg
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120

tcatatcttc ttggtggtgc aggggagaga gggttgacta ttgaaggaaa cttcatcaag
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ttcactgcc taggagtata ttggaagat gnannanggg ntncnntn
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120
gtgattactt ctccgggtcaa cggttaagtca tattttcttg gtggtgcagg ggagagaggt
180
ttgactattg aaggaaaactt catcaagttc actgccatag gagtatattt ggaagatgta
240
gcagtggctt cacttgccac taaatggaag ggcaaatcct ctgaagagtt gcttcagacc
300
cttgacttct acagagatat catttcagga ccatttgaga agttgattcg aggatccaag
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420
ttaaatactg ttgggactta tggagatgca gaagttgaag ctatgcaaaa atttgttgaa
480
gccttcaagc ctattaattt tccacctggt gcctctgttt tttcacagga atcacctgat
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120

gtcgagaacc ttgaattccc ggcggtgatt acttctccgg tcaacggtaa gtcatatttt
180

cttggctggtg caggggagag aggttngact attgaaggaa acttcatcaa gttcactgcc
240

ataggagtat atttgaaga tgtacgaggg gottcacttg ccactaaatg gaagggcaga
300

tcctctgaag agngcttgag accctngact nc
332

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20 25 30

Gly Glu Arg Gly Xaa Thr Ile Glu Gly Asn Phe Ile Lys Phe Thr Ala
35 40 45

Ile Gly Val Tyr Leu Glu Asp Val Ala Gly Ala Ser Leu Ala Thr Lys
50 55 60

Trp Lys Gly Arg Ser Ser Glu Glu Xaa Leu Arg Pro Xaa Thr
65 70 75

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gtcgagaacc ttgaattccc ggcggtgatt acttctccgg tcaacggtaa gtcataattt
180

cttgggtggtg caggggagag aggtttgact attgaaggaa acttcatcaa gttcactgcc
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300

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50

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120

tcgagaacct tgaattcccg gcggtgatta cttctccggt caacggtaag tcatattttc
180

ttggtggtgc aggggagaga ggttngacta ttgaaggaaa cttcatcaag ttcactgcca
240

taggagtata tttggaagat gtagcagggg cttcacttgc cactaaatgg aagggcana
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nctctgaaga gtgcttgaga cccttgactt c
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120

cgagagattac ttctnoggg aanggggaagg gatattntct tgggtggnga ggnnaganng
180

nntngn
186

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120

tgttgggact tatggagatg cagaagctga agctatgcaa aaatttggtg aagccttcaa
180

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 35 40 45

Phe Val Glu Ala Phe Lys Pro Ile Asn Phe Pro Gly Ala Ser Val
 50 55 60

Phe Tyr Arg Gln Ser Pro Asp Gly Ile Leu Gly Val Ser Ile Ala Asn
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tggtgggact tatggagatg cagaagctga agctatgcaa aaatttggtg aagccttcaa
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120

tatggagatg cagaagctga agctatgcaa aaatttgttg aagccttcaa gcctattaat
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gcaggagagc ggggtcttca aattcaagac aaatttgtca aattcacgcg tattgggtgt
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gagctaaccg aaactgttcc tttcttcagg gacatcgta caggtcctatt tgagaaattt
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 35 40 45

Thr Ala Ile Gly Val Tyr Leu Gln Asp Ile Ala Val Pro Tyr Leu Ala
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Thr Lys Trp Lys Gly Lys Thr Ala Gln Glu Leu Thr Glu Thr Val Pro
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Phe Phe Arg Asp Ile Val Thr Gly Pro Phe Glu Lys Phe Met Gln Val
 85 90 95

Thr Met Ile Leu Pro Leu Thr Gly Gln Gln Tyr Ser Glu Lys Val Ser
 100 105 110

Glu Asn Cys Val Ala Ile Trp Lys Ser Leu Gly Ile Tyr Thr Asp Glu
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Glu Ala Lys Ala Ile Glu Lys Val Ser Val Phe Lys Glu Thr Phe Pro
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Pro Gly Ser Ser Ile Leu Phe Thr Leu Pro Lys Gly Leu Gly Ser Leu
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Thr Ile Xaa Phe Ser Lys Asp Gly Ser Ile Pro Glu Thr Glu Ser Ala
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Val Ile Glu Asn Lys Leu Leu Ser Gln Ala Val Xaa Glu Ser Met Ile
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Gly Ala His Gly Val Ser Pro Ala Ala Lys Gln Ser Phe Gly His Gln
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 120

atctatctcc tcctaccgtc acaccanccg gatccaccaa caattttctc ctccggcggtg
 180

caggagagcg gggctctcaa attcaagaca aatttgtcaa attcaccgnt attggtgttt
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atctacagga cattgtgtgt ccttacctcg ccactaaatg gaagggtnag actgctcaag
 300

agctaacgga aactgncctt ttcttcaggg acatngnnac aggtccattt gagaaattta
 360

tgcagggtgac aatgatcttg ccattgactg ggcaacaata ctccagagaaa gtgtcanaaa
 420

attgtgtacc tatntgnaag tctcttcgga ttatatacca ccaagaagcc aaagcaattg
 480

agaagnntgt ttctgtcttc aaagangaaa cattccccacc aggtcctctc atccttttca
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cagnattacc caaaggatta ngatcactaa cgataagntt ctctaaagat ggatccattc
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cagagaccga gtctgcagtt atagngaata agctactctc acaagctgtg ctngagtcga
 660

tgataggggc anncggtgtc tnnntgcan caaancatag ttttggnac caggntancc
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ccctgcagca aaacagagtt tggccaccag gttatccgag ttattcaacg aggttggtga
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120

tccactgaca acttcttcct cggcgggtgca ggagagaggg gtcttcaaat ccaagacaaa
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ttcgtcaaat tcaccgctat tgggtgttat ctgcaggaca ttgctgttcc ttacctcgca
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gctaaatgga agggtagac tgctcaagag ctaactcaaa ctgttccttt cttcaggga
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atcgttacag gtccatttga gaaatttatg caggtgacaa tgatcttgcc attgactggg
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caacaatact cagagaaagt gtcagaaaat tgtgtagcta ttggaagtc tcttgggata
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acaacaacct ataactanac atattatttt tatntattta gtatataatt gaaataaact
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gctaaagata nttattaaga tatggtgagt gtagctgaaa ttgcgaagcg tcagagggct
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gaaggccctg caaccatttt ggccattggc actgcaaact cagcaaacgg tggtagagcg
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gaagagattt tgaagaaaa tcctagtctt tgtgaatata tggcaccttc attggatgct
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35 40 45

Lys Thr Glu Leu Lys Glu Lys Phe Gln Arg Met Cys Asp Lys Ser Met
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acaacaanct ataacttinn ctgttatnta naccaattga gntcaaat nacatacata
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gcggaacata ctaaatacaa catggttagt gtttctgaaa ttgcgaaggc tcaaagggct
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gaaggccctg caactatttt ggccattggt actgcaaato cagcaaatcg tgttgaccag
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420

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480

aggcaagaca tgggtggtgt tgaggtaact agacttggga aggaggctgc agtgaaagct
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atcaaagaat ggggtcaacc aaagtcaaag attactcact taatcttttg caccacaagt
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120
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180
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240
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120

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180

atccagcaaa ccgtgttgat cagagcacat atcctgattt ctacttcaaa atcactaaca
240

gtgaacataa agttgagctc aaagagaaat tccagcgcat gtgtgataaa tctatgatca
300

agagcgagata catgtatcta acagaagaga ttttgaaaga aaatcctagt ctttgtgagc
360

acatggcacc ttcatgggat gctaggcaag acatggtggt ggttgaggta cctagacttg
420

ggaaggaggc tgcagtgaaa gctataaaag aatggggcca accaaagtca aagattactc
480

acttaatctt ttgcaccaca agtgggtgtg acatgcctgg tgcgtattac caactcacia
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120

aaagggcaga aggcctctgca acaatcttgg ccattggcac tgcaaatcca gcaaacctg
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240

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atctaacaga agagattttg aaagaaaatc ctagtctttg tgagcacatg gcaccttcac

360

tggtatgctag gcaagacatg gtggtggttg aggtacctag acttggaag gaggtgtag
420

tgaagctat aaaagaatgg ggtcaaccaa agtcaaagat tactcactta atcttttgca
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ccacaagtgg tgttgacatg cctgggtgctg attaccaact cacaaaaactc ttaggtcttc
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120

caaagggcag aagccctgc aaccatttta gccattgcta ctgcaaatcc agcaaacctg
180

gtagaccaga gcacatatcc tgatttctac ttcaaaatca ctaacagtga gcataagggt
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gaagcttaag agaaattcca gcgcatgtgt gataaatcta tgatcaagag cagatacatg
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tatctaacag aagagatttt gaaagaaaat cctagtcttt gtgaatacat ggcaccttca
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ttggatgcta ggcaagacat ggtggtggtt gaggtacctt gactaggaaa ggaggctgca
420

gtcaaggcca ttaagaatg gggtaacca aagtcaaaga ttactcactt aatcttttgc
480

accacaagtg gtgtagacat gcctgggtgt gattaccaac tcacaaaact cttgggactt
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120

gccctgcaac cattttggcc attggcactg caaatccacc aaacctgtgt gagcagagca
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catatcctga tttctacttc aaaattacaa acagtgtgca caagactgag ctcaaagaga
240

agttccaacg catgtgtgac aaatccatga tcaagagcag atacatgtat ctaacagaag
300

agattttgaa agaaaatcct agtctttgtg aatacatggc accttcattg gatgctaggc
360

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aagatttgcc cgagaacaac aaaggtgctc gtgtgctagt tgtttgtctt gaagtcaccg
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ctgaaggccc tgcaaccatt ttggccattg gcaactgcaaa tccaccaaac cgtgttgagc
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agagcacata tcttgatttc tacttcaaaa ttacaaacag tgagcacaag actgagctca
240

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aagagaagtt ccaacgcatg tgtgacaaat ccatgatcaa gagcagatac atgtatctaa
300

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cagaagagat ttgaaagaa aatcctagnc ttgtgaata catgncacct tcattggatg
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407

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120

gcctcgcaac cattttggcc atgggcactg caaatccacc aaaccgtgtt gagcagagca
180

catatcctga tttctacttc aaaattacaa acagtgcgca caagactgag ctcaagagaga
240

agttccaacg catgtgtgac aaatccatga tcaagagcag atacatgtat ctaacagaag
300

agattttgaa agaaaatcct agtctttgtg aatacatggc accttcattg gatgctaggc
360

aagacatgggt ggtgggtgag gtacctanac ttgggaagga ggctgcannc aagccatta
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120

ctgaaggccc tgcaaccatt ttggccattg gcactgcaaa tccaccaaac cgtgttgagc
180

agagcacata tcctgatttc tacttcaaaa ttacaacacag tgagcacaag actgagctca
240

aagagaagtt ccaacgcatg tgtgacaaat ccatgatcaa gacgagatag atgtatctaa
300

cagaagagat tttgaagaaa aatcctagtc tttgtgaata catggcacct tcattggatg
360

ctagacaaga catgggtggtg gttgaggtac ctgacttgg gaaggaggct gcagtcaagg
420

ctatcaaaga atgggggtcaa ccaaaatcta agattacaca ttgatcttt tgcaccacaa
480

gtgggtgtaga catgcctggt gctgattacc aactcacaaa actcttagga ctctgtccat
540

atgtgaagag gtacatgatg taccaacaag ggtgctttgc aggtgg
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gaaggccctg caactatttt ggccattggc actgc aaatc cagcaaacg tgtgatcag
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agcacatatc ctgattttta cttcaaaatc actaacagtg agcataagggt tgagcttaaa
240

gagaaatttc agcgcatgtg tgataaatct atgatcaaga gcagatacat gtatctaaca
300

gaagagattt tgaagaaaaa tcctagtett tgtgaataca tggcaccttc attggatgct
360

aggcaagaca tgggtggtgg tgaggtaacct agacttggga aggagggtgc agtgaaagct
420

atcaaaagaat ggggtcaacc aaagtcaaag attactcact taatcttttg caccacaagt
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ggtgtagaca tgcctggagc tgattaccaa ctcacaaaaa tcttaggtct tcgcccatat

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gcaaccattt tggccattgg tactgcaaat ccaccaaacc gtgttgagcg gacacatat

180

cctgatttct acttcaaaat tacaacacgt gacacacaaga ctgagctcaa agagaagttc

240

caacgcattgt gtgacaaatc catgatcaag agcagatata tgatatcaac agaagagatt

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ttgaaagaaa atcctagttt ttgtgaatac atggcacctt cattggatgc taggcaagac

360

atgggtggtg ttgaggtacc tagacttggg aaggaggctg cagtgaagc tatcaaagaa

420

tggggtcaac caaagtcaaa gattactcac ttaatctttt gcaccacaag tgggtgtagac

480

atgcctggag ctgattacca actcacaaaa ctcttaggtc ttccgccata tgtgaaaaag

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604

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120

caactatctt ggccattggt actgcaaatc cagcaaatcg tgttgaccag agtacatatc
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ctgatttcta ctcaaaaatc actaacagtg agcataaggt tgagcttaaa gagaaatttc
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agcgcatgtg tgataaatct atgatcaaga gcagatacat gtatctaaca gaagagattt
300

tgaagaaaaa tcttagtctt tgtgaatata tggcaccttc attggatgct aggcaagaca
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tgggtgggtg tgaggtacct agacttggga aggagggtgc agtgaagct atcaaagaat
420

ggggtcaacc aaagtcaaag attactcact taatcttttg caccacaagt ggtgttgaca
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tgccctggtc cgattaccaa ctcaaaaaac tcttaggtct tgcgccatat gtgaagaggt
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aaggccctgc aactattttg gccattggta ctgcaaatcc agcaaatcgt gttgaccaga
180

gtacatatcc tgatttctac ttcaaaatca ctaacagtga gcataaggtt gagcttaaag
240

agaaatttca gcgcattgtg gataaatcta tgatcaagag cagatacatg tatctaacag
300

aagagatttt gaaagaaaat cctagtcctt gtgaatacat ggcaacctca ttggatgcta
360

ggcaagacat ggtggtggtt gaggtaccta gacttgggaa ggaggctgca gtgaaagcta
420

tcaagaatg gggtaacca aagtcaaaga ttactcactt aatcttttgc accacaagtg
480

gtgtagacat gcctggagct gattaccaac toacaaaact cttagggttt cgcccatatg
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120

ggccctgcaa ccattttggc cattggcact gcaaatccac caaacctgt tgagcagagc
180

acatatcctg atttctactt caaaattaca aacagtgtg acaagactga gctcaaagag
240

aagttccaac gcattgtgtga caaatccatg atcaagagca gatacatgta tctaacagaa
300

gagattttga aagaaaatcc tagtctttgt gaatacatgg caccttcatt ggatgctagg
360

caagacatgg tgggtggtga ggtacctaga cttgggaagg aggctgcagt caaggccatt
420

aaagaatggg gtcaacaaa gtcaaagatt actcacttaa tcttttgcac cacaagtgg
480

gttgacatgc ctgggtgtga ttaccaactc acaaaactct taggtcttcg cccatatgtg
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aaaagggtata tgatgtacca acaaggttgt tttgcaggag gcacgggtgt tcggttggca
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120

caactatttt ggccattggt actgcaaatc cagcaaatcg tgttgaccag agtacatata
180

ctgattttcta cttcaaaatc actaacagtg agcataaggt tgagcttaaa gagaatttc
240

agcgcatgtg tgataaatct atgatcaaga gcagatacat gtatctaaca gaagagattt
300

tgaaagaaaa tccctagtctt tgtgaatata tggnaccttc attgnatgnt agncaagaca
360

tgntgtgnc ngaggnaccn agacttgccn
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<210> 40

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120
aggccctgca accatttttg ccattggcac tgcaaatcca ccaaaccgtg ttgagcagag
180
cacatatcct gatttctact tcaaaattac aaacagtgag cacaagactg agctcaaga
240
gaagttccaa cgcgtgtgtg acaaatccat gatcaagagc agatacatgt atctaacaga
300
agagattttg aaagaaaatc ctagtctttg tgaatacatg gcaccttcat tggatgctag
360
acaagacatg gtgggtggtg aggtacctag acttgggaag gaggctgcag tcaaggctat
420
caaagaatgg ggtcaaccaa aatctaagat tacacatttg atcttttgca ccacaagtgg

480

tgtanacatg cctggtgctg attaccnact ngcaaaaactn ttaggacttn gcccatatgt
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gangaggcgc gtgntgnccc n
561

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120
ggccctgcaa ctattttggc cattgggtact gcaaatccag caaatcgtgt tgaccagagt
180
acatactctg atttctactt caaaatcact aacagtgagc ataagggtga gcttaaagag
240
aaatttcagc gcattgtgtga taaatctatg atcaagagca gatacatgta tctaacagaa
300
gagattttga aagaaaatcc tagtctttgt gaatacatgg caccttcatt ggatgctagg
360
caagacatgg tgggtggtga ggtacctaga cttgggaagg aggtctcagt gaaagctatc
420
aaagaatggg gtcaacaaa gtcaaagatt actcacttaa tcttttgcac cacaagtggg
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120

gcctcgcaac tatittggcc attggtactg caaatccagc aaacgtgtt gatcagagta
180

catatcctga ttctacttc aaaatcacta acagtgaaca taaagttgag ctcaaagaga
240

aattccagcg catgtgtgat aaatctatga tcaagagcag atacatgtat ctaacagaag
300

agattttgaa agaaaatcct agtctttgtg aatacatggc accttcattg gatgctaggc
360

aagatatggt ggcggttgag gtacctanac ttgnaaagga ggctgcnntg aaggtatta
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aagaatgggg ccancn
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<210> 43

<211> 607

<212> DNA

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120

ccttgcaaco attttggcca ttggcactgc aaatccacca aacogtggtg agcagagcac
180

atctcctgat ttctacttca aaattacaaa cagtgcagcac aagactgagc tcaaagagaa
240

gttccaacgc atgtgtgaca aatccatgat caagagcaga tacatgtatc taacagaaga
300

gattttgaaa gaaaatccta gtctttgtga atacatggca ccttcattgg atgctaggca
360

agacatgggt gtggttgagg tacctagact tgggaaggag gctgcagtga aagctatcaa
420

agaatggggg caaccaaagt caaagattac tcacttaatc ttttgcacca caagtgggtg
480

agacatgcct ggagctgatt accaactcac aaaactctta ggtcttcgcc catatgtgaa
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aaggatatg atgtaccaac aagggtgttt tgcaggaggc acgggtgcttc gtttggcaaa
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120

ctgcaaccat tttggccatt ggcaactgcaa atccacaaaa ccgtgttgag cagagcacat
180

atcctgtatt ctacttcaaa attacaaca gtgagcacia gactgagctc aaagagaagt
240

tccaacgcac gtgtgacaaa tccatgatca agagcagata catgtatcta acagaagaga
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ttttgaaaga aaatcctagt ctttgtgaat acatggcacc ttcattggat gctaggcaag
360

acatgggtgtt ggttgaggta cctagacttg ggaaggaggc tgcagtcaag gccattaaag
420

aatgggggtca accaaagtca aagattactc acttaattctt ttgcaccaca agtgggtgtt
480

acatgcctgg tgctgattac caactcacia aactcttagg tcttcgccca tatgtgaaaa
540

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120

tgcaaccatt ttggccattg gcaactgcaaa tccaccaaac cgcgttgagc agagcacata
180

tcctgatttc tacttcaaaa ttacaaacag tgagcacaag actgagctca aagagaagtt
240

ccaacgcatg tgtgacaaat ccatgatcaa gacgagatac atgtatctaa cagaagagat
300

tttgaagaa aatcctagtc tttgtgaata catggcacct tcattggatg ctaggcaaga
360

catgggtggtg gttgaggtac ctgactctgg gaaggaggct gcaagtcaagg ctatcaaaaga
420

atgggggtcaa caaaaatcta agattacaca ttgatcttt tgaccacaa gtgggtgtaga
480

catgcctggt gctgattacc aactcacaaa actcttgga cttcgtccat atgtgaagag
540

attcatgatg taccaacaag gctgctttgc aggtgggacg gttcttcg
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<210> 46

<211> 613

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120

aaccattttg gccattggca ctgcaaatcc accaaaccgt gttgagcaga gcacatatcc

180

tgatttctac ttcaaaatta caaacagtga gcacaagact gagctcaaaag agaagttcca
240

acgcattgtgt gacaaatcca tgatcaagag cagatacatg tatctaacag aagagatttt
300

gaaagaaaaat cctagtcttt gtgaatacat ggcaccttca ttggatgcta ggcaagacat
360

ggtgggtggtt gaggtacctt gacttgggaa ggaagctgca gtcaaggcca ttaaaagaatg
420

gggtcagcca aagtcaaaga ttactcactt aatcttttgc accacaagtg gtgttgacat
480

gcctggagct gattaccaac tcacaaaact cttaggtctt cgcccatatg tgaaaaggta
540

tatgatgtac caacaagggt gttttgcagg aggcacggtg cttcgttttg caaaagattt
600

ggccgagaac aac
613

<210> 47
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120

tttggccatt ggtactgcaa atccagcaaa ccgtgttgat cagagtacat atcctgattt
180

ctacttcaaa atcactaaca gtgagcataa gggtgagctc aaggagaaat tccagcgcat
240

gtgtgacaaa tctatgatca agagcagata catgtatcta acagaagaga ttttgaaga
300

aaatcctagt ctttgtgaat acatggcacc ttcattggat gctaggcaag atatggtggg
360

cggttgagsta cctagactgg gaaaggaagc tgcagtgaag gctattaaag aatgggggtca
420

accaaagtca aagattactc acttaatctt ttgcactaca agtgggtgtag acatgcctgg
480

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540

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544

<210> 48
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120

ccattttggc cattgggtact gcaaatccag caaacogtgt tgatcagagt acatatcctg
180

atttctactt caaaatcact aacagtgagc ataaggttga gctcaaggag aaattccagc
240

gcatgtgtga taaatctatg atcaagagca gatacatgta tctaacagaa gagattttga
300

aagaaaaatcc tagtctgtgt gagtacatgg caccttcatt ggatgctagg caagacatgg
360

tgttggttga ggtacctaga cttggaaaagg aggetgcagt caaggccatt aaagaatggg
420

gtcaacacaa gtcaaagatt actcacttaa tcttttgcac cacaagtggg gtagacatgc
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ctgggtgctga ttaccaactc acaaaactct tangtcttgc tccatacgtg aagagggaca
540

tgatgtacca acaag
555

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120

ccatttttggc cattggcact gcaaatccac caaacctgtg tgagcagagc acatatcctg
180

atttctactt caaaattaca aacagtggag acaagactga gctcaaagag aagttccaac
240

gcagtgtgtga caaatccatg atcaagagca gatacatgta tctaacagaa gagattttga

300

aagaaaatcc tagtctttgt gaatacatgg caccttcatt ggatgctagg caagacatgg
360

tggtggttga ggtacctaga cttgggaagg aggctgcagt caaggccatt aaagaatggg
420

gtcaacaaa gtcaaagatt actcacttaa tcttttgcac cacaagtggg gttgacatgc
480

ctggtgctga ttaccaactc aaaaaactct taggtcttcg cccatatgtg aaaagggtata
540

tgatgtacca acaagggttg tttgcaggag
570

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120

ccattggtac tgcaaatcca gcaaacctg tttgatcagag tacatatcct gattttctact
180

tcaaaatcac taacagttag cataagggtg agctcaagga gaaattccag cgcattgtgtg
240

ataaatctat gatcaagagc agatacatgt atctaacaga agagattttg aaagaaaatc
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ctagtctgtg tgagtacatg gcaccttcac tggatgctag gcaagacatg gttgtggttg
360

aggtagcctag acttggaag gaggtgcag tcaaggccat taaagaatgg ggtagcaacaa
420

agtagaagat tactcactta atcttttgca ccacaagtgg tgtagacatg cctgggtgctg
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<210> 51
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120

ttggtactgc aaatccagca aaccgtgttg atcaaagtac atatcctgat ttctacttca
180

aaatcactaa cagtgcagcat aaggttgagc tcaaagagaa attccagcgc atgtgtgata
240

aatctatgat caagagcaga tacatgtatc caacagaaga gattttgaaa gaaaatccta
300

gtcttttgta atacatggca ccttcattgg atgctagaca agacatggtg gtgggtgagg
360

tacctagact tggaaaggag gctgcagtga aggccattaa agaatggggt caacaaaaat
420

ctaagattac acatttgatc ttttgacca caagtgggtg agacatgcct ggtgctgatt
480

accagctcac aaaactctta ggtcttcgtc catatgtgaa aaggtatatg atgtaccaac
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aagggtgctt tgcaggtggg acggtgcttc gtttgccaa gg
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<210> 52
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120

ttggccattg ctactgcaaa tccagcaaac cgtgttgatc aaagtacata tcttgatttc
180

tacttcaaaa tcaactaacag tgagcataag gttgagctca aagagaaatt ccagcgcnng
240

tgtgataaat ctatgatcaa gagcagatac atgtatctaa cagaagagat tttgaaagaa
300

aatcctagtc tttgtgaata catggcacct tcattggatg ctagacaaga catggtgggtg
360

gttgaggtag ctgacttgg aaaggaggct gcagtgaagg ccattaaaga atgggggtcaa
420

ccaaaatcta agattacaca ttgatcttt tgcaccacaa gtggtgtana catgcctggg
480

gctgattacc agctcacaaa actcttaggt ctctgtccat atgtgaaaag ggatatgatg
540

taccaacaag ggtgctttgc aggtgggacc gtgcttcntt tggccaanga tttggcccan
600

aacaacaaan gngctcgngn gttggntggt tggctctnaan tcaccgcan
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120

caaacctgtg tgagcagagc acatatcttg atttctactt caaaattaca aacagtggagc
180

acaagactga gctcaaagag aagttccaac gcatgtgtga caaatccatg atcaagagca
240

gatacatgta tctaacagaa gagattttga aagaaaaatcc tagtctttgt gaatacatgg
300
caccttcatt ggatgctagg caagacatgg tgggtggttga ggtacctaga cttgggaagg
360
aggctgcagt gaaagctatc aaagaatggg gtcaaccaaa gtcaaagatt actcacttaa
420
tcttttgcac cacaagtggg gtagacatgc ctggagctga ttaccaactc acaaaactct
480
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120

gagcacatat cotgatttct acttcaaaat tacaacagtg gagcacaaga ctgagctcaa
180

agagaagttc caacgcattg gtgacaaatc catgatcaag agcagataca tgtatctaac
240

agaagagatt ttgaaagaaa atoctagtct ttgtgaatac atggcacctt cattggatgc
300

taggcaagac atggtggtgg ttgaggtacc tagacttggg aaggaggctg cagncnaggc
360

cattaaanaa tggggncnac caaagncaaa gattactcac ttaatctttt gccaccacaa
420

tggtgctgac atgnctgggt ctgattacca actcacaata ctottaggnc tteccccata
480

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<210> 55

<211> 504

<212> DNA

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120
cacatatcct gatttctact tcaaaattac aaacagttag cacaagactg agctcaaaga
180
gaagttccaa cgcattgtgtg acaaatccat gatcaagagc agatacatgt atctaacaga
240
agagattttg aaagaaaatc ctagtctttg tgaatacatg gcaccttcac tggatgctag
300
gcaagacatg gtggtggttg aggtacctag acttgggaag gaggtgcag tcaaggccat
360
taaagaatgg ggtnaaccaa agtgaaagat tactnactta atcttttgca ccacaagtgg
420
tgttagcatg nctgggtctg attaccaact cacaaaactc ttaggnnttg gncatattg
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gaaaaggctc atgatgcacc aacn
504

<210> 56
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<212> DNA
<213> *Trifolium repens*

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120
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180
gaagttccaa cgcattgtgtg acaaatccat gatcaagagc agatacatgt atctaacaga
240
agagattttg aaagaaaatc ctagtctttg tgaatacatg gcaccttcac tggatgctag
300
gcaagacatg gtggtggttg aggtacctag acttgggaag gaggtgcag tgaaggctat
360
caagaatgg ggtaaccaa agtcaagat tactcactta atcttttgca ccacaagtgg
420
tgttagcatg cctggagctg attaccaact cacaaaactc ttaggtcttc gccatattg
480
gaaaagggtat atgatgtacc aacaagggtg ttttgaggga ggcacgggtc ttcgtttggc
540
aaaagatttg gccgagaaca acaagggtgc tcgtgtgttg gttgtttgtt ctgaagtcac
600

tcagttaca ttccgtggcc cgagtgacac tcacttggac agtcttgttg gacaagcatt
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gtttggagat ggagcagctg cacttatcgt tggttctgat ccagtgccag aaattgagaa
720

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<210> 57
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120

cacatatcct gatttctact tcaaaattac aaacagtggag cacaagactg agctcaaaaga
180

gaagttccaa cgcattgttg acaaatccat gatcaagagc agatacatgt atctaacaga
240

agagattttg aaagaaaatc ctagtctttg tgaatacatg gcaccttcat tggatgctag
300

acaagacatg gtgggtggtg aggtacctag acttgggaag gaggctgcag tcaaggctat
360

caaagaatgg ggtcaaccaa aatctaagat tacacatttg atcttttgca ccacaagtgg
420
tgtagacatg cctggtgctg attaccaact cacaaaactc ttaggacttc gtccatatgt
480
gaagaggtag atgatgtacc aacaagggtg ctttgcaggt ggggcgggtc ttggtttggc
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<210> 58
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ctgagctcaa agagaagttc caacgcatgt gtgacaaatc catgatcaag agcagataca
180
tgtatctaac agaagagatt ttgaaagaaa atcctagtct ttgtgaatac atggcacctt
240
cattggatgc tagacaagac atgggtggtg ttgaggtacc tagacttggg aaggaggccg
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cagtcaaggc tatcaaagaa tggggccaac caaaatctaa gattacacat ttgatctttt
360
gcaccacaag tggtgtgagac atgcctgggt ctgattacca actcacaaaa ctcttaggac
420
ttcgtccata tgtgaagagg tacatgatgt accaacaagg gtgctttgca ggtgggacgg
480
ttcttcgttt ggctaagat ttggccgaga acaacaaagg tgctcgtgtg ttggttgttt
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ggcaagacat ggtggtggtt gaggtaccta gacttgggaa ggaggctgca gtgaaagcta
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tcaaagaatg gggccaacca aagtcaaaga ttactcactt aatcttttgc accacaagtg
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gtgttgacat gcctggtgct gattaccaac tcacaaaaact cttaggctct cgcccatatg
420
tgaagaggta catgatgtac caacaagggt gctttgcagg tgggacggtt cttcgtttgg
480
ccaaggattt ggccgagaac aacaaagggt ctcggtgtgt gttgttttgc tctgaagtaa
540
ccgcagtcac attccgcggc ccagtgaca ctcatttgga cagccttggt ggacaagcac
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120
aaatttcagc gcattgtgtga taaatctatg atcaagagca gatacatgta tctaacagaa
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gagattttga aagaaaaatcc tagtctttgt gaatacatgg caccttcatt ggatgctagg
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360
gttgacatgc ctgggtgctga ttaccaactc aaaaactct taggtcttcg cccatatgtg
420
aagggttaca tgatgtacca acaagggtgc ttgacagtg ggacgggtct tcgtttggcc
480
aaggatttgg ccgagaacaa caaagggtct cgtgtgttgg ttgttgtctc tgaagtaacc
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caccttcatt ggatgctagg caagacatgg tgggtggtga ggtacctaga cttgggaagg
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aggctgcagt gaaagctatc aaagaatggg gtcaacaaa gtcaagatt actcacttaa
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tcttttgcac cacaagtggg gtagacatgc ctggagctga ttaccaactc acaaaactct
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taggtcttcg cccatatgtg aagagggtaca tgatgtacca acaaggggtgc tttgcagggtg
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ggacgggttct tcgtttggcc aaggatttgg ccgagaacaa caaagggtgct cgtgtgttgg
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ttgtttgtgc tgaagtaacc gcagtcacat tccggggccc cagtgcact catttggaca
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gtcttgttgg acaagcacta ttccggagatg gagctgctgc actcattgtt ggctcagacc
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<210> 62

<211> 553

<212> DNA

<213> *Trifolium repens*

<400> 62

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120

cttggaaagg aggctgcagt caaggccatt aaagaatggg gtcaacaaa gtcaagatt
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actcacttaa tcttttgcac cacaagtggg gtagacatgc ctgggtgtga ttaccaactc
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acaaaaactct taggtcttcg tccatcagtg aagagggtaca tgatgtacca acaaggggtc
300

tttgcagggtg ggacgggtgct tcgtttggcc aaggatttgg ccgagaacaa caaagggtgct
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cgtgtgttgg ttgtttgttc tgaagtcaco gcagtcacat tccgtggccc tagtgacact
420

catttggaca gtcttgttgg acaagcacta ttggagatg gagctgctgc tctcattgtt
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120

tgtgaagagg tatatgatgt atcaacaagg ttgctttgca ggaggcacgg tgcttcgttt
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ggctaaagat ttggcggaga acaacaaagg tgctcgtgtg ctagtgttt gttctgaagt
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aacagcagtc acattccgcg gtccaagtga cactcacttg gacagtcttg ttggacaagc
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actattcgga gatggagctg ctgctctcat tgttgggtca gacctgtac cagaaatgca
360

gaaacctata tttagatgg tatggaccgc acagacaatt gctccggaca gtgaagggtc
420

cattgatggt caccttcgtg aagctggact aacatttcat cttcttaaag atgttctgtg
480

gattgtatca aagaacatta ataaagcatt ggtcgaggct ttccaacat taggaatttc
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480
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<400> 65

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Ile Val Ser Lys Asn Ile Asp Lys Ala Leu Val Glu Ala Phe Gln Pro
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Leu Asn Ile Ser Asp Tyr Asn Ser Ile Phe Trp Ile Ala His Pro Gly
 35 40 45

Gly Pro Ala Ile Leu Asp Gln Val Glu Ile Lys Leu Gly Leu Lys Pro
 50 55 60

Glu Lys Met Lys Ala Thr Arg Asp Val Leu Ser Glu Tyr Gly Asn Met
 65 70 75 80

Ser Ser Ala Cys Val Leu Phe Ile Leu Asp Glu Met Gln Lys Lys Ser
 85 90 95

Ala Glu Asn Gly Leu Lys Thr Thr Gly Glu Gly Leu Asp Trp Gly Val
 100 105 110

Leu Phe Gly Phe Gly Pro Gly Leu Thr Ile Glu Thr Val Val Leu His
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Ser Val Ala Ile
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360
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60
ggtgtgttgt ttggatttgg accaggactt accattgaaa ctgtgtgtct acatagtgtg
120
gctatatgag aatgcgagac ttgattgttt tgtattgtat tgtattgtat tgtattactt
180
ttaactctgc ttgaatttcc atttaacaat aaatatggag ttcaataagt accatcagtg
240
ttaaaataat atatcggtta tagctattat tttagtgtct gttttttttt actaaactat
300
attttatttt agtatttggc attgatttga aataaatatt gtccctcttaa ctgaaaaaaa
360

aaa

363

<210> 68
<211> 363
<212> DNA
<213> *Trifolium repens*

<400> 68
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60

gggtgtgtgt ttggatttgg accaggactt accattgaaa ctgttgttct acatagtgtg
120

gctatatgag aatgcgagac ttgattgttt tgtattgtat tgtattgtat tgtattactt
180

ttaattcttc ttgaatttcc atttaacaat aaatatggag ttcaataagt accatcagtg
240

ttaaaaaaat atatcgtaa tagctattat tttagtgtct gtttcttttt actaaactat
300

attttatttt agtatttgct attgatttga aataaatatt gtcctcttaa ctgaaaaaaa
360

aaa
363

<210> 69
<211> 897
<212> DNA
<213> *Trifolium repens*

<220>
<221> misc_feature
<222> (2)..(2)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (26)..(26)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (33)..(33)
<223> Any nucleotide

<400> 69
gnttcaatct gtgtgcatata aaatttcttt gcnatagaaa accatacaca ttatgatcttg
60

caaagaagaa atatgggaga cgaaggatata gtgagagggt tcacaaagca gacaacccct
120

gggaaggcta ctatatgggc tottggcaag gcattccctc accaacttgt gatgcaagag
180

tatttagttg atgggtattt tagggacact aattgtgaca atcctgaact taagcagaaa
240

ctgtctagac ttgttaagac aaccacggtg aaacaaggt atgttggtat gaatgaggag
 300
 atactaaaga aatatccaga acttggtgtc gaaggcgctt caactgtaaa acaacgttta
 360
 gagatatgta atgaggcagt aacacaaatg gcaattgaag ctcccaagt ttgcctaaag
 420
 aattggggta gatccttatt ggacataact catgtgggtt atgtttcatc tagtgaagct
 480
 agattaccgg gtggtgacct atacttgtca aaaggactag gactaaaccc taaaattcaa
 540
 agaaccatgc tctatttctc tggatgctcg ggaggogtag ccggccttcg cgttgcgaaa
 600
 gacatagctg agaacaaccc tgggaagtag gttttgcttg ctacttctga aactacaatt
 660
 attggattca agccaccaag tgttgataga ccttatgac ttgttggtgt ggcactcttt
 720
 ggagatgggt ctggtgctat gataattggc tcagacccaa tacttgaaac tgagactcca
 780
 ttgtttgagc ttcatacttc agctcaggag tttataccag acacagagaa gaaaatagat
 840
 gggcggctga cggaggaggg cataagtctc acgctagcga gggaactgcc gcagata
 897

<210> 70
 <211> 275
 <212> PRT
 <213> *Trifolium repens*

<400> 70

Met Gly Asp Glu Gly Ile Val Arg Gly Val Thr Lys Gln Thr Thr Pro
 1 5 10 15

Gly Lys Ala Thr Ile Leu Ala Leu Gly Lys Ala Phe Pro His Gln Leu
 20 25 30

Val Met Gln Glu Tyr Leu Val Asp Gly Tyr Phe Arg Asp Thr Asn Cys
 35 40 45

Asp Asn Pro Glu Leu Lys Gln Lys Leu Ala Arg Leu Cys Lys Thr Thr
 50 55 60

Thr Val Lys Thr Arg Tyr Val Val Met Asn Glu Glu Ile Leu Lys Lys
 65 70 75 80

Tyr Pro Glu Leu Val Val Glu Gly Ala Ser Thr Val Lys Gln Arg Leu
 85 90 95

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Glu Ile Cys Asn Glu Ala Val Thr Gln Met Ala Ile Glu Ala Ser Gln
 100 105 110
 Val Cys Leu Lys Asn Trp Gly Arg Ser Leu Ser Asp Ile Thr His Val
 115 120 125
 Val Tyr Val Ser Ser Ser Glu Ala Arg Leu Pro Gly Gly Asp Leu Tyr
 130 135 140
 Leu Ser Lys Gly Leu Gly Leu Asn Pro Lys Ile Gln Arg Thr Met Leu
 145 150 155 160
 Tyr Phe Ser Gly Cys Ser Gly Gly Val Ala Gly Leu Arg Val Ala Lys
 165 170 175
 Asp Ile Ala Glu Asn Asn Pro Gly Ser Arg Val Leu Leu Ala Thr Ser
 180 185 190
 Glu Thr Thr Ile Ile Gly Phe Lys Pro Pro Ser Val Asp Arg Pro Tyr
 195 200 205
 Asp Leu Val Gly Val Ala Leu Phe Gly Asp Gly Ala Gly Ala Met Ile
 210 215 220
 Ile Gly Ser Asp Pro Ile Leu Glu Thr Glu Thr Pro Leu Phe Glu Leu
 225 230 235 240
 His Thr Ser Ala Gln Glu Phe Ile Pro Asp Thr Glu Lys Lys Ile Asp
 245 250 255
 Gly Arg Leu Thr Glu Glu Gly Ile Ser Phe Thr Leu Ala Arg Glu Leu
 260 265 270
 Pro Gln Ile
 275

<210> 71
 <211> 577
 <212> DNA
 <213> *Trifolium repens*

<220>
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 <222> (2)..(2)
 <223> Any nucleotide

<220>
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 <222> (26)..(26)
 <223> Any nucleotide

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<221> misc_feature
<222> (33)..(33)
<223> Any nucleotide

<220>
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<222> (43)..(43)
<223> Any nucleotide

<400> 71
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caaagaagaa atatgggaga cgaagggtata gtgagagggtg tcacaaagca gacaaccctt
120
gggaaggcta ctatatgggc tcttggcaag gcattccctc accaacttgt gatgcaagag
180
tgtttagttg atgggtattt tagggacact aattgtgaca atcctgaact taagcagaaa
240
cttgctagac tttgtaagac aaccacggt aaaaacagggt atgttggttat gaatgaggag
300
atactaaga aatatccaga acttgtgtgc gaaggcgct caactgtaaa acaacgttta
360
gagatatgta atgaggcagt aacacaaatg gcaattgaag ctcccgaagt ttgcctaaag
420
aattggggta gatccttctc ggacataact catgtgggtt atgttctcct tagtgaagct
480
agattaccgc gtggtagacct atacttgtca aaaggactag gactaaacct taaaattcaa
540
agaaccatgc tctattttctc tggatgctcg ggaggcg
577

<210> 72
<211> 599
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (12)..(12)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (20)..(20)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (23)..(23)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (30)..(30)
<223> Any nucleotide

<400> 72
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60
agaagaaata tgggagacga aggtatagtg agagggtgca caaagcagac aacccctggg
120
aaggctacta tattggctct tggcaaggca ttccctcacc aacttgtgat gcaagagtgt
180
ttagttgatg gttatttttag ggacactaat tgtgacaatc ctgaacttaa gcagaaactt
240
gtagactttt gtaagacaac cacggtaaaa acaagggtatg ttgttatgaa tgaggagata
300
ctaaagaaat atccagaact tgtgtcgaa ggcgcctcaa ctgtaaaaca acgttttagag
360
atatgtaatg aggcagtaac acaaatggca attgaagctt cccaagtttg cctaagaat
420
tggggtagat ccttatcgga cataactcat gtggtttatg ttcatctag tgaagctaga
480
ttaccgggtg gtgacctata cttgtcaaaa ggactaggac taaacctaa aattcaaaga
540
accatgctct atttctctgg atgctcgga ggcgtagccg gccttcgcgt tgcgaaaga
599

<210> 73
<211> 581
<212> DNA
<213> *Trifolium repens*

<220>
<221> misc_feature
<222> (10)..(11)
<223> Any nucleotides

<220>
<221> misc_feature
<222> (19)..(19)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (26)..(26)
<223> Any nucleotide

<400> 73
tctgttctgn ntaacattnc ttccnttag aaaactatac acatttgatc ttgcaaagaa
60
gaaatatggg agacgaaggt atagtggag gtgtcacaaa gcagacaacc cctgggaagg

120

ctactatatt ggctcttggc aaggcattcc ctcaccaact tgtgatgcaa gagtatttag
180

ttgatggta ttttagggac actaattgtg acaatcctga acttaagcag aaacttgcta
240

gactttgtaa gacaaccacg gtaaaaaaa ggtatgtgt tatgaatgag gagatactaa
300

agaaatatcc agaacttggt gtogaaggcg cctcaactgt aaaacaacgt ttagagatat
360

gtaatgagcg agtaacacaa atggcaattg aagcttccca agtttgccta aagaattggg
420

gtagatcctt atcggacata actcatgtgg tttatgtttc atctagttaa gctagattac
480

cgggtggtag cctatacttg tcaaaaggac taggactaaa ccctaaaatt caaagaacca
540

tgctctattt ctctggatgc togggaggcg tagccgcct t
581

<210> 74

<211> 588

<212> DNA

<213> *Trifolium repens*

<220>

<221> misc_feature

<222> (11)..(11)

<223> Any nucleotide

<220>

<221> misc_feature

<222> (13)..(13)

<223> Any nucleotide

<220>

<221> misc_feature

<222> (25)..(27)

<223> Any nucleotides

<220>

<221> misc_feature

<222> (36)..(36)

<223> Any nucleotide

<400> 74

tctgtgtgc ntnaaattac ttgmnntag aaaacnctac acatttgatc ttgcaaagaa
60

gaaatatggg agacgaaggt atagtgagag gtgtcacaaa gcagacaacc cctgggaagg
120

ctactatatt ggctcttggc aaggcattcc ctcaccaact tgtgatgcaa gagtgtttag
180

ttgatgggta ttttagggac actaattgtg acaatcctga acttaagcag aaacttgcta
240

gactttgtaa gacaaccacg gtaaaaacaa ggtatgtgtg tatgaatgag gagatactaa
300

agaaatatcc agaacttggt gtcgaaggcg cctcaactgt aaaacaacgt ttagagatat
360

gtaatgaggc agtaacacaa atggcaattg aagcttccca agtttgcta aagaattggg
420

gtagatcctt atcggacata actcatgtgg tttatgtttc atctagttaa gctagattac
480

ccggtgggta cctatacttg tcaaaaggac taggactaaa ccctaaaatt caaagaacca
540

tgctctatct ctctggatgc tcgggaggcg tagccggcct tcgcggtg
588

<210> 75

<211> 563

<212> DNA

<213> *Trifolium repens*

<400> 75

ttacatcttt tttattgtag aaaatatata ttgatcttag caaagaagaa atatgggaga
60

cgaaggata gtgagaggtg tcacaaggca gccaacccct gggaaggcta ctatattggc
120

tcttggcaag gcattccctc accaacttgt gatgcaagag tatttagttg atgggtattt
180

tagggacact aattgtgaca atcctaagct taagcagaaa ctgtctagac ttgcaagac
240

aaccacagtg aaaacaaggt atgttggtat gaatgaagag atactaaaga aatatccaga
300

acttactatc ggaggcacct cgacggtaaa acaacattta gagatatgta atgaggcagt
360

aacacaaatg gcaattgaag cttcccaagt ttgctaaag aattgggga gaacctatc
420

agacataact catgtggttt atgtttcatc tagtgaagct agattacctg gtggtagacct
480

atacttgta aaaggactag gactaaacct taaaattcaa agaaccatgc tctatttctc
540

gggatgctcg ggaggcgtag ccg
563

<210> 76

<211> 603

<212> DNA

<213> *Trifolium repens*

<220>

<221> misc_feature

<222> (4)..(4)
<223> Any nucleotide

<400> 76
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gtgagaggtg tcacaaagca gacaaccctt gggaaggcta ctatatgggc tcttggcaag
120
gcattccctc accaacttgt gatgcaagag tathtagttg atggttattt tagggacact
180
aattgtgaca atcctgacct taagcagaaa ctgtctagac ttgttaagac aaccacggta
240
aaaacaaggat atgtgtttat gaatgaggag atactaaaga aatatccaga acttgttgtc
300
gaaggcgcct caactgtaaa acaacgttta gagatatgta atgaggcagt aacacaaatg
360
gcaattgaag cttcccaagt ttgcctaaag aattgggcta gatccttacc ggacataact
420
catgtgggtt atgtttctac tagtgaagct agattaccog gtgggtgacct atacttgtca
480
aaaggactag gactaaaccc taaaattcaa agaaccatgc tctatttctc tggatgctog
540
ggaggcgtag ccggccttcg cgttgcgaaa gacatagctg agaacaacco tggaagtaga
600
gtt
603

<210> 77
<211> 584
<212> DNA
<213> *Trifolium repens*

<220>
<221> misc_feature
<222> (1)..(1)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (5)..(5)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (40)..(40)
<223> Any nucleotide

<400> 77
ntcngaact tactgtggaa ggcgcctcga ctgtaaaacn acgtttagag atatgtaatg
60

aggcagtaac acaaatggca attgaagctt cccaagtttg cctaagaat tggggtagac
120
cettatcaga cataactcat gtggtttatg ttctctctag tgaagctaga ttaccgggtg
180
gtgacctata ttgtcaaaa ggactaggac taaatcctaa aattcaaaga accatgctct
240
atttctctgg atgctcagga ggcgtagccg gccttcgcgt tgcgaagac atagctgaga
300
acaaccctgg aagtagagtt ttgcttgcta ctctgaaac tacaattatt ggattcaagc
360
caccaagtgt tgatagacct tatgatcttg ttggtgtggc actctttgga gatgggtgctg
420
gtgctatgat aattggctca gaccaatac ttgaaactga gactccattg tttagacctc
480
atacttcago tcaggagttt ataccagaca cagagaagaa aatagatggg cggtcgacgg
540
aggagggcat aagtttcacg ctacggaggg aactgccga gata
584

<210> 78
<211> 735
<212> DNA
<213> *Trifolium repens*

<220>
<221> misc_feature
<222> (47)..(47)
<223> Any nucleotide

<400> 78
gtagcaacac acactttgat ttctttttga gtcttgcta cgtggcnnta ccaaaaaacg
60
ttgctaagtc atcaaccatt ccaattcctt aatataacct atcagtactc accatctttt
120
cttcctccct gctaacttta tacttagaga agatgggtgaa agttaatgag atccgccagg
180
cacagagagc tgaaggccct gccactgtgt tggcaatcgg cactgcaact cctccaaact
240
gtgttgatca gagtacatac ccgactact acttcgcgat cacaaacagt gagcacaaga
300
cagagctcaa agaaaaatto cagcgcatgt gtgacaaatc tatgattaag aagagataca
360
tgcatttgac agaagagatt ttgaaggaga atccaagttt atgtgagtac atggcacctt
420
cattggatgc aagacaagac atggtgggtt tggaagtacc aaggctagga aaagaggcag
480
caacaaaggc aatcaaggaa tgggggtcaac ctaagtccaa gattacccac ctcatctttt
540

gcaccacaag tgggtgtggac atgcccggtg ccgactatca gcttacaaag cttttaggcc
600

ttcgtccgca tgtgaagcgt tacatgatgt accaacaagg ttgttttctt ggtggcacgg
660

tgcttcgttt ggctaaagac ttggctgaaa acaacaaagg tgcccggtga ttggtgggtt
720

gttcagagat aactg
735

<210> 79
<211> 194
<212> PRT
<213> Trifolium repens

<400> 79

Met Val Lys Val Asn Glu Ile Arg Gln Ala Gln Arg Ala Glu Gly Pro
1 5 10 15

Ala Thr Val Leu Ala Ile Gly Thr Ala Thr Pro Pro Asn Cys Val Asp
20 25 30

Gln Ser Thr Tyr Pro Asp Tyr Tyr Phe Arg Ile Thr Asn Ser Glu His
35 40 45

Lys Thr Glu Leu Lys Glu Lys Phe Gln Arg Met Cys Asp Lys Ser Met
50 55 60

Ile Lys Lys Arg Tyr Met His Leu Thr Glu Glu Ile Leu Lys Glu Asn
65 70 75 80

Pro Ser Leu Cys Glu Tyr Met Ala Pro Ser Leu Asp Ala Arg Gln Asp
85 90 95

Met Val Val Val Glu Val Pro Arg Leu Gly Lys Glu Ala Ala Thr Lys
100 105 110

Ala Ile Lys Glu Trp Gly Gln Pro Lys Ser Lys Ile Thr His Leu Ile
115 120 125

Phe Cys Thr Thr Ser Gly Val Asp Met Pro Gly Ala Asp Tyr Gln Leu
130 135 140

Thr Lys Leu Leu Gly Leu Arg Pro His Val Lys Arg Tyr Met Met Tyr
145 150 155 160

Gln Gln Gly Cys Phe Ala Gly Gly Thr Val Leu Arg Leu Ala Lys Asp
165 170 175

Leu Ala Glu Asn Asn Lys Gly Ala Arg Val Leu Val Val Cys Ser Glu

180

185

190

Ile Thr

<210> 80
<211> 574
<212> DNA
<213> *Trifolium repens*

<220>
<221> misc_feature
<222> (47)..(47)
<223> Any nucleotide

<400> 80
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ttgctcactc atcaaccatt ccaattcctt aatataacct atcagtactt accatctttt
120
cttctccctt gctaacttta gaatcagaga agatggtgaa tgттаатgag atccgccagg
180
cacagagagc tgaaggccct gccactgtgt tggcaatcgg cactgcaact cctccaaact
240
gtgtcgatca gagtacatac ccggactact acttcgcat cacaacacgt gaggacaaga
300
cagagctcaa agaaaaattc cagcgcatgt gtgacaaatc tatgattaag aagagatata
360
tgcatattgac agaagagatt ttgaaggaga atccaagttt atgtgagtac atggcacctt
420
cattgggatgc aagacaagac atgggtggttg tggagttacc aaggctagga aaagaggcag
480
caacaaaggc aattaaggaa tgggggtcaac ctaagtccaa gattaccacac ctcacttttt
540
gcaccaccag tgggtgtgac atgcccggtg ccgc
574

<210> 81
<211> 597
<212> DNA
<213> *Trifolium repens*

<400> 81
gtagcaacac acactttgat ttctttttga gtccttgcta cgtggcctta ccaaaaaaacg
60
ttgctaagtc atcaaccatt ccaattcctt aatataacct atcagtactc accatctttt
120
cttctccctt gctaacttta gactcagaga agatggtgaa tgттаатgag atccgccagg
180
cacagagagc tgaaggccct gccaccgtgt tggcaatcgg cactgcaact cctccaaact

240

gtgtcgatca gactacatac ccagactact acttccgcat cacaacacagt gagcacaaga
300

cagagctcaa agaaaaattc cagcgcatgt gtgacaaatc tatgattaag aagagatata
360

tgcatttgac agaagagatt ttgaaggaga atccaagttt atgtgagtac atggcacctt
420

cattggatgc aagacaagac atggtggttg tggaaagtacc aaggctagga aaagaggctg
480

caacaaaggc tatcaaggaa tgggggtcaac ctaagtccaa gattactcac ctcatctttt
540

gcaccacaag tgggtgtggac atgcctggcg ccgactatca gcttacaaag ctttttag
597

<210> 82

<211> 616

<212> DNA

<213> *Trifolium repens*

<220>

<221> misc_feature

<222> (70)..(70)

<223> Any nucleotide

<220>

<221> misc_feature

<222> (616)..(616)

<223> Any nucleotide

<400> 82

gtagcaacac acactttgat ttctttttga gtccttgcta cgtggcttta ccaaaaaacg
60

ttgctaagtn atcaaccatt ccaattcctt aatataacct atcagtactc accatctttt
120

cttcctccct gctaacttta gactcagaga agatggtgaa tgtaatatgag atccgccagg
180

cacagagagc tgaaggccct gccaccgtgt tggcaatcgg cactgcaact cctccaaact
240

gtgtcgatca gactacatac ccagactact acttccgcat cacaacacagt gagcacaaga
300

cagagctcaa agaaaaattc cagcgcatgt gtgacaaatc tatgattaag aagagatata
360

tgcatttgac agaagagatt ttgaaggaga atccaagttt atgtgagtac atggcacctt
420

cattggatgc aagacaagac atggtggttg tggaaagtacc aaggctagga aaagaggctg
480

caacaaaggc tatcaaggaa tgggggtcaac ctaagtccaa gattactcac ctcatctttt
540

gcaccacaag tgggtgtggac atgcctggcg ccgactatca gcttacaaag cttttaggcc
600

ttcgtccgca tgtgan
616

<210> 83
<211> 585
<212> DNA
<213> *Trifolium repens*

<220>
<221> misc_feature
<222> (1)..(3)
<223> Any nucleotides

<220>
<221> misc_feature
<222> (7)..(7)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (20)..(20)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (37)..(37)
<223> Any nucleotide

<220>
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<222> (61)..(61)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (451)..(451)
<223> Any nucleotide

<220>
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<222> (507)..(507)
<223> Any nucleotide

<400> 83
nnncacncac acttttttgn atccctgcta cgtggcntta ccaaaaaacg ttgctaagtc
60

ntcaaccatt ccaattcctt aatataacct atcagtactc accatctttt ctctctcctt
120

gctaaacttta gactcagaga agatggtgaa tgттаатgag atccgccagg cacagagagc
180

tgaaggccct gccaccgtgt tggcaatcgg cactgcaact cctccaaact gtgttgatca
240

gagtacatac ccggactact acttccgcat cacaacacagt gagcacaaga cagagctcaa
300

agaaaaatcc cagcgcatgt gtgacaaatc tatgattaag aagagatata tgcatttaac
360

agaagagatt ttgaaggaga atccaagttt atgtgagtac atggcacctt cattggatgc
420

aagacaagac atgggtggtg tgggaagtacc naggctagga aaagaggcag taacaaaggc
480

aattagggaa tgggggtcaac ctaagtncaa gattaccac ctcactcttt gcaccaccag
540

tgggtgtggac atgcccggtg ccgactatca gctcacaaag ctctt
585

<210> 84
<211> 596
<212> DNA
<213> *Trifolium repens*

<220>
<221> misc_feature
<222> (3)..(3)
<223> Any nculeotide

<220>
<221> misc_feature
<222> (14)..(14)
<223> Any nculeotide

<220>
<221> misc_feature
<222> (37)..(37)
<223> Any nculeotide

<400> 84
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atccgccagg cacagagagc tgaaggccct gcaactgtgt ttgcaatcgg cactgcaact
120

cctaaaaact gtgttgatca gagtacttac ccgactact atttccgaat cacaacacag
180

gaacacaaga ctgaactcaa agaaaaatcc cagcgcatgt gtgacaaatc tatgattaag
240

aagagatata tgcatttgac agaagagatt ttgaaggaga attcaagttt atgtgagtac
300

atggcacctt cattggatgc aagacaagac atgggtggtg tgggaagtacc aaggctagga
360

aaagaggctg caacaaaggc tatcaaggaa tgggggtcaac ctaagtccaa gattactcac
420

ctcactcttt gcaccacaag tgggtgtggac atgcctgggt ccgactatca gcttacaaag

480

cttttaggcc ttcgtccgca tgtgaagcgt tatatgatgt accaacaagg ttgttttgc
540

ggtggcacgg tgcttcggtt ggctaaagac ttggctgaaa acaacaaagg tgcccg
596

<210> 85
<211> 618
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<213> *Trifolium repens*

<220>
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<222> (14)..(14)
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<222> (37)..(37)
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<400> 85
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atccgcgagg cacagagagc tgaaggccct gcaactgtgt ttgcaatcgg cactgcaact
120

cctaaaaaact gtgttgatca gactacttac cccgactact atttccgaat cacaaacagc
180

gaacacaaga ctgaactcaa agaaaaatc cagcgcatgt gtgacaaatc tatgattaag
240

aagagatata tgcatttgac agaagagatt ttgaaggaga attcaagttt atgtgagtac
300

atggcacctt cattggatgc aagacaagac atggtggttg tggaagtacc aaggctagga
360

aaagaggctg caacaaaggc tatcaaggaa tgggggtcaac ctaagtccaa gattactcac
420

ctcatctttt gcaccacaag tgggtgtggac atgcctgggt cggactatca gcttacaaag
460

cttttaggcc ttctgctcgca tgtgaagcgt tatatgatgt accaacaagg ttgttttgc
540

ggtggcacgg tgcttcggtt ggctaaagac ttggctgaaa acaacaaagg tgcccgtgta
600

ttggtggttt gttcagag
618

<210> 86
<211> 609
<212> DNA
<213> *Trifolium repens*

<220>
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<222> (4)..(4)
<223> Any nucleotide

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<222> (10)..(10)
<223> Any nucleotide

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<222> (32)..(33)
<223> Any nucleotides

<400> 86
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gccaggcaca gagagctgaa ggcctgcaa ctgtgtttgc aatcggcact gcaactccta
120

aaaactgtgt tgatcagagt acttaccctg actactattt ccgaatcaca aacagcgaac
180

acaagactga actcaaagaa aaattccagc gcattgtgtga caaatctatg attaagaaga
240

gatacatgca tttagacagaa gagattttga aggagaattc aagttttgt gagtacatgg
300

caccttcatt ggatgcaaga caagacatgg tgggtgtgga agtaccgaagg ctaggaaaaa
360

aggctgcaac aaaggctatc aagggaatggg gtcaacctaa gtccaagatt actcacctca
420

ttttttgcac cacaagtggt gtggacatgc ctgggtgccga ctatcagctt acaaagcttt
480

taggccttgg tccgcatgtg aagcgttata tgatgtacca acaaggttgt ttgtctgggt
540

gcacgggtgct tcgttttggct aaagacttgg ctgaaaacaa caaaggtgcc cgtgtattgg
600

tggtttggtt
609

<210> 87
<211> 571
<212> DNA
<213> *Trifolium repens*

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<222> (247)..(247)
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<222> (571)..(571)
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<400> 87
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agctgaaggc cctgccactg tgttggnant nggcactgca actcctccaa actgtgtcga
120
tcagagtaca taccoggact actacttccg catcacaaac agtgagcaca agacagagct
180
caaagaaaaa ttccagcgca tgtgtgacaa atctatgatt aagaagagat acatgcattt
240
gacagangag attttgaagg agaatccaag tttatgtgag tacatggcac cttoattgga
300
tgcaagacaa gacatgggtg ttgtggaagt accaaggcta ggaagaggag cagcaacaaa
360
ggcaatttag gaatggggcc aacctaagtc caagattacc cacctcatct tttgccacc
420
cagtgggtgc gacatgcccg gtgocgacta tcagctcaca aagctcttag gcctgcgtcc
480
atatgtgaag cgttacatga tgtatcaaca aggttgtttt gctgggtggca cgggtgcttcg
540
tttggctaaa gacttggctg aaaacaacaa n
571

<210> 88
<211> 603
<212> DNA
<213> *Trifolium repens*

<220>
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<223> Any nucleotides

<220>
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<222> (9)..(9)
<223> Any nucleotide

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<222> (13)..(14)
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<222> (594)..(594)
<223> Any nucleotide

<400> 88
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aaggccctgc cactgtgttg gcaatcggca ctgcaactcc tccaaactgt gtcgatcaga
120

gtacataccc ggactactac ttccgcatca caaacagtga gcacaagaca gagctcaaaag
180

aaaaattcca gcgcatgtgt gacaaatcta tgattaagaa gagatacatg cattttgacag
240

aagagatddd gaaggagaat ccaagtttat gtgagtacat ggcaccttca ttggatgcaa
300

gacaagacat ggtggttgtg gaagtaccaa ggctaggaaa agaggcagca acaaaaggcaa
360

ttaaggaatg gggccaacct aagtccaaga ttaccacact catctttttgc accaccagtg
420

gtgtcgacat gcccggtgcc gactatcagc tcacaaagct cttaggcctg cgtccatatg
480

tgaagcgtda catgatgtat caacaaggtd gttttgctgg tggcacgggt cttcgttttg
540

ctaaagactt ggctgaaaac aacaaangtg cccgtgtgtd ggtgggttgt tcanagataa
600

ctg
603

<210> 89
<211> 588
<212> DNA
<213> *Trifolium repens*

<220>
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<222> (7)..(7)
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<222> (12)..(12)
<223> Any nucleotide

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<222> (43)..(43)

<223> Any nucleotide

<220>
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<222> (68)..(68)
<223> Any nucleotide

<400> 89
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120
cttaccocga ctactatttc cgaatcacia acagogaaca caagactgag ctcaaagaaa
180
aattccagcg catgtgtgac aaatctatga ttaagaagag atacatgcat ttgacagaag
240
agattttgaa ggagaatcca agtttatgtg agtacatggc accttcattg gatgcaagac
300
aagacatggt ggtagtggaa gtaccaaggc taggaaaaga ggcagcaaca aaggcaatta
360
aagaatgggg tcaacctaa gccaagatta cccacctcat cttttgcacc accagtgtgtg
420
tggaatgcc cgtgtccgac tatcagctca caaagctctt aggcctgogt ccatatgtga
480
agcgttacat gatgtatcaa caaggttgtt ttgctggtgg cacggtaact cgtttggcta
540
aagactggc tgaaaaaac aaagggtgcc gtgtgttggt ggtttgtt
588

<210> 90
<211> 250
<212> DNA
<213> *Trifolium repens*

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<222> (247)..(247)
<223> Any nucleotide

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<222> (250)..(250)
<223> Any nucleotide

<400> 90
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cacaagactg agctcaaaga aaaattccag cgcagtgtg acaaatctat gattaagaag
120

agatacatgc atttgacaga agagattttg aaggagaatc caagnttatg tgagtacatg

180

gcaccttnat tggatgcaag acaagacatg gnggcgcgcc accnnccntc cncncaccn
240

caacccnccn
250

<210> 91
<211> 583
<212> DNA
<213> *Trifolium repens*

<220>
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<222> (47)..(47)
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<222> (552)..(552)
<223> Any nucleotide

<400> 91
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tgctaagtca tcaaccattc caattcctta atataaccta tcagtactca ccattctttc
120

ttcctccctg ctaacttttag actcagtaga agatggtgaa tgtaatatgag atccgccagg
180

cacagagagc tgaaggccct gccaccgtgt tggcaatcgg cactgcaact cctccaaact
240

gtgttgatca gagtacatac ccggactact acttccgcat cacaacacgt gagcacaaga
300

cagagctcaa agaaaaattc cagcgcacgt gtaagatatt tatcttatac tccatgcagt
360

ttctttctcg ctgactgccg tgtttatata ttgttttgtt ttgttcctta aatttgttat
420

gtcactctca catgtacaaa aacttaaga ctaaactgca tatcattttt ttcagggaca
480

aacttatgat taagaagaga tacatgcatt tgacagaaga gattttgaag gagaatccaa
540

gtttatgtga gnacatggca ccttcttggg atgcaagaca agt
583

<210> 92
<211> 95

<212> PRT
 <213> Trifolium repens

<220>
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 <222> (86)..(86)
 <223> Any amino acid

<400> 92

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Ala Thr Val Leu Ala Ile Gly Thr Ala Thr Pro Pro Asn Cys Val Asp
 20 25 30

Gln Ser Thr Tyr Pro Asp Tyr Tyr Phe Arg Ile Thr Asn Ser Glu His
 35 40 45

Lys Thr Glu Leu Lys Glu Lys Phe Gln Arg Thr Arg Asp Lys Ser Met
 50 55 60

Ile Lys Lys Arg Tyr Met His Leu Thr Glu Glu Ile Leu Lys Glu Asn
 65 70 75 80

Pro Ser Leu Cys Glu Xaa Met Ala Pro Ser Trp Asp Ala Arg Gln
 85 90 95

<210> 93
 <211> 582
 <212> DNA
 <213> Trifolium repens

<220>
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 <223> Any nucleotide

<220>
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 <222> (551)..(551)
 <223> Any nucleotide

<400> 93

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 120

ttctctccctg ctaacttttag actcagagaa gatgggtgaat gttaagtgaga tccgccaggc
 180

acagagagct gaaggccctg ccaccgtgtt ggcaatcggc actgcaacte etccaaactg
 240

tgttgatcag agtacatacc cggactacta cttccgcata acaaacagtg agcacaagac

300

agagctcaaa gaaaaattcc agcgcacgtg taagatatatt atctttatact ccatgcatgt
360

ctttttctgc tgactgcgct gtttatatat tgttttgttt tgttccttaa atttggtatg
420

tcactctcac atgtacaaaa cacttaagac taaactgcat atcatttttt tcagggacaa
480

atctatgatt aagaagagat acatgcattt gacagaagag attttgaagg agaatccaag
540

tttatgtgag nacatggcac cttcttgggg tgcaagacaa gt
582

<210> 94
<211> 167
<212> DNA
<213> *Trifolium repens*

<220>
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<222> (17)..(17)
<223> Any nucleotide

<220>
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<222> (34)..(34)
<223> Any nucleotide

<220>
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<222> (38)..(38)
<223> Any nucleotide

<400> 94
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60

aacctatcag tactcaccat cttttcttcc tccctgctaa ctttagactc agtagaagat
120

ggtgaatggt aatgagatcc gccaggcaca gagagctgaa ggccctg
167

<210> 95
<211> 613
<212> DNA
<213> *Trifolium repens*

<220>
<221> misc_feature
<222> (3)..(3)
<223> Any nucleotide

<220>
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<222> (16)..(16)

<223> Any nucleotide

<400> 95
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 120
 acgtgctcct actcagggaa aggcaacgat acttgcatga ggaaggcct tccccgccca
 180
 agtcctccct caagagtgtc tgggtgaagg attcattcgc gacactaagt gtgacgatac
 240
 ttatatgaag gagaaattgg agcgtctttg caaaaacaca actgtaaaaa caagatacac
 300
 agtaatgtca aaggagatct tagacaacta tccagagcta gccatagatg gaacaccaac
 360
 aataaggcaa aagcttgaaa tagcaaatcc agcagtagtt gaaatggcaa caagagcaag
 420
 caaagattgc atcaaagaat ggggaagggtc acctcaagat atcacacaca tagtctatgt
 480
 ttctctgagc gaaattcgtc taccgggtgg tgacctttat cttgcaaatg aactcggtt
 540
 aaacagcgat gttaatcgcg taatgtctta ttctctcggt tgctacggcg gtgtcactgg
 600
 cttacgtgtc gcc
 613

<210> 96
 <211> 182
 <212> PRT
 <213> *Trifolium repens*

<400> 96

Met Pro Gln Gly Asp Leu Asn Gly Ser Ser Ser Val Asn Gly Ala Arg
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 Ala Arg Arg Ala Pro Thr Gln Gly Lys Ala Thr Ile Leu Ala Leu Gly
 20 25 30
 Lys Ala Phe Pro Ala Gln Val Leu Pro Gln Glu Cys Leu Val Glu Gly
 35 40 45
 Phe Ile Arg Asp Thr Lys Cys Asp Asp Thr Tyr Ile Lys Glu Lys Leu
 50 55 60
 Glu Arg Leu Cys Lys Asn Thr Thr Val Lys Thr Arg Tyr Thr Val Met
 65 70 75 80
 Ser Lys Glu Ile Leu Asp Asn Tyr Pro Glu Leu Ala Ile Asp Gly Thr

85

90

95

Pro Thr Ile Arg Gln Lys Leu Glu Ile Ala Asn Pro Ala Val Val Glu
 100 105 110

Met Ala Thr Arg Ala Ser Lys Asp Cys Ile Lys Glu Trp Gly Arg Ser
 115 120 125

Pro Gln Asp Ile Thr His Ile Val Tyr Val Ser Ser Ser Glu Ile Arg
 130 135 140

Leu Pro Gly Gly Asp Leu Tyr Leu Ala Asn Glu Leu Gly Leu Asn Ser
 145 150 155 160

Asp Val Asn Arg Val Met Leu Tyr Phe Leu Gly Cys Tyr Gly Gly Val
 165 170 175

Thr Gly Leu Arg Val Ala
 180

<210> 97

<211> 613

<212> DNA

<213> *Trifolium repens*

<220>

<221> misc_feature

<222> (3)..(3)

<223> Any nucleotide

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<221> misc_feature

<222> (16)..(16)

<223> Any nucleotide

<400> 97

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 120

acgtgctcct actcagggaaggcaacgat acttgcatta gaaaggctt tccccgccca
 180

agtcctccct caagagtgc tgggtggaagg attcattgcg gacactaagt gtgacgatac
 240

ttatattaag gagaaattgg agcgtctttg caaaaacaca actgtaaaaa caagatacac
 300

agtaatgtca aaggagatct tagacaacta tccagagcta gccatagatg gaacaccaac
 360

aataaggcaa aagcttgaaa tagcaaatcc agcagtagtt gaaatggcaa caagagcaag
 420

caagagattgc atcaagaagt ggggaaggtc acctcaagat atcacacaca tagtctatgt
480

ttctctgagc gaaattcgtc taccgggtgg tgacctttat ctgc aaatg aactcggtt
540

aaacagcgat gttaatcgcg taatgcteta ttctctcggt tgctacggcg gtgtcaactgg
600

cttacgtgtc gcc
613

<210> 98

<211> 570

<212> DNA

<213> *Trifolium repens*

<220>

<221> misc_feature

<222> (13)..(13)

<223> Any nucleotide

<400> 98

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120

tgctcctact cagggaaaagg caacgatact tgcattagga aaggctttcc ccgccagggt
180

cctccctcaa gagtgcttgg tggaaggatt cattcgcgac actaagtgtg acgatactta
240

tattaaggag aaattggagc gtctttgcaa aaacacaact gtgaaaacaa gatacacagt
300

aatgtcaaag gagatcttag acaactatcc agagctagcc atagatggaa caccaacaat
360

aaggcaaaag cttgaaatag caaatccagc agtagttgaa atggcaacaa gagcaagcaa
420

agattgcac aaagaatggg gaaggtcacc tcaagatc acacacatag tctatgtttc
480

ctcgagcgaa attcgtctac ccggtgggtga cctttatctt gcaaatgaac tcggcttaaa
540

cagcgaatgtt aatcgcgtaa tgctctatct
570

<210> 99

<211> 575

<212> DNA

<213> *Trifolium repens*

<220>

<221> misc_feature

<222> (33)..(33)

<223> Any nucleotide

<400> 99
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gcctcaaggt gatttgaatg gaagttcctc ggtgaatgga gcacgtgcta gacgtgctcc
120
tactcagggg aaggcaacga tacttgcatt aggaaaggct tccccgcccc aggtcctccc
180
tcaagagtgc ttggtggaag gattcattcg cgacactaag tgtgacgata cttatattaa
240
ggagaaattg gagcgtcttt gcaaaaacac aactgtgaaa acaagatata cagtaatgtc
300
aaaggagatc ttagacaact atccagagct agccatagat ggaacaccaa caataaggca
360
aaagcttgaa atagcaaacc cagcagtagt tgaatggca acaagagcaa gcaagattg
420
catcaaagaa tgggggaagg cacctcaaga tatcacacac atagtctatg ttctctcgag
480
cgaaattcgt ctaccgggtg gtgaccttta tcttgcaaat gaactcggt taaacagcga
540
tgттаатсгс gтаатсгст atttctctcg ttgct
575

<210> 100
<211> 573
<212> DNA
<213> *Trifolium repens*

<400> 100
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120
aaaggcaacg atacttgcac taggaaaggc ttccccgcc caagtcctcc ctcaagagtg
180
cttggtggaa ggattcattc gcgacactaa gtgtgacgat acttatatta aggagaaatt
240
ggagcgtctt tgcaaaaaca caactgtaaa aacaagatc acagtaatgt caaaggagat
300
cttagacaac tatccagagc tagccataga tggaacacca acaataaggc aaaagcttga
360
aatagcaaat ccagcagtag ttgaaatggc aacaagagca agcaagatt gcatcaaga
420
atgggggaagg tcacctcaag atatcacaca catagtctat gtttctctga gcgaaattcg
480
tctaccgggt ggtgaccttt atcttgcaaa tgaactcggc ttaaacagcg atgttaatcg
540

cgtaatgctc tatttcctcg gttgctacgg cgg
573

<210> 101
<211> 607
<212> DNA
<213> *Trifolium repens*

<400> 101
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aacaacaaag gtgcccgtgt gttggtggtt tgttcagaga taactgcagt tactttccgt
120

ggaccagtg acactcacct tgatagcctt gtggggcaag cattgtttgg agatggtgca
180

gcagctgtga ttgttggttc agaccctttg ccagaagttg agaagccttt gttgaattg
240

gtatggacgg cacaacaat cgctccagat agtgaaggag ccattgatgg tcaccttcgc
300

gaagcagggc tgacattcca tctctcaag gatgttccta gccttgtctc aaataacatt
360

gagaaagcgc ttgttgatgc ctttcaacct ttgaatatt ctgactacaa ttccatcttt
420

tgattgcac acccaggcgg accagcaatt cttgaccaag ttgaagctaa gttaggctta
480

aagccagaga aaatgcaagc cactcgacat gtacttagcg aatatggtaa catgtcaagt
540

gcgtgtgtgt tatttatctt ggatgagatg aggaggaagt caaaagaaga cggacttgcc
600

acaacag
607

<210> 102
<211> 202
<212> PRT
<213> *Trifolium repens*

<400> 102

Val Tyr Gln Gly Cys Phe Ala Gly Gly Thr Val Leu Arg Leu Ala Lys
1 5 10 15

Asp Leu Ala Glu Asn Asn Lys Gly Ala Arg Val Leu Val Val Cys Ser
20 25 30

Glu Ile Thr Ala Val Thr Phe Arg Gly Pro Ser Asp Thr His Leu Asp
35 40 45

Ser Leu Val Gly Gln Ala Leu Phe Gly Asp Gly Ala Ala Ala Val Ile
50 55 60

Val Gly Ser Asp Pro Leu Pro Glu Val Glu Lys Pro Leu Phe Glu Leu
65 70 75 80

Val Trp Thr Ala Gln Thr Ile Ala Pro Asp Ser Glu Gly Ala Ile Asp
85 90 95

Gly His Leu Arg Glu Ala Gly Leu Thr Phe His Leu Leu Lys Asp Val
100 105 110

Pro Ser Leu Val Ser Asn Asn Ile Glu Lys Ala Leu Val Asp Ala Phe
115 120 125

Gln Pro Leu Asn Ile Ser Asp Tyr Asn Ser Ile Phe Trp Ile Ala His
130 135 140

Pro Gly Gly Pro Ala Ile Leu Asp Gln Val Glu Ala Lys Leu Gly Leu
145 150 155 160

Lys Pro Glu Lys Met Gln Ala Thr Arg His Val Leu Ser Glu Tyr Gly
165 170 175

Asn Met Ser Ser Ala Cys Val Leu Phe Ile Leu Asp Glu Met Arg Arg
180 185 190

Lys Ser Lys Glu Asp Gly Leu Ala Thr Thr
195 200

<210> 103
<211> 607
<212> DNA
<213> *Trifolium repens*

<220>
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<222> (12)..(12)
<223> Any nucleotide

<220>
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<222> (46)..(46)
<223> Any nucleotide

<400> 103
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60

aacaacaaag gtgcccggtg tttggtggtt tgttcagaga taactgcagt tactttccgt
120

ggacccagtg acactcatct tgatagcctt gtggggcaag cattgtttgg agatgggtga
180

gcagctgtga ttgttggttc agacccttgc ccagaagttg agaagccttt gtttgaattg
240

gtatggaccg cacaacaat cgctccagat agtgaaggag ccattgatgg tcaccttcgc
300

gaagcagggc tgacattcca tctcctcaag gatgttccta gccttgcttc aaataacatt
360

gagaaagctc ttgttgatgc ctttcaacct ttgaatatct ccgattacaa ttccatcttt
420

tggattgcac acccaggcgg accagcaatt cttgaccaag ttgaagctaa gttaggctta
480

aagccagaga aaatgcaatc cactcgacat gtacttagcg aatatggtaa catgtcgagt
540

gcgtgtgtgt tatttatctt ggatgagatg aggaggaagt caaaagaaga cggacttgcc
600

acaacag
607

<210> 104
<211> 591
<212> DNA
<213> *Trifolium repens*

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<222> (587)..(587)
<223> Any nucleotide

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<222> (589)..(589)
<223> Any nucleotide

<400> 104
ccaaggttgt tttgctgggt gcacggctact tcgtttggct aaagacttgg ctgaaaacaa
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caaaggtgcc cgtgtgttgg tggtttgttc agagataact gcagttactt tccgtggacc
120

cagtgcactc caccttgata gccttggtgg gcaagcattg ttgggagatg gtgcagcagc
180

tgtgattggt gggtcagacc ctttgccaga agttgagaag cctttgtttg aattgggtatg
240

gaccgcacaa acaatcgctc cagatagtga aggagccatt gatggtcacc ttccggaagc
300

agggtgaca ttccatctcc tcaaggatgt tcctagcctt gtctcaaata acattgagaa
360

agcgcttggt gatgccttcc aacctttgaa tatttctgac tacaattcca tcttttgat

420

tgcacaccca ggcggaaccag caattcttga ccaagttgaa gctaagttag gottaaagcc
480

agagaaaaatg caagccactc gacatgtact tagcgaatat ggtaacatgt caagtgcgtg
540

tgtgttatatt atcttggatg anatgaggag gaagtcaaaa gaacacngnc t
591

<210> 105

<211> 590

<212> DNA

<213> *Trifolium repens*

<220>

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<222> (55)..(55)

<223> Any nucleotide

<400> 105

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gggtcccgtg tgttgggtgt ttgttcagag ataactgcag ttactttccg tggaccagtg
120

gacatcacc ttgatagcct tgtggggcaa gcattgtttg gagatggtgc agcagctgtg
180

attgttgggt cagacccttt gccagaagtt gagaagcctt tgtttgaatt ggtatggacc
240

gcacaaacaa tcgctccaga tagtgaagga gccattgatg gtcacottcg cgaagcaggg
300

ctgacattcc atctcctcaa ggatgttccct agccttgtct caaataacat tgagaaagcg
360

cttgttgatg cctttcaacc tttgaatatt totgactaca attccatctt ttggattgca
420

cacccaggcg gaccagcaat tcttgaccaa gttgaagcta agttaggctt aaagccagag
480

aaaatgcaag ccaactcgaca tgtacttagc gaatatggta acatgtcaag tgcggtgtgtg
540

ttatttatct tggatgagat gaggaggaag tcaaaagaag acggacttgc
590

<210> 106

<211> 510

<212> DNA

<213> *Trifolium repens*

<220>

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<222> (4)..(4)

<223> Any nucleotide

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<223> Any nucleotide

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<223> Any nucleotide

<400> 106
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60

ttggtacatc ttttgttacc tccaacaaaa aaatggtgac cgtagaagag attcgtaacg
120

cccaacgttc aaatggcctt gacactatct tagcttttgg cacagccact ccttctaact
180

gtgtcactca agctgattat cctgattact actttcgtat caccaacagc gaacatatga
240

ctgatcttaa ggaaaaattc aagcggatgt gtgatagatc aatgataaag aaacgttaca
300

tgcacctaac agaagacttt ctgaaggaga atocaaatat gtgtgaatac atggcaccat
360

cactagatgt aagacgagac atagtgggtg ttgaagnacc aaagctaggt aaagaancac
420

caaaaaaagc catatgngaa tggggacaac caaaatcnaa aatcacacat gcttggtttc
480

tgaccacttc cggtgntgac atgcccgggg
510

<210> 107
<211> 137
<212> PRT
<213> *Trifolium repens*

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<223> Any amino acid

<220>
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<222> (121)..(121)
<223> Any amino acid

<400> 107

Met Val Thr Val Glu Ile Arg Asn Ala Gln Arg Ser Asn Gly Pro
1 5 10 15

Ala Thr Ile Leu Ala Phe Gly Thr Ala Thr Pro Ser Asn Cys Val Thr
20 25 30

Gln Ala Asp Tyr Pro Asp Tyr Tyr Phe Arg Ile Thr Asn Ser Glu His
35 40 45

Met Thr Asp Leu Lys Glu Lys Phe Lys Arg Met Cys Asp Arg Ser Met
50 55 60

Ile Lys Lys Arg Tyr Met His Leu Thr Glu Asp Phe Leu Lys Glu Asn
65 70 75 80

Pro Asn Met Cys Glu Tyr Met Ala Pro Ser Leu Asp Val Arg Arg Asp
85 90 95

Ile Val Val Val Glu Xaa Pro Lys Leu Gly Lys Glu Pro Lys Lys Ala
100 105 110

Ile Xaa Glu Trp Gly Gln Pro Lys Xaa Lys Ile Thr His Ala Trp Phe
115 120 125

Leu Thr Thr Ser Gly Asp Met Pro Gly
130 135

<210> 108
<211> 240
<212> DNA
<213> *Trifolium repens*

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<222> (217)..(218)
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<222> (231)..(231)
<223> Any nucleotide

<400> 108
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60

aagatgcaat cggtgaagcc atcaaacaaag gttatagaca ctttgatact gctgctgctt
120

atgggtcana acaagctctt ggtgaagggtt tgaaagaagc anttgaactt ggtcttgtca
180

ctanagaaga gctntttggt acttctaacc ttggggnnac tgaaaatcat ntaaaccttg
240

<210> 109
 <211> 79
 <212> PRT
 <213> *Trifolium repens*

<220>
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 <223> Any amino acid

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<220>
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<220>
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 <222> (77)..(77)
 <223> Any amino acid

<400> 109

Gln Met Xaa Val Val Gly Met Gly Ser Ala Pro Asp Phe Thr Cys Lys
 1 5 10 15

Lys Asp Thr Lys Asp Ala Ile Val Glu Ala Ile Lys Gln Gly Tyr Arg
 20 25 30

His Phe Asp Thr Ala Ala Ala Tyr Gly Ser Xaa Gln Ala Leu Gly Glu
 35 40 45

Gly Leu Lys Glu Ala Xaa Glu Leu Gly Leu Val Thr Xaa Glu Glu Xaa
 50 55 60

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Phe Val Thr Ser Lys Leu Trp Xaa Thr Glu Asn His Xaa Asn Leu
 65 70 75

<210> 110
 <211> 604
 <212> DNA
 <213> Trifolium repens

<220>
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 <222> (13)..(13)
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 tgttattgaa ttcaggacac aaaatgccag tcataggaat gggaacatca gtagacaatc
 120
 gtccatcaaa tgatgttctt gcttcaatct ttgttgatgc aattgaagtt gggtatcgcc
 180
 attcgattc tgcttctgtg tatggaacag aggaagccat aggaattgct ttagcaaaa
 240
 ctttagaaaa agggcttatt aagagtagag atgaagtttt catcacttca aagccatgga
 300
 atactgatgc agattatgaa cttattgttc cagctctcaa gaccacattg aaaaagctgg
 360
 ggacggagta tgtggatctt tatctgatcc attggccagt gagacttaga catgatcttg
 420
 aaaacctgtg tgttttcacc aaagaagatt tacttccctt tgatatagaa gggacatgga
 480
 aagctatgga agaattgttat aagttaggct tagcaaaatc tattggtata tgcaattatg
 540
 gtacaaaaaa actcacaaa ctcttggaag cagccaccat tacccttgca gtcaatcagg
 600
 tgga
 604

<210> 111
 <211> 189
 <212> PRT
 <213> Trifolium repens

<400> 111

Met Ala Gly Lys Lys Ile Pro Glu Val Leu Leu Ser Gly His Lys
 1 5 10 15

Met Pro Val Ile Gly Met Gly Thr Ser Val Asp Asn Arg Pro Ser Asn
 20 25 30

Asp Val Leu Ala Ser Ile Phe Val Asp Ala Ile Glu Val Gly Tyr Arg

35

40

45

His Phe Asp Ser Ala Ser Val Tyr Gly Thr Glu Glu Ala Ile Gly Ile
 50 55 60
 Ala Leu Ala Lys Ala Leu Glu Lys Gly Leu Ile Lys Ser Arg Asp Glu
 65 70 75 80
 Val Phe Ile Thr Ser Lys Pro Trp Asn Thr Asp Ala Asp Tyr Glu Leu
 85 90 95
 Ile Val Pro Ala Leu Lys Thr Thr Leu Lys Lys Leu Gly Thr Glu Tyr
 100 105 110
 Val Asp Leu Tyr Ile His Trp Pro Val Arg Leu Arg His Asp Leu
 115 120 125
 Glu Asn Pro Val Val Phe Thr Lys Glu Asp Leu Leu Pro Phe Asp Ile
 130 135 140
 Glu Gly Thr Trp Lys Ala Met Glu Glu Cys Tyr Lys Leu Gly Leu Ala
 145 150 155 160
 Lys Ser Ile Gly Ile Cys Asn Tyr Gly Thr Lys Lys Leu Thr Lys Leu
 165 170 175
 Leu Glu Thr Ala Thr Ile Thr Pro Ala Val Asn Gln Val
 180 185

<210> 112
 <211> 334
 <212> DNA
 <213> *Trifolium repens*

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 <223> Any nucleotide

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 <222> (17)..(17)
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 <222> (246)..(246)
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<222> (277)..(277)
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<222> (281)..(281)
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<222> (328)..(328)
<223> Any nucleotide

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<222> (330)..(330)
<223> Any nucleotide

<220>
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<222> (334)..(334)
<223> Any nucleotide

<400> 112
gtgttagcagn attaganaaa natataaaaa aaaacatggc aggaagagaa atcccagaag
60

tgttattgaa ttcaggacac aaaatgccag tcataggaat gggaacatca gtagacaatc
120

gtccatcaaa tgatgttctt gcttcaatct ttgttgatgc aattgaagtt ggttatogcc
180

atttcgattc tgcttctgtg tatggaacag aggaagccat aggaattgct tttagcaaaag
240

ctttanaaaa agggcttatt aagagtanag atgaagnntt natcacttgc aagncatgga
300

atactgatgc acattatgaa cttattgntn caan
334

<210> 113
<211> 602

<212> DNA
<213> *Trifolium repens*

<220>
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<222> (8)..(8)
<223> Any nucleotide

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<222> (14)..(14)
<223> Any nucleotide

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<222> (16)..(16)
<223> Any nucleotide

<220>
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<222> (20)..(20)
<223> Any nucleotide

<220>
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<222> (22)..(22)
<223> Any nucleotide

<400> 113
gtagcagngt tagnanaagn gngaaaaaaa aacatggcag gaaagaaaaa cccagaagtg
60

ttattgaatt caggacacaa aatgccagtc ataggaatgg gaacatcagt agacaatcgt
120

ccatcaaatg atgttcttgc ttcaatcttt gttgatgcaa ttgaagtgg ttatcgccat
180

ttcgattctg cttctgtgta tggaacagag gaagccatag gaattgcttt agcaaaagct
240

ttagaaaaag ggcttattaa gagtagagat gaagttttca tcaactcaaa gccatggaat
300

actgatgcag attatgaact tattgttcca gctctcaaga ccacattgaa aaagctgggg
360

acggagtatg tggatcttta totgatccat tggccagtga gacttagaca tgatcttgaa
420

aaccctgttg ttttcaccaa agaagattta cttcccttgg atatagaagg gacatggaaa
480

gctatggaag aatgttataa gttaggctta gcaaagtcta ttggtatatg caattatggt
540

accaaaaaac tcaccaaact cttggaaaca gccaccatta cccctgcagt caatcaggtg
600

ga
602

<210> 114
<211> 584
<212> DNA
<213> *Trifolium repens*

<220>
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<222> (4)..(5)
<223> Any nucleotides

<220>
<221> misc_feature
<222> (27)..(27)
<223> Any nucleotide

<400> 114
agtnngaaaa agagagaaaa aaaaacntgg caggaaagaa aatcccagaa gtgttattga
60
attcaggaca caaaatgcc a gtcattaggaa tgggaacatc agtagacaat cgtccatcaa
120
atgatgttct tgettcaatc ttgtttgatg caattgaagt tggttatcgc catttcgatt
180
ctgtttctgt gtatggaaca gaggaagcca taggaattgc tttagcaaaa gcttttagaaa
240
aaggggcttat taagagtaga gatgaagttt tcatcacttc aaagccatgg aatactgatg
300
cagattatga acttattggt ccagctctca agaccacatt gaaaaagctg gggacggagt
360
atgtggatct ttatctgac cattggccag tgagacttag acatgatctt gaaaacctg
420
ttgttttcac caaagaagat ttacttcct ttgatataga agggacatgg aaagctatgg
480
aagaatgtta taagttaggc tttagcaagt ctattggtat atgcaattat ggtacaaaa
540
aactcaccaa actcttggaa acagccacca ttacctctgc agtc
584

<210> 115
<211> 547
<212> DNA
<213> *Trifolium repens*

<220>
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<222> (4)..(5)
<223> Any nucleotides

<220>
<221> misc_feature
<222> (27)..(27)
<223> Any nucleotide

<400> 115
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attcaggaca caaaatgccg gtcataaggaa tgggaacatc agtagacaat cgtccatcaa
120
atgatgttct tgettcaatc ttgtttgatg caattgaagt tggttatcgc catttcgatt
180
ctgcttctgt gtatggaaca gaggaagcca taggaattgc tttagcaaaa gctttagaaa
240
aagggttat taagagtaga gatgaagttt tcataccttc aaagccatgg aatactgatg
300
cagattatga acttattgtt ccagctctca agaccacatt gaaaaagctg gggacgsgat
360
atgtggatct ttatctgac cattggccag tgagacttag acatgatctt gaaaacctg
420
ttgttttcac caaagaagat ttacttcctt ttgatataga agggacatgg aaagctatgg
480
aagaatgtta taagttaggc ttagcaaatg ctattggtat atgcaattat ggtacaaaa
540
aactcac
547

<210> 116
<211> 334
<212> DNA
<213> *Trifolium repens*

<220>
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<222> (295)..(295)
<223> Any nucleotide

<400> 116
acatggcagg aaagaaaatc ccagaagtgt tattgaattc aggacacaaa atgccagtca
60
taggaatggg aacatcagta gacaatcgtc catcaaatga tgttcttctt tcaatctttg
120
ttgatgcaat tgaagttggt tatcgtcatt tcgattctgc ttctgtttat ggaacagagg
180
aagctatagg aattgcttta gcaaaagctt tagaaaaagg gcttattaag agtagagatg
240
aagttttcat cacttcaaag ccatggaata ctgatgcaga ttatgatctt attgtccag
300
ctctcaagac cacattgaaa aagctgggga caga
334

<210> 117

<211> 694
<212> DNA
<213> *Trifolium repens*

<220>
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<222> (11)..(11)
<223> Any nucleotide

<220>
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<222> (23)..(23)
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<222> (101)..(101)
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<222> (105)..(106)
 <223> Any nucleotide

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 gncctaaagt gtgtaacata ttcttaactt aaannntttt naccncaaa aaaaaacaa
 120
 agacaataac atgggtagtg ttgaaattcc aacaaagggtt cttactaaca cttctagtc
 180
 agtgaaaatg cctgtggttg gaatgggatc agctcctgat ttcacatgta agaagatac
 240
 aaaagatgca atcattgaag ccatcaaaca aggttataga cactttgata ctgctgctgc
 300
 ttatggctca gaacaagctc ttggtgaagg ttgaaagaa gcaattgaac ttggccttgc
 360
 cactagagaa gagctttttg ttacttctaa actttgggtc actgaaaatc atcctcacct
 420
 tgttgttctt gctcttcaaa aatctctcaa gactcttcaa ttggagtact tggacttgta
 480
 ttgatccat tggccactta gttctcagcc tggaaagttt tcatttccaa ttgatgtggc
 540
 agatctcttg ccatttgatg tgaagggtgt ttgggaatcc atggaagaag gcttgaact
 600
 tggactcact aaagctattg gtgttagtaa cttctctgtc aagaaacttc aaaatcttgc
 660
 ctcagttgcc accgttcttc ctgcggtcaa tcag
 694

<210> 118
 <211> 188
 <212> PRT
 <213> *Trifolium repens*

<400> 118
 Met Gly Ser Val Glu Ile Pro Thr Lys Val Leu Thr Asn Thr Ser Ser
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 Gln Val Lys Met Pro Val Val Gly Met Gly Ser Ala Pro Asp Phe Thr
 20 25 30
 Cys Lys Lys Asp Thr Lys Asp Ala Ile Ile Glu Ala Ile Lys Gln Gly
 35 40 45
 Tyr Arg His Phe Asp Thr Ala Ala Ala Tyr Gly Ser Glu Gln Ala Leu
 50 55 60
 Gly Glu Gly Leu Lys Glu Ala Ile Glu Leu Gly Leu Val Thr Arg Glu

65 70 125/390 75 80

Glu Leu Phe Val Thr Ser Lys Leu Trp Val Thr Glu Asn His Pro His
85 90 95

Leu Val Val Pro Ala Leu Gln Lys Ser Leu Lys Thr Leu Gln Leu Glu
100 105 110

Tyr Leu Asp Leu Tyr Leu Ile His Trp Pro Leu Ser Ser Gln Pro Gly
115 120 125

Lys Phe Ser Phe Pro Ile Asp Val Ala Asp Leu Leu Pro Phe Asp Val
130 135 140

Lys Gly Val Trp Glu Ser Met Glu Glu Gly Leu Lys Leu Gly Leu Thr
145 150 155 160

Lys Ala Ile Gly Val Ser Asn Phe Ser Val Lys Lys Leu Gln Asn Leu
165 170 175

Val Ser Val Ala Thr Val Leu Pro Ala Val Asn Gln
180 185

<210> 119
<211> 576
<212> DNA
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gnctnaaagt gtgtaacata ttcttaactt aaacnatttt cacccaacaa aaaaaaacaa
120
agacaataac atgggtagtg ttgaaattcc aacaaagggtt cttactaaca cttctagtca
180
agtgaataatg cctgtggttg gaatgggatc agctcctgat ttcacatgta agaaagatac
240
aaaagatgca atcattgaag ccatcaaaca aggttataga cactttgata ctgctgctgc
300
ttatggctca gaacaagctc ttggtgaagg ttgaaagaa gcaattgaac ttggtcttgt
360
cactagagaa gagctttttg ttgcttctaa actttgggtc actgaaaatc atcctcatct
420
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480
tttgattcac tggccactta gttctcagcc cggaaagttt tcatttccaa ttgaggtggc
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120

gttgaaattc caacaaaggt tcttactaac acttctagtc aagtgaaaat gcctgtggtt
180

ggaatgggat cagctcctga tttcacatgt aagaagata caaaagatgc aatcattgaa

240

gccatcaaac aaggttatag acactttgat actgctgctg cttatggctc agaacaagct
300

cttggtgaag gtttgaaaga agcaattgaa cttggtcttg tcactagaga agagcttttt
360

gttgcttcta aactttgggt cactgaaaat cactctcctc ttgttggtcc tgctcttcaa
420

aaatctctca agactcttca attggagtac ttggacttgt atttgattca ctggccactt
480

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120

acacttctag tcaagtgaag atgcctgtgg ttggaatggg atcagctcct gatttcacat
180

gtaagaaaga taaaaaagat gcaatcattg aagccatcaa acaaggttat agacactttg
240

atattgtgc tgcttatggc tcagaacaag ctcttggtga aggtttgaaa gaagcaattg
300

aacttggtct tgtcactaga gaagaccttt ttgttacttc taaactttgg gtcactgaaa
360

atcatctca cctgttatt cctgctcttc aaaaatctct caagactctt caattggagt
420

acttggaact gtatttgatc cactggccac ttagttctca gcccggaag ttttcatttc
480

caattgaggt ggcagatctc ttgccatttg atgtgagggg tgtttggcaa tccatggaag
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120

acttctagtc aagtgaaaaat gcctgtggtt ggaatgggat cagctcctga ttccacatgt
180

aagaagata caaaagatgc aatcattgaa gccatcaaac aagggttatg acactttgat
240

attgctgctg cttatggctc agaacaagct cttgggtgaag gtttgaaaga agcaattgaa
300

cttggctctg tcactagaga agaccttttt gttacttcta aactttgggt cactgaaaaat
360

catcctcacc ttgttattcc tgctcttcaa aaatctctca agactcttca attggagtagc
420

ttggacttgt atttgatcca ctggccactt agttctcagc ccggaaggtt ttcatttcca
480

attgagggtg cagatctctt gccatttgat gtgaggggtg ttggcaatc catggaagaa
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120

gttctagtca agtgaaaatg cctgtggttg gaatgggatc agtccttgac ttcacatgta
180

agaaagacac aaaagatgca atcattgaag ccatcaaaca aggntataga cactttgaaa
240

ctgctgctgn ttatgcntca caacaagctc ttgnnnnnann cttcnatgcc ccn
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120
cttctagtca agtgaaaaatg cctgtgggtg gaatgggatc agctcctgat ttacatgta
180
aaaagacac aaaagatgca atcattgaag ccatcaacaa aggttataga cactttgata
240
ctgntgctgc ttatggctca naacaagctc ttgggtgaagg ttgaaagaa gcaattgaac
300
ttggccttgt cactagaaaa gagctttttg ttacttctaa actttgggtc actgaaaaatc
360
atctcacct tgtgttctc gctcttcaaa aatctctcaa gactcttcaa ttggagtact
420
tggacttgta ttgatccat tggccactta attctcancc tggaaagttt tcatttccca
480
ttgangtggc aaatctcttg ccatttnatg tgaanggtgt ttgggaatcc atggaaaaan
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gcttnaaact tggactcact aaagctattg gtgncannaa cttctctntc aanaaacttc
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120
tagtcaagtg aaaatgcctg tggttggaat gggatcagca cctgatttca catgtaagaa
180
agacacaaaa gatgcaatca ttgaagccat caaacaaggt tatagacact ttgatactgc
240
tgctgcttat ggctcagaac aagctcttgg tggagggttg aaagaagcaa ttgaacttgg
300
ccttgtcact agagaagagc tttttgttac ttctaaactt tgggtcactg aaaatcatcc
360
tcaccttggt gttcctgcto ttcaaaaatc tctcaagact cttcaattgg agtacttgga
420
cttgatattg atccattggc cacttagttc tcagcctgga aagttttcat ttccaattga
480
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tcaagtgaat atgcctgtgg ttggaatggg atcagctctt gatttcacat gtaagaaaga
180
tacaaaagat gcaatcattg aagccatcaa acaagggtat agacactttg atactgctgc
240
tgcttatggc tcagaacaag ctcttggtga aggtttgaaa gaagcaattg aacttgccct
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tgtcactaga gaagagcttt ttgttacttc taaactttgg gtcaactgaaa atcatctca
360
tcttggtgtt cctgctcttc aaaaatctct caagactctt caattggagt acttggaact
420
gtatttgatc cattggccac ttagttctca gcctggaaaag ttttcatttc caattgatgt
480
ggcagatctc ttgccatttg atgtgaaggg tgtttgggaa tccatggaag aaggcttgaa
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caagtgaata tgccctgtgtg tggaatggga tcagcacctg atttcacatg taagaagac
180
acaaaagatg caatcattga agccatcaaa caagggtata gacactttga tactgctgct
240
gcttatggct cagaacaagc tcttggtgaa gggttgaaag aagcaattga acttggcctt
300
gtcactagag aagagctttt tggtacttct aaactttggg tcactgaaaa tcatcctcac
360
cttggtgttc ctgctcttc aaaaatcttc aagactcttc aattggagta cttggacttg
420
tattgatcc attggccact tagttctcag cctggaaagt ttctattcc aattgatgtg
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120

caagtgaata tgctgtgtgt tggaatggga tcagctcctg atttcacatg taagaagatg
180

acaaaagatg caatcattga agccatcaaa caaggttata gacactttga tactgctgnt
240

gcttatggct cagaacaagc tcttggtgaa ggtttgaaag aagcaattga acttgacctt
300

gtcactagag aagagctttt tggtacttct aaactttggg tcaactgaaa tcatcctcac
360

cttggtattc ctgctcttca aaaatctctc aagactcttc aattggagta cttggacttg
420

tatttgatcc attggccact tagttctcag cctggaaagt ttctatttcc aattgatgtg
480

gcagatctct tgccatttga tgtgaagggt gtttgggaat ccattggaaga aggcctgaaa
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120

caagtga aaa tgccgtgtgt tggaatggga tcagcacctg atttcacatg taagaaagac
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acaaaagatg caatcattga agccatcaaa caggggtata gacactttga tactgtgtgt
240

gcttatggct cagaacaagc tcttggtgaa gggttgaaag aagcaattga acttggtctt
300

gtcactagag aagacctttt tggtacttct aaactttggg tcaactgaaa tcatcctcat
360

cttggtgttc ctgctcttca aaaatctctc aagactcttc aattggagta cttggacttg
420

tatttgatcc attggccact tagttctcag cctggaaagt ttctatttcc aattgatgtg
480

gcagatctct tgccatttga tgtgaagggt gtttgggaat ccatggaaga aggcttgaaa
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caagtgaaaa tgcctgtggt tggaatggga tcagcacctg atttcacatg taagaagac
180

acaaaagatg caatcattga agccatcaaa caagggtata gacactttga tactgctgt
240

gcttatggct cagaacaagc tcttggtgga gggttgaaag aagcaattga acttggcctt
300

gtcactagag aagagctttt tgttactttc aaactttggg tcactgaaaa tcatectcac
360

ctgtgtgttc ctgctcttca aaaatctctc aagactcttc aattggagta cttggacttg
420

tatttgatcc attggccact tagttctcag cctggaaagt ttctatttcc aattgatgtg
480

gcagatctct tgccatttga tgtgaagggt gtttggcaat ccatggaaga aggcctgaaa
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597

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120

tgccgtggtg tggaatggga tcagctcctg atttcacatg taagaaagat acaaaagatg
180

caatcattga agccatcaaa caagggtata gacactttga tactgctgct gcttatggct
240

cagaacaagc tcttggtgaa ggtttgaaag aagcaattga acttggcctt gtcactagag
300

aagagctttt tgttacttct aaactttggg tcactgaaaa tcactcctcac cttgttgttc
360

ctgctcttca aaaatctctc aagactcttc aattggagta cttggacttg tatttgatcc
420

attggccact tagttctcag cctggaaagt ttctatttcc aattgatgtg gcagatctct
480

tgccatttga tgtgaagggt gtttgggaat ccatggaana aggccttgaaa cttggactcn
540

ctaaagctat tgggtgtann nacttctntg tnan
574

<210> 132
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<400> 132
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120
tgcctgtggt tggaatggga tcagctctcg atttcacatg taagaaagat acaaaagatg
180
caatcattga agccatcaaa caagggtata gacactttga tactgctgct gcttatggct
240
cagaacaagc tcttggtgaa ggtttgaaag aagcaattga acttggcctt gtcactagag
300
aagagctttt tgttacttct aaactttggg tcaactgaaaa tcatctctac cttgttgctc
360
ctgctcttca aaaatctctc aagactcttc aattggagta cttggacttg tatttgatcc
420
attggcact tagttctcag cctggaaggt ttctatttcc aattgatgtg gcagatctct
480
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540
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578

<210> 133
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<220>

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<222> (57)..(59)

<223> Any nucleotides

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120

tgccctgtggt tggaaatgga tcagcacctg atttcacatg taagaagac acaaaagat
180

caatcattga agccatcaaa caaggttata gacacttga tactgtgtgt gcttatggct
240

cagaacaagc tcttggtgaa ggtttgaaag aagcaattga acttgccctt gtcactagag
300

aagagctttt tgttacttct aaactttggg tcaactgaaa tcatcctcac cttgtgttgc
360

ctgctcttcca aaaatctctc aagactcttc aattggagta cttggacttg tatttgatcc
420

attggccact tagttctcag ccgaaaaagt ttctatttcc aattgatgtg gcagatctct
480

tgccatttga tgtgaagggt gtttggaat ccatggaaga aggcttgaaa cttggactca
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ctaaagctat tgggtgcagt aacttctctg tcaagaaact tcaaaatctt gtctcagttg
600

<210> 134
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120

atggggatcag ctctgtatt cacaatgaag aaagatacaa aagatgcaat cattgaagcc
180

atcaaaacaag gttatagaca ctttgatact gctgctgctt atggctcaga acaagctctt
240

ggtgaaggtt tgaagaagc aattgaactt ggccttgtca ctagagaaga gctttttgtt
300

acttctaacc tttgggtcac tgaaaatcat cctcaccttg ttgttctgc tottcaaaaa
360

tctctcaaga ctcttcaatt ggagtacttg gacttgtatt tgatccattg gccacttagt
420

tctcagcctg gaaagtttct atttccaatt gatgtggcag atctcttgcc atttgatgtg
480

aagggtgttt gggaatccat ggaagaagc ttgaaacttg gactcactaa agctattggt
540

gttagtaact tctctgtcaa gaaacttcaa aatcttgtct cagttgccac cgttcttctt
600

gcgggtcaatc ag
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<210> 135

<211> 610

<212> DNA

<213> Trifolium repens

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<222> (30)..(30)

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 120
 cggctacatt gtccacgcca ccatccaaga tctcgaggat gagaacgaga caaaacattt
 180
 ggaagcaatg gaaggagcaa agggtcattc caaatttttc gaaatggatc ttcttaacag
 240
 cgactctatt gcggccgccc tgaaagggtg tgccggagtt atacatcttg catgtcctaa
 300
 catcattggg gaagtcaaa accccgagaa gcaaattttg gaaccggcaa ttcaaggaac
 360
 ggtaatatgt ttgaagggtg caaaggaagc aggggtggag cgtgtgtgtg cgacatcgtc
 420
 gatctccgcc atcataccga gtctaattg gccagctgat aagattaagg gagaagattg
 480
 ttggacagac cttgattatt gcaaggaaaa gaagttatac taccctattg caaagacact
 540
 agcagaaaaa gctgggtggg aatttgctaa agagaccggg tttgatgttg ttatgattaa
 600
 ccctgggtact
 610

<210> 136
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<400> 136

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20	25	30
Ile Gln Asp 35	Leu Glu Asp Glu Asn Glu Thr Lys His 40	Leu Glu Ala Met 45
Glu Gly Ala Lys Gly His 50	Leu Lys Phe Phe Glu Met Asp 55 60	Leu Leu Asn
Ser Asp Ser Ile Ala Ala Ala Val Lys Gly Cys Ala Gly Val Ile His 65 70 75 80		
Leu Ala Cys Pro Asn Ile Ile Gly Glu Val Lys Asp Pro Glu Lys Gln 85 90 95		
Ile Leu Glu Pro Ala Ile Gln Gly Thr Val Asn Val Leu Lys Val Ala 100 105 110		
Lys Glu Ala Gly Val Glu Arg Val Val Ala Thr Ser Ser Ile Ser Ala 115 120 125		
Ile Ile Pro Ser Pro Asn Trp Pro Ala Asp Lys Ile Lys Gly Glu Asp 130 135 140		
Cys Trp Thr Asp Leu Asp Tyr Cys Lys Glu Lys Lys Leu Tyr Tyr Pro 145 150 155 160		
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Thr Gly Phe Asp Val Val Met Ile Asn Pro Gly Thr 180 185		

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120

cggctacatt gtccacgcca ccatccaaga tctcgaggat gagaacgaga caaaacattt
180

ggaagcaatg gaaggagcaa aggggtcatct caaatatttc gaaatggatc ttcttaacag
240

cgactctatt gcggnccgcg tgaagggttg ngccggaggtt atacatnttg nctgtcctac
300

cccccttggg gangagnnng caccenn
327

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120
cgggtacatc gtccacgcca ccattccaaga tctcgaggat gagaacgaga caaaacattt
180
ggaagcaatg gaaggggcaa aggggtcatct taaatttttc gaaatggatc ttcttaacag
240
tgactctatt gcggcgccgc tgaaagggtg tgccggagtt atacatnttg catgtgctaa
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catcattgct gaangnaaan accnoganaa cnggatatttg naacnngnn
349

<210> 139
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120
cggctacatt gtccacgcca ccatccaaga tctcgaggat gagaacgaga caaacattt
180
ggaagcaatg gaaggagcaa aggggtcatct caaatTTTTT gaaatggatc ttcttaacag
240
cgaetctatt gcggccgccc tgaaagggtg tgccggagtt atacatcttg catgtcctaa
300
catcattggt gaagtcaaag accccgagaa gcaaatTTTg gaaccggcaa ttcaaggaa
360
ggttaatggt ttgaagggtg caaaggaagc aggggtggag cgtgtggtgg cgacatcgtc
420
gatctccgcc atcataccga gtcctaattg gccagctgat aagattaagg gagaagattg
480
ntggacagac cttgattatt gcaangaaaa gaagttatac taccocattg caaagacatt
540
ancagaaaaa gctgggtggg aatttgctaa agagaccggg ttgatgttg tt
592

<210> 140
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<213> *Trifolium repens*

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120

cggctacatt gtccacgcca ccatccaaga tctcagggat gagaacgaga caaaacattt
180

ggaagcaatg gaaggagcaa agggatcatct caaatttttc gaaatggatc ttctcaacag
240

cgactctatt gcggccgccc tgaaagggtg tgccggagtt atacatcttg catgtcctag
300

catcattggt gaagtcaaag accccgagaa gcaaattttg gaaccggcaa ttcaaggaac
360

ggttaatgtg ttgaagggtg caaaggaagc aggggtggag cgtgtggtgg cgacatcgtc
420

gatctccgcc atcataccga gtctctaattg gccacgtgat aagattaagg gagaagattg
480

ttggacagac cttgattatt gcaaggaaaa gaagttatac taccocattg caaagacact
540

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594

<210> 141

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gtctacattgt ccacgccacc atccaagatc tcgaggatga gaacgagaca aaacatttgg
180
aagcaatgga aggagcaaag ggtcatctca aattttttcga aatggatctt cttaacagcg
240
actctattgc ggccgccgtg aaagggtgtg ccggagttat acatcttgca tgtcctaaca
300
tcattggtga agtcaaagac ccgagaagc aaatttttga accggcaatt caaggaacg
360
ttaatgtgtt gaaggtggca aaggaagcag ggggtggagcg tgtggtggcg acatcgtcga
420
tctctgccat cataccgagt cctaattggc cagctgataa gattaagga gaagattgtt
480
ggacagacct tgattattgc aaggaaaaga agttatacta cccattgca aagacactag
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583

<210> 142
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gctacattgt ccacgcccacc atccaagatc tcgaggatga gaacgagaca aaacatttgg
180
aagcaatgga aggagcaaaag ggtcatctca aatttttcga aatggatctt ctcaacagcg
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actctattgc ggccgcccgtg aaagggtgtg ccggagttaa acatcttgca tgtcctagca
300
tcattggtga agtcaaagac ccgagaagc aaattttggg accggcaatt caaggaacgg
360
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ttcccgccat cataccgagt cctaattggc cagctgataa gattaaggga gaagattgtt
480
ggacagacct tgattattgc aaggaaaaga agttatacta cccattgca aagacactag
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120

acattgtcca cgccaccatc caagatctcg aggatgagaa cgagacaaaa catttggaag
180

caatgggaagg agcaaagggt catctcaaatt tttttgaaat ggatcttctt aacagcgact
240

ctattgcgco cgcogtgaaa ggttggtgccg gagtataca tcttgcatgt cctaacatca
300

tgtgtgaagt caaagacccc gagaagcaaa ttttggaacc ggcaattcaa ggaacggtta
360

atgtgttgaa ggtggcaaaag gaagcagggg tggagcgtgt ggtggcgaca tcgtcgatct
420

cgcgcacat accgagtcct aattggccag ctgataagat taagggagaa gattgttgga
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aaaaagctgg ttgggaattt gctaaagaga c
571

<210> 144
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acatcggtcca cgccaccatc caagatctcg aggatgagaa cgagacaaaa catttggaag
180

caatggaagg ggcaaagggt tatcttaaat ttttcgaaat ggatcttctt aacagtgact
240

ctattgcggc cgccgtgaaa ggttgtgccc gagttatata tcttgcatgt cctaacatca
300

ttggtgaagt caaagacccc gagaagcaaa ttttgaacc ggcgattcaa ggaacggtta
360

acgtgttgaa ggtggcaaag gaagcagggg tggagcgtgt ggtggcgacg tcatcgatct
420

ccgccatcat accgagtcct aattggccag ctgataagat taaggggagaa gattgttgga
480

cggaacctga ttattgcaag gaaaagaagt tacactaccc catcgcaaag acactagcag
540

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<400> 145
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naccggagcc ngcggagcca tcgggttcag ggtgggtcgc ctctctctcg aacggcgcta
120

cattgtccac gccaccatcc aagatctcga ggatgagaac gagacaaaac atttgggaagc
180

aatggaagga gcaaagggtc atctcaaatt ttttgaaatg gatcttctta acagcgactc
240

tattgcgync gccgtgaaag gttgtgccgg agttatacat cttgcatgng ctaacatcat
300

tggggaagcn aaagnactcn ataagnan
328

<210> 146
<211> 232
<212> DNA
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<222> (186)..(186)
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<220>
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<222> (232)..(232)
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<400> 146
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60

ccacgcggnt acattgtcca cgccaccatc caagatctcg aggatgagaa cgagacaaaa
120

catttggaag caatggaagg agcaaagggt catntnaaat ttttcgaaat ggatcttntt
180

aacangact ctattgcggc cgccgtgaaa ggttggtgccg gagttataca tn
232

<210> 147

<211> 623

<212> DNA

<213> *Trifolium repens*

<220>

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<223> Any nucleotide

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<222> (14)..(14)

<223> Any nucleotide

<400> 147
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gttttgggtt acagggggca ctggcttcat agcagcctac ctagtgaag cottattaga
120

aaagggtcac acagtaagga ctactgtaag aaaccagat gatttggaag aggttggtta
180

tctaaactgaa ctaagtgaag acaaagagag attgaagatt ttaaaagcag atctattggt
240

ggaagggagt tttgatgagg cagtgaagtg tgttgatggt gtgtttcata cagcttcccc
300

tggtctgtgt ccacatgatg acaacattca gggttacttg attgatccat gtataaaagg
360

aacacaaaa gtgcttaact catgcatcaa agcaaagggt aaacgtgtgg tggttaacatc
420

ttcatgctct tcataagat acogtgaoga tgtgcaacaa atttctctc ttaatgaatc
480

tcattggagt gattctgaat actgcaaacg ctataacctg tggatgcat atgcaagac
540

tttagggagaa aaagaagcat ggaggattgc aaaggaaagt ggaattgac tagttgtagt
600

taacccctct tttgttggtg gtc
623

<210> 148
 <211> 190
 <212> PRT
 <213> *Trifolium repens*

<400> 148

Met Pro Glu Phe Cys Val Thr Gly Gly Thr Gly Phe Ile Ala Ala Tyr
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Leu Val Lys Ala Leu Leu Glu Lys Gly His Thr Val Arg Thr Thr Val
 20 25 30

Arg Asn Pro Asp Asp Leu Glu Lys Val Gly Tyr Leu Thr Glu Leu Ser
 35 40 45

Glu Asp Lys Glu Arg Leu Lys Ile Leu Lys Ala Asp Leu Leu Val Glu
 50 55 60

Gly Ser Phe Asp Glu Ala Val Ser Gly Val Asp Gly Val Phe His Thr
 65 70 75 80

Ala Ser Pro Val Leu Val Pro His Asp Asp Asn Ile Gln Val Thr Leu
 85 90 95

Ile Asp Pro Cys Ile Lys Gly Thr Gln Asn Val Leu Asn Ser Cys Ile
 100 105 110

Lys Ala Lys Val Lys Arg Val Val Leu Thr Ser Ser Cys Ser Ser Ile
 115 120 125

Arg Tyr Arg Asp Asp Val Gln Gln Ile Ser Pro Leu Asn Glu Ser His
 130 135 140

Trp Ser Asp Ser Glu Tyr Cys Lys Arg Tyr Asn Leu Trp Tyr Ala Tyr
 145 150 155 160

Ala Lys Thr Leu Gly Glu Lys Glu Ala Trp Arg Ile Ala Lys Glu Ser
 165 170 175

Gly Ile Asp Leu Val Val Val Asn Pro Ser Phe Val Gly Gly
 180 185 190

<210> 149
 <211> 570
 <212> DNA
 <213> *Trifolium repens*

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120
aaaggggtcac acagtaagga ctactgtaag aaaccagat gatttgaga aggttggtta
180
tctaactgaa ctaagtgaag acaagagag attgaagatt ttaaaagcag atctattggt
240
ggaagggag tttgatgagg cagtgagtg tggtgatggt gtgtttcata cagcttcccc
300
tgtttctgtt ccacatgatg acaatattca gggtactttg attgatccat gtataaaagg
360
aacacaaaaa gtgcttagct catgcacaa agcaaaggbg aaacgtgtgg tggttaacatc
420
ttcatgctct tccataagat accgtgacga tggtaacaa atttaccac ttaatgaatc
480
tcattggagt gattctgaat actgcaaacy ctataacctg tggatgcat atgcaaagac
540
attaggagaa aaagaagcat ggaggattgc
570

<210> 150
<211> 572
<212> DNA
<213> *Trifolium repens*

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<222> (2)..(2)
<223> Any nucleotide

<220>
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<222> (8)..(9)
<223> Any nucleotides

<400> 150
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60
ttcatagcag cctacctagt gaaagcccta ttagaaaagg gtcacacagt aaggactact

120

gtaagaaacc cagatgattt ggagaaggtt ggttatctaa ctgaactaag tgaagacaaa
180

gagagattga agattttaaa agcagatcta ttggtggaag ggagttttga tgaaggcagt
240

agtgggtgtg atggtgtgtt tcatacagct tccctgttcc ttgtccaca tgaatgacaa
300

attcagggtta ctttgattga tccatgtata aaaggaacac agaattgtgt taactcatgc
360

atcaaaagaa aggtgaaacg tgtggtgtta acatcctcat gctcttccat aagataccgt
420

gacgatgtgc aacaaatttc tcctcttaat gaatctcatt ggagtgtatc tgattactgc
480

aaacgctata acctgtggta tgcataatgca aagactttag gagaaaaaga agcatggagg
540

attgcaaagg aaagtgggat taatctagtt gt
572

<210> 151

<211> 572

<212> DNA

<213> *Trifolium repens*

<400> 151

ggaaagagat gcctgagttt tgtgttacag ggggcactgg ctccatagca gcttacctag
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tgaagccctt attagaaaag ggtcacacag taaggactac tgtaagaaac ccagatgatt
120

tggagaaggt tggttatcta actgaactta gtgaagacaa agagagattg aagattttaa
180

aagcagatct attggtggaa gggagttttg atgaggcagt gagtgggtgt gatgggtgtg
240

ttcatagcag tccccctgtt cttgttccac atgatgacaa cattcagggt actttgattg
300

atccatgtat aaaaggaaca caaatgtgc ttaactcatg catcaaagca aaggtgaaac
360

gtgtgggtgt aacatcttca tgctcttcca taagataccg tgacgatgtg caacaatttt
420

ctcctcttaa tgaatctcat tggagtgtt ctgaatactg caaacgctat aacctgtggt
480

atgcatatgc aaagacttta ggagaaaaag aagcatggag gattgcaaag gaaagtggaa
540

ttgatctagt tgtagttaac cctcttttgg tt
572

<210> 152

<211> 574

<212> DNA
<213> *Trifolium repens*

<220>
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gccttattag aaaaggggtca cacagtaagg actactgtaa gaaaccaga tgctttggag
120
aagggttggt atctaactga acttagtgaa gacaagaga gattgaagat tttaaaagca
180
gatctattgg tggaagggag tttgatgag gcagtgaagt gtgttgatgg tgtgtttcat
240
acagcttccc ctgttcttgt tccacatgat gacaacatto aggttacttt gattgatcca
300
tgtataaaag gaacacaaaa tgtgcttaac tcatgcatca tagcaaaggt gaaacgtgtg
360
gtgttaacat cttcatgctc ttccataaga tacogtgaag atgtgcaaca aatttctcct
420
cttaatgaat ctcatggag tgattctgaa tactgcaaac gctataacct gtggtatgca
480
tatgcaaaga cttaggaga aaaagaagca tggaggattg caaaggaaag tggaattgat
540
ctagttgtag ttaaccctc tttgttggt ggtc
574

<210> 153
<211> 641
<212> DNA
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<223> Any nucleotide

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60

ccctactcca aaaactactac aaaattcacg ccacaattctt cccaatttc aacgcattct
120

atctcttcac actccaccgg gaagctcaat ccggatcac aattttccct gtcgatatcc
180

tcgactccac gcgcgtcttc tccgctatca ataactgtc aggtgtcttt catgccgtt
240

ctccatgtac cctcgaagat ccaactgatc cgcaaaaaga gcttctagaa cctgctgtac
300

aagggaacctt aaatgttcta gaagcatcca gcgcgcaggt accaaacctt aattggccgg
360

agaaaaaggc gatcgatgag gcgtcgtgga cggatgttga gtactgtaaa ttgagaggga
420

atgggtatct ggtgtcgaaa acggaggcgg agaaggcggc ttgggatttt cgagagaaaa
480

atgggtggtgt tgatgtgggg gcggntcatc cggggacttg ttggggagag ttgatacaga

540

aggagttgaa tgcgagttca gcggnntttac agaggttgat gatggggagt gaggatactc
600

aagagtgnta ttggnngggg ggctgnnnat gntaaagatg n
641

<210> 154
<211> 206
<212> PRT
<213> Trifolium repens

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<222> (204)..(204)
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<400> 154

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Leu Val Lys Thr Leu Leu Gln Lys His Tyr Lys Ile His Ala Thr Ile
20 25 30

Phe Pro Asn Ser Asn Ala Ser His Leu Phe Thr Leu His Pro Glu Ala
35 40 45

Gln Ser Arg Ile Thr Ile Phe Pro Val Asp Ile Leu Asp Ser Thr Ala
50 55 60

Val Phe Ser Ala Ile Asn Asn Cys Ser Gly Val Phe His Ala Ala Ser
65 70 75 80

Pro Cys Thr Leu Glu Asp Pro Thr Asp Pro Gln Lys Glu Leu Leu Glu
85 90 95

Pro Ala Val Gln Gly Thr Leu Asn Val Leu Glu Ala Ser Ser Ala Gln
100 105 110

Val Pro Asn Pro Asn Trp Pro Glu Lys Lys Ala Ile Asp Glu Ala Ser
115 120 125

Trp Thr Asp Val Glu Tyr Cys Lys Leu Arg Gly Lys Trp Tyr Leu Val
130 135 140

Ser Lys Thr Glu Ala Glu Lys Ala Ala Trp Asp Phe Arg Glu Lys Asn
145 150 155 160

Gly Gly Val Asp Val Gly Ala Xaa His Pro Gly Thr Cys Leu Gly Glu
165 170 175

Leu Ile Gln Lys Glu Leu Asn Ala Ser Ser Ala Leu Gln Arg Leu Met
180 185 190

Met Gly Ser Glu Asp Thr Gln Glu Xaa Tyr Trp Xaa Gly Gly
195 200 205

<210> 155
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<212> DNA
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120
tcctccggcg ctacactgtt caccgccacg tccaaaatct caatgatgag aacgaaacga
180
agcatctaga agctctcgaa ggagcacaaa ctaactctcg tctcttccag atcgatctcc
240
ttaactcga cacaatcttc gctgctgtcc gcggttgcgt cggaattttc cacctcgctt
300
caccttgca cgttagacaaa gttcatgata ctccagaagga gcttttgat cctgcaatta
360
aagggacttt gaattgtgctt actgcagcta aggaagtagg ggtgaagcgt gtggttgtaa
420
ctcgtctgt ctcggcgatt actcctagtc ctgattggcc tctgatggt gttaaaagag
480
aggattgttg gactgatgtt gaatattgca agaaaaaga gttgggggat ccgttgcca
540
aaacattggc tgaaaaagct gcgtgggatt tttncaaaga aaatggtttg gatgttcttg
600
nggtgaatcc cgggactgng atgggtcctg tttttccacc acggcataat gcaagcatgc
660
tcactgcctt ggaaactttt ttgaaggctg gnnctgaaac atttgaagac tattttatgg
720
gattggccnn ctttaaagat gtngcattgg cncatnnttt ggggtatgag aacaaanann
780
ctttgggana catngngggg ttgaaactat cnnctcttac gg
822

<210> 156
<211> 256
<212> PRT
<213> Trifolium repens

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<400> 156

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Trp Leu Val His Leu Leu Leu Arg Gly Tyr Thr Val His Ala Thr
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Val Gln Asn Leu Asn Asp Glu Asn Glu Thr Lys His Leu Glu Ala Leu
 35 40 45

Glu Gly Ala Gln Thr Asn Leu Arg Leu Phe Gln Ile Asp Leu Leu Asn
 50 55 60

Tyr Asp Thr Ile Leu Ala Ala Val Arg Gly Cys Val Gly Ile Phe His
 65 70 75 80

Leu Ala Ser Pro Cys Thr Val Asp Lys Val His Asp Pro Gln Lys Glu
 85 90 95

Leu Leu Asp Pro Ala Ile Lys Gly Thr Leu Asn Val Leu Thr Ala Ala
 100 105 110

Lys Glu Val Gly Val Lys Arg Val Val Val Thr Ser Ser Val Ser Ala
 115 120 125

Ile Thr Pro Ser Pro Asp Trp Pro Ser Asp Val Val Lys Arg Glu Asp
 130 135 140

Cys Trp Thr Asp Val Glu Tyr Cys Lys Lys Lys Glu Leu Gly Tyr Pro
 145 150 155 160

Leu Ser Lys Thr Leu Ala Glu Lys Ala Ala Trp Asp Phe Xaa Lys Glu
 165 170 175

Asn Gly Leu Asp Val Val Xaa Val Asn Pro Xaa Thr Xaa Met Gly Pro
 180 185 190

Val Phe Pro Pro Arg His Asn Ala Ser Met Leu Met Pro Trp Glu Thr
 195 200 205

Phe Leu Lys Ala Xaa Xaa Glu Thr Phe Glu Asp Tyr Phe Met Gly Leu
 210 215 220

Ala Xaa Phe Lys Asp Xaa Ala Leu Xaa His Xaa Leu Gly Tyr Glu Asn
 225 230 235 240

Lys Xaa Xaa Leu Gly Xaa Xaa Xaa Gly Leu Lys Leu Xaa Xaa Leu Thr
 245 250 255

<210> 157
<211> 535
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<223> Any nucleotide

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120

tcctccggcg ctacactggt caccgcaccg tccaaaatct caatgatgag aacgaaacga
180

agcatctaga agctctcgaa ggagcacaaa ctaatctcgg tctcttccag atcgatctcc
240

ttaactacga cacaatcctc gctgctgtcc gcggttgctg cggaattttc cacctcgctt
300

caccttgcac tgtagacaaa gttcatgata ctacagaagga gcttttggat cctgcaatta
360

aaagggaactt gaatgtgctt actgcagcta aggaagtagg ggtgaagcgt gtggttgcta
420

ctcgtctgt ctcggcgatt actoctagtc ctgattggcc ttctgatgtt gttaaaagag
480

aggattgttg gactgatgtt gaatattgca agaaaaaaga gttgtggtat ccggt
535

<210> 158
<211> 801
<212> DNA
<213> *Trifolium repens*

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gnggcggatg catcggttca tggctagtcc atctccttct cctccggcgc tacactgttc
120

acgccaccgt ccaaaatctc aatgatgaga acgaaacgaa gcatctagaa gctctcgaag
180

gagcacaaac taatctccgt ctcttcacaga tcgatctcct taactacgac acaatcctcg
240

ctgctgtccg cggttcgctg ggaattttcc acctcgcttc accttgact gtagacaaag
300

ttcatgatcc tcagaaggag cttttggatc ctgcaattac agggactttg aatgtgctta
360

ctgcagctaa ggaagtaggg gtgaagcgtg tggttgttac ctcgctgtgc tcggcgatta
420

ctcctagtcc tgattggcct tctgatgttg ttaaaagaga ggattgttgg actgatgttg
480

aatattgcaa gaaaaaagag ttggggatc cggtgtccaa aacattggct gaaaaagctg
540

cggtgggattt ttncaaagaa aatggtttgg atgttgttgn ggtgaatccc ggnactgnga
600

tgggtcctgt tttccacca cggcataatg caagcatgct catgccttgg gaaacttttt
660

tgaaggctgg nntgaaaca ttgaagact attttatggg attggcennn tttaaagatg
720

tngcattggc ncatnnttgg gggtatgaga acaaanannn ttggganac atngnggggt
780

tgaaactatc nntccttacg g
801

<210> 159

<211> 582

<212> DNA

<213> *Trifolium repens*

<400> 159

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60

tttttagcat cttggottat taagaaactt cttttgtctg gctatcaagt cattggaaca
120

gttagagatt tagggaagaa gaagaaagtt gaacatttat ggaatttga aggagcaaca
180

gaaagactag aactaatcca agctgattta ttggaagaaa atagtttcga caaagcgatc
240

atgggatgca aagggtgtctt ccacattgcc tctccagtac tcaatcatat atcagataat
300

cctaaggcgg aaatcttggg accggcagtc caagggtacgc taaatgtgtt cggttcttgt
360

aagaggaacc ccatcttctg tcgagtgggtg ctaggctcat catctctggc tgtagagta
420

agagctgatt ttgatccaag cataccaatt gatgaatcat cttggagctc cttggaattg
480

tgcgagaaac tcaaggcatg gtaccacaatg tcaagacaa tggcagaaaa agcagcttgg
540

gaatatagca aagagaatgg aatagactta gtgactatct tc
582

<210> 160

<211> 190

<212> PRT

<213> *Trifolium repens*

<400> 160

Met Glu His Lys Gly Gly Asp Lys Val Cys Val Thr Gly Ala Ser Gly
1 5 10 15

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Phe Leu Ala Ser Trp Leu Ile Lys Lys Leu Leu Leu Ser Gly Tyr Gln
      20                      25                      30

Val Ile Gly Thr Val Arg Asp Leu Gly Lys Lys Lys Lys Val Glu His
      35                      40                      45

Leu Trp Lys Leu Glu Gly Ala Thr Glu Arg Leu Glu Leu Ile Gln Ala
      50                      55                      60

Asp Leu Met Glu Glu Asn Ser Phe Asp Lys Ala Ile Met Gly Cys Lys
      65                      70                      75                      80

Gly Val Phe His Ile Ala Ser Pro Val Leu Asn His Ile Ser Asp Asn
      85                      90                      95

Pro Lys Ala Glu Ile Leu Glu Pro Ala Val Gln Gly Thr Leu Asn Val
      100                     105                     110

Leu Arg Ser Cys Lys Arg Asn Pro Asp Leu Val Arg Val Val Leu Ala
      115                     120                     125

Ser Ser Ser Ser Ala Val Arg Val Arg Ala Asp Phe Asp Pro Ser Ile
      130                     135                     140

Pro Ile Asp Glu Ser Ser Trp Ser Ser Leu Glu Leu Cys Glu Lys Leu
      145                     150                     155                     160

Lys Ala Trp Tyr Tyr Pro Met Ser Lys Thr Met Ala Glu Lys Ala Ala Trp
      165                     170                     175

Glu Tyr Ser Lys Glu Asn Gly Ile Asp Leu Val Thr Ile Phe
      180                     185                     190

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<210> 161
<211> 572
<212> DNA
<213> Trifolium repens

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<222> (4)..(5)
<223> Any nucleotides

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 <223> Any nucleotide

<400> 161
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tatatatatt tgtgtttcaa gaacccaaaa aatagaatag tgatggaaa gagttgcaag
 120

gtttgtgtca ccggtgggtgc tggttatatt ggttctcttt tagtcaaaaa gcttttgga
 180

aagggttaca ccgttcattgc tactcttaga aacttgaagg acgaatccaa agtagatttt
 240

ttgagaggct ttccacatgc agatactaga cttatgttat ttgaagctga tatatacaaa
 300

tcagatgaat ttggccgc aattcaaggt tgtgagtttg tttttcacct tgetactcct
 360

tttcaacatc aaactgattc tcagttaaag agcatagagg aagctgcaat agcaggggta
 420

aaaagcatag ctgaaaattg cataaaatca ggaacagtga gaaaattgat atacactgga
 480

actgtaattg cttctcttc tctgaaagat gatggaagtg gctacaaaga cttcattgat
 540

gaaacttggt ggacacctct ccattctcct ct
 572

<210> 162
 <211> 156

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<212> PRT
<213> Trifolium repens

<400> 162

Met Glu Arg Ser Cys Lys Val Cys Val Thr Gly Gly Ala Gly Tyr Ile
1           5           10           15

Gly Ser Leu Leu Val Lys Lys Leu Leu Glu Lys Gly Tyr Thr Val His
20           25           30

Ala Thr Leu Arg Asn Leu Lys Asp Glu Ser Lys Val Asp Phe Leu Arg
35           40           45

Gly Phe Pro His Ala Asp Thr Arg Leu Met Leu Phe Glu Ala Asp Ile
50           55           60

Tyr Lys Ser Asp Glu Phe Trp Pro Ala Ile Gln Gly Cys Glu Phe Val
65           70           75           80

Phe His Leu Ala Thr Pro Phe Gln His Gln Thr Asp Ser Gln Phe Lys
85           90           95

Ser Ile Glu Glu Ala Ala Ile Ala Gly Val Lys Ser Ile Ala Glu Asn
100          105          110

Cys Ile Lys Ser Gly Thr Val Arg Lys Leu Ile Tyr Thr Gly Thr Val
115          120          125

Ile Ala Ser Ser Ser Leu Lys Asp Asp Gly Ser Gly Tyr Lys Asp Phe
130          135          140

Ile Asp Glu Thr Cys Trp Thr Pro Leu His Leu Pro
145          150          155

<210> 163
<211> 714
<212> DNA
<213> Trifolium repens

<220>
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<222> (4)..(4)
<223> Any nucleotide

<220>
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<222> (131)..(131)
<223> Any nucleotide

<220>
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<222> (147)..(147)
<223> Any nucleotide

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<400> 163
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ttaataattg gaagggagaa taaatagttg aaaaacacac agtgggagtg tttttgttgt
120

taaagaagct ngaaaatgga ggaagcnaca aagatggatga aaaagagtg acaaatgttt
180

ccttagtcca aatactgtgt tacaggagca acagggtata ttggttcattg gcttgttgaa
240

gctcttcttc aaagagggtg cactgttcat gctactgtta gagatcctga aaaatcgtaa
300

cacctcctgt cgttgtggaa aggtagtac caattgagaa tttccgtgc ggatttgcaa
360

gaagaaggaa gtttcgatga tgcgtaaaa ggaatgtattg gtgtgttcca tgttcagct
420

tcaatgcaat tcaatattag tgacaagaa aacactgagg acttgttgta agcaaatata
480

attgaccctg caatcaaagg aaccataaat ctctcaaat catgcttgaa atcaaattca
540

gtgaaaaggg ttgttttcac atcttcata agtactatta ctgttaaaga caacgacgga
600

aaatggaaac ctattgttga tgaatcttgc caaacaaaaa ctgagattct gtggaataca
660

caaccaagtg gatgggttta tgcactttca aagcttcattg cagaagaagc ggct
714

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<210> 164
<211> 187
<212> PRT
<213> Trifolium repens

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<400> 164

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Met Val Lys Lys Ser Gly Gln Ile Val Pro Thr Ala Lys Tyr Cys Val
1           5           10           15

```

```

Thr Gly Ala Thr Gly Tyr Ile Gly Ser Trp Leu Val Glu Ala Leu Leu
20           25           30

```

```

Gln Arg Gly Cys Thr Val His Ala Thr Val Arg Asp Pro Glu Lys Ser
35           40           45

```

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Leu His Leu Leu Ser Leu Trp Lys Gly Ser Asp Gln Leu Arg Ile Phe
50           55           60

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```

Arg Ala Asp Leu Gln Glu Glu Gly Ser Phe Asp Asp Ala Val Lys Gly
65           70           75           80

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Cys Ile Gly Val Phe His Val Ala Ala Ser Met Gln Phe Asn Ile Ser
85 90 95

Asp Lys Glu Asn Thr Glu Asp Phe Val Glu Ala Asn Ile Ile Asp Pro
100 105 110

Ala Ile Lys Gly Thr Ile Asn Leu Leu Lys Ser Cys Leu Lys Ser Asn
115 120 125

Ser Val Lys Arg Val Val Phe Thr Ser Ser Ile Ser Thr Ile Thr Ala
130 135 140

Lys Asp Asn Asp Gly Lys Trp Lys Pro Ile Val Asp Glu Ser Cys Gln
145 150 155 160

Thr Lys Thr Glu Ile Leu Trp Asn Thr Gln Pro Ser Gly Trp Val Tyr
165 170 175

Ala Leu Ser Lys Leu His Ala Glu Glu Ala Ala
180 185

<210> 165
<211> 289
<212> DNA
<213> Trifolium repens

<220>
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<223> Any nucleotide

<400> 165
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60

ttaataattg gaagggagaa taaatagttg aaaaacacac agttggagtg tttttgtgtg
120

taaagaagct ataaaaatgga ggaaacaaca aagatgggtga aaaatagtg acaaaatgtt
180

cctatagcca aatactgtgt cacaggagcc acaggctata ttggttcatg gctgttgtaa
240

gctcttcttc aaagaggttg cactgttcat gctactgtta gagatcctg
289

<210> 166
<211> 591
<212> DNA
<213> Trifolium repens

<220>
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<222> (8)..(8)
<223> Any nucleotide

<220>
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<222> (23)..(24)
<223> Any nucleotides

<400> 166
agaagctnga aaatggagga agnnacaaag atggtgaaaa agagtggaca aattgttcct
60

actgccaaat actgtgttac aggagcaaca ggctatatattg gtccatggct tgttgaagct
120

cttcttcaaa gaggttgacac tgttcatgct actgttagag atcctgaaaa atcgttacac
180

ctcctgtcgt tgtggaaaagg tagtgaccaa ttgagaattt tccgtgcgga tttgcaagaa
240

gaagggaagtt tcgatgatgc cgtaaaagga tgtattgggtg tgttccatgt tgcagcttca
300

atgcaattca atattagtga caaagaaaac actgaggact ttgttgaagc aaatataatt
360

gaccttgcaa tcaaaggaac cataaatctt ctcaaatcat gcttgaaatc aaattcagtg
420

aaaagggttg ttttcacatc ttccataagt actattactg ctaaagacaa cgacggaaaa
480

tggaaaccta ttgttgatga atcttgccaa acaaaaaactg agattctgtg gaatacacaa
540

ccaagtggtat ggggttatgc actttcaaag ctctatgcag aagaagcggc t
591

<210> 167
<211> 572
<212> DNA
<213> *Trifolium repens*

<220>
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<222> (3)..(3)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (19)..(19)
<223> Any nucleotide

<400> 167
ctngaaaatg gaggaagcna caaagatggt gaaaaagagt ggacaaaattg ttcctactgc
60

caaatactgt gttacaggag caacaggcta tattggttca tggcttggtg aagctctttc
120

tcaaagaggt tgcaactgttc atgctactgt tagagatcct gaaaaatcgt tacacctcct
180

gtcgttgtagg aaaggtagtg accaattgag aatttttcgt gcggatttgc aagaagaagg
240
aagtttcgat gatgccgtaa aaggatgtat tgggtgtgtc catgttgcag cttcaatgca
300
attcaatatt agtgacaaag aaaacactga ggactttgtt gaagcaaata taattgaccc
360
tgcaatcaaa ggaaccataa atcttctcaa atcatgtctt aaatcaaatt cagtgaanaa
420
gggtgttttc acatcttcca taagtactat tactgctaaa gacaacgacg gaaaatggaa
480
acctattgtt gatgaattct gccaaacaaa aactgagatt ctgtggaata cacaaccaag
540
tggatgggtt tatgcacttt caaagcttca tg
572

<210> 168
<211> 976
<212> DNA
<213> *Trifolium repens*

<220>
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<222> (2)..(3)
<223> Any nucleotides

<220>
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<222> (5)..(5)
<223> Any nucleotide

<220>
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<222> (16)..(16)
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<223> Any nucleotide

<400> 168
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agtgaagtga aaacatacat gggttccgaa tcagaaatag tttgtgttac cggagcttca
120
gggttccatg gatcgtggct tggttatgaga cttatagagc gtggctacac ggttcgagcc

180

accgttcgcg acccagataa catgaagaag gtgaagcatt tgggtggaact gccgggtgca
240

aaaagcaaat tgtctctttg gaaggctgat cttgataaag aggggagttt tgatgaagca
300

attaagggtt gcacaggagt ttttcatggt gctacaccaa tggattttga atccaaggac
360

cctgagaatg aagtgataaa gctacaata aatggattaa tagacatact gaaagcatgc
420

gaaaaggcaa aaacagttag aaaattgggt ttcacatcat cggctggaac tgtggacgtt
480

actgaacatc caaagtctat tattgatgaa acatgctgga gtgacgttga cttttgccgt
540

agagtcaaga tgaccgggtg gatgtatttt gtttcaaaga ccctagcaga gcaagaagct
600

tggaagtatt cgaagagca caacatagac tttgtctcca tcattccacc tcttgttgtt
660

ggcccttttc ttatggcctc aatgccacct agtctaata cttgctcttc tcttatcaca
720

ggaatgagg ccattactc aatcataaag caagggcaat acgtccattt agatgacctt
780

tgcttctgctc atatatttct gtatgagaat ccaaagctc aaggagata catttgcgtg
840

tcacatgaag caaccattca tcaagttgca aaactatta aagaaaataa cccagagttc
900

aatgtcccaa caaaattcaa tgatatccca gatgaattgg aaattattaa attttctaaa
960

aagaagatca cagact
976

<210> 169

<211> 299

<212> PRT

<213> Trifolium repens

<400> 169

Met Gly Ser Glu Ser Glu Ile Val Cys Val Thr Gly Ala Ser Gly Phe
1 5 10 15

Ile Gly Ser Trp Leu Val Met Arg Leu Ile Glu Arg Gly Tyr Thr Val
20 25 30

Arg Ala Thr Val Arg Asp Pro Asp Asn Met Lys Lys Val Lys His Leu
35 40 45

Val Glu Leu Pro Gly Ala Lys Ser Lys Leu Ser Leu Trp Lys Ala Asp
50 55 60

Leu Asp Lys Glu Gly Ser Phe Asp Glu Ala Ile Lys Gly Cys Thr Gly
65 70 75 80

Val Phe His Val Ala Thr Pro Met Asp Phe Glu Ser Lys Asp Pro Glu
85 90 95

Asn Glu Val Ile Lys Pro Thr Ile Asn Gly Leu Ile Asp Ile Leu Lys
100 105 110

Ala Cys Glu Lys Ala Lys Thr Val Arg Lys Leu Val Phe Thr Ser Ser
115 120 125

Ala Gly Thr Val Asp Val Thr Glu His Pro Lys Ser Ile Ile Asp Glu
130 135 140

Thr Cys Trp Ser Asp Val Asp Phe Cys Arg Arg Val Lys Met Thr Gly
145 150 155 160

Trp Met Tyr Phe Val Ser Lys Thr Leu Ala Glu Gln Glu Ala Trp Lys
165 170 175

Tyr Ser Lys Glu His Asn Ile Asp Phe Val Ser Ile Ile Pro Pro Leu
180 185 190

Val Val Gly Pro Phe Leu Met Ala Ser Met Pro Pro Ser Leu Ile Thr
195 200 205

Ala Leu Ser Leu Ile Thr Gly Asn Glu Ala His Tyr Ser Ile Ile Lys
210 215 220

Gln Gly Gln Tyr Val His Leu Asp Asp Leu Cys Leu Ala His Ile Phe
225 230 235 240

Leu Tyr Glu Asn Pro Lys Ala Gln Gly Arg Tyr Ile Cys Cys Ser His
245 250 255

Glu Ala Thr Ile His Gln Val Ala Lys Leu Ile Lys Glu Lys Tyr Pro
260 265 270

Glu Phe Asn Val Pro Thr Lys Phe Asn Asp Ile Pro Asp Glu Leu Glu
275 280 285

Ile Ile Lys Phe Ser Lys Lys Lys Ile Thr Asp
290 295

<210> 170

<211> 586

<212> DNA

<213> Trifolium repens

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60

agtgaagtga aaacatacat gggttccgaa tcagaaatag tttgtgttac cggagcttca
120

tggttcacgc gatcgtggct tgttatgaga cttatagagc gtggctacac gggtcgagcc
180

accggttcgac acccagataa catgaagaag gtgaagcatt tgggtggaact gccgggtgca
240

aaaagcaaat tgtctctttg gaaggctgat cttgataaag aggggagttt tgatgaagca
300

attaaagggc gcacaggagt ttttcacggt gctacaccaa tggatttga atccaaggac
360

cctgagaatg aagtgataaa gctacaata aatggattaa tagacatact gaaagcatgc
420

gaaaaggcaa aaacagttaa aaaattgggt ttcacatcat cggctggaac tgtggacggt
480

actgaacatc caaagtctat tattgatgaa acatgctgga gtgacgttga cttttgccgt
540

agagtcaaga tgaccgggtg gatgtatttt gtttcaaaga ccctag

586

<210> 171
<211> 569
<212> DNA
<213> *Trifolium repens*

<220>
<221> misc_feature
<222> (24)..(24)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (209)..(209)
<223> Any nucleotide

<400> 171
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60

ctggagtgaa aatatacatg gggtctgaat cggaaatagt ttgtgttacc ggagcttcag
120

gtttcatcgg gtcgtggcct gttatgagac ttatggagca tggctacact gttcgagcca
180

ccgttcgtga ccagataaac atgaagaang tgaagcattt gctggaactg ccagggtgcaa
240

aaagcaaat gtctctttgg aaggctgac ttgataaaga ggggagttt gatgaagcaa
300

ttaagggtg cacaggagtt ttcatgttg ctacaccaat ggattttgag tccaaggacc
360

ctgagaatga agtgataaag cctacaataa acggattaat agacatactg aaagcatgag
420

aaaaggcaaa aacagttaga aaattggttt tcacatcatc ggctggaact gtggacgtta
480

ctgaacatcc aaagtctatt attgatgaaa catgctggag tgacgttgac ttttgccgta
540

gagtcaaaat gaccggttgg atgtatttt
569

<210> 172
<211> 493
<212> DNA
<213> *Trifolium repens*

<220>
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<222> (2)..(2)
<223> Any nucleotide

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<222> (19)..(19)

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<222> (161)..(161)

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<222> (322)..(322)

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<223> Any nucleotide

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<221> misc_feature

<222> (493)..(493)

<223> Any nucleotide

<400> 172

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60

gaagtgaana catacatggg ttccgaatca gaaatagttt gngttaccgg agcttcattg
120

ttnatcggat cgtggcttgt tatgagactt atanagcgtg nctacacggc tcgagccacc
180

gttcgcgacc cagataacat gaagaagggtg aagcatttgg tggaactgcc ggggtcaaaa
240

agcaaattgt ctctttggaa ggctgatctt gataaagagg ggagttttga tgaagcaatt
300

aaaggggtgca caggagtttt tnatgttgct acaccaatgg attttgaatc caaggaccct
360

gagaatgaag tgataaagcc tacaataaat ggattaatag acatactgaa agcatgcnaa
420

aaggcaaaaa cagttaaaaa attggttttc acatcatcgg ctgnaactgt ggacgttact
480

gaacatccaa agn

493

<210> 173

<211> 580

<212> DNA

<213> Trifolium repens

<220>

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<222> (2)..(2)

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<222> (13)..(13)

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<222> (19)..(19)

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 <222> (546)..(546)
 <223> Any nucleotide

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 <222> (576)..(576)
 <223> Any nucleotide

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 gaagtgaata catacatggg ttccgaatca gaaatagttt gtgttaccgg agcttcatgt
 120
 ttcacggat cgtggcttgt tatgagactt atagagcgtg gctacacggt tcgagccacc
 180
 gttcgcgacc cagataacat gaagaagggt aagcatttgg tgggaactgcc gggtgcaaaa
 240
 agcaaatgtt ctctttggaa ggctgatctt gataaagagg ggagttttga tgaagcaatt
 300
 aaagggtgca caggagtttt tcatgttgct acaccaatgg attttgaatc caaggaccct
 360
 gagaatgaag tgataaagcc tacaataaat ggattaatag acatactgaa agcatgcgaa
 420
 aaggcaaaaa cagttaaaaa attggttttc acatcatcgg ctggaactgt ggaagttact
 480
 gaacatccaa agtctattat tgatgaacaa tgctggagtg acgttgactt ttgccgtana
 540
 gtcaaanatga ccggctggat gtattttgtt tcaaanaccc

580

<210> 174
<211> 581
<212> DNA
<213> *Trifolium repens*

<220>
<221> misc_feature
<222> (2)..(2)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (13)..(13)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (22)..(22)
<223> Any nucleotide

<220>
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<222> (50)..(52)
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<222> (54)..(55)
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60

gaagtgaaaa catacatggg ttccgaatca gaaatagttt gtgttaccgg agcttcaggt
120

ttcatcggat cgtggcctgt tatgagactt atagagcgtg gctacacggt tcgagccacc
180

gttcgcgacc cagataacat gaagaagggt aagcatttgg tggaaactgcc ggggtcaaaa
240

agcaaatgt ctctttggaa ggctgatctt gataaagagg ggagtttga tgaagcaatt
300

aaagggtgca caggagtttt tcatgttgct acaccaatgg attttgaatc caaggaccct
360

gagaatgaag tgataaagcc tacaataaat ggattaatag acatactgaa agcatcgcaa
420

aaggcaaaaa cagttagaaa attggttttc acatcatcgg ctgggaactgt ggacgttact
480

gaacatccaa agtctattat tgatgaaaca tgctggagtg acgttgactt ttgccgtaga
540

gtcaagatga cgggttgat gtattttgtt tcaagaccc t
581

<210> 175
<211> 592
<212> DNA
<213> *Trifolium repens*

<220>
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<220>
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<222> (13)..(13)
<223> Any nucleotide

<220>
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<222> (16)..(16)
<223> Any nucleotide

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<222> (22)..(22)
<223> Any nucleotide

<220>
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<222> (36)..(36)
<223> Any nucleotide

<220>
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<222> (50)..(52)
<223> Any nucleotides

<220>
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<222> (54)..(55)
<223> Any nucleotides

<400> 175
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gaagtgaaaa catacatggg ttccgaatca gaaatagttt gtgttaccgg agcttcaggt
120

ttcatcggat cgtggcttgt tatgagactt atagagcgtg gctacacggt tcgagccacc
180

gttcgcgacc cagataacat gaagaagggtg aagcatttgg tggaaactgcc ggggtgcaaaa
240

agcaaatgtt ctctttggaa ggctgatctt gataaagagg ggagttttga tgaagcaatt
300

aaagggtgca caggagtttt tcattgttgc acaccaatgg attttgaatc caaggaccct
360

gagaatgaag tgataaagcc tacaataaat ggattaatag acatactgaa agcatcgcaa
420

aaggcaaaaa cagttagaaa attggttttc acatcatcgg ctggaactgt ggacgttact
480

gaacatccaa agtctattat tgatgaaaca tgctggagtg acgttgactt ttgccgtaga
540

gtcaagatga cgggttggtt gtattttgtt tcaaagacct tagcagagca ag
592

<210> 176
<211> 598
<212> DNA
<213> *Trifolium repens*

<220>
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<223> Any nucleotide

<220>
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<222> (13)..(13)
<223> Any nucleotide

<220>
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<222> (19)..(19)
<223> Any nucleotide

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<222> (22)..(22)
<223> Any nucleotide

<400> 176
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gaagtgaaaa catacatggg ttctgaatca gaaatagttt gtgttaccgg agcatcagggt
120

ttcatcggat cgtggcttgc tatgagactt atagagcgtg gctacacggt tcgagccact
180

gttcgcgacc cagataacat gaagaagggtg aagcatttgg tggaaactgcc ggggtgcaaaa
240

agcaaatgtt ctctttggaa ggctgatctt gataaagagg ggagttttga tgaagcaatt

300

aaagggtgca caggagtgtt tcatgttgct acaccaatgg attttgaatc caaggaccct
360

gagaatgaag tgataaagcc tacaataaat ggattaatag acatactgaa agcatgcgaa
420

aaggcaaaaa cagttaaaaa attggttttc acatcatcgg ctgggaactgt ggacgttact
480

gaacatccaa agtctattat tgatgaaaca tgctggagtg acgttgactt ttgccgtaga
540

gtcaagatga cgggttgat gtattttgtt tcaaagaccc tagcagagca agaagctt
598

<210> 177

<211> 576

<212> DNA

<213> *Trifolium repens*

<220>

<221> misc_feature

<222> (9)..(9)

<223> Any nucleotide

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<222> (12)..(12)

<223> Any nucleotide

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<222> (18)..(18)

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<220>

<221> misc_feature

<222> (21)..(21)

<223> Any nucleotide

<400> 177

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aagtgaatat atacatgggt tccgaatcgg aaatagtgtg tgttacogga gcttcaggtt
120

tcatcgggtc gtggcttggt atgagactta tggagcgcgg ctacacggtt cgagccactg
180

ttcgcgaccc agataacatg aagaaggtga agcatttgat ggaactgcgg ggtgcaaaaa
240

gcaaattgtc tctttggaag gctgatcttg ataaagaggg gagttttgat gaagcaatta
300

aagggtgcac aggagtgttt catgttgcta caccaatgga ttttgaatcc aaggaccctg
360

196/390

agaacgaagt gataaagcct acaataaatg gactaataga catactgaga gcattgtgaaa
420

aggcaaaaaac aattagaaga ttgggtttca catcatcagc tggaactgtg gacgttaactg
480

aacactcaaa atcaattggt gatgaaacat gttggagtga cggtgacttt tgcgctagag
540

tcaaaatgac cggttggatg tattttgttt caaaga
576

<210> 178

<211> 587

<212> DNA

<213> *Trifolium repens*

<220>

<221> misc_feature

<222> (12)..(12)

<223> Any nucleotide

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<222> (21)..(21)

<223> Any nucleotide

<400> 178

ggtcttccgt tnaatttaag nctatatgta aaaagaaaaa aagagtagag aagtgaagtg
60

aagtgaaaaac atacatgggt tctgaatcag aaatagtgtg tggtaccgga gcattcagggt
120

tcattcggatc gtggtttgtt atgagactta tagagcgtgg ctacacggtt cgagccactg
180

ttcgcgaccc agataacatg aagaaggatg agcatttggt ggaactgccg ggtgcaaaaa
240

gcaaatgtgc tctttggaag gctgatcttg ataaagaggg gagttttgat gaagcaatta
300

aagggtgcac aggagttttt catgttgcta caccaatgga ttttgaatcc aaggaccctg
360

agaatgaagt gataaagcct acaataaatg gattaataga catactgaaa gcattcgaaga
420

aggcaaaaaac agttaaaaaa ttgggtttca catcatcggc tggaactgtg gacgttactg
480

aacatccaaa gtctattatt gatgaaacat gctggagtga cggtgacttt tgcgctagag
540

tcaagatgac cggttggatg tattttgttt caaagaccct agcagag
587

<210> 179

<211> 630

<212> DNA

<213> *Trifolium repens*

<220>
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<222> (12)..(13)
<223> Any nucleotides

<220>
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<222> (21)..(21)
<223> Any nucleotide

<400> 179
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aagtgaaaaac atacatgggtg tctgaatcag aaatagtttg tgttaccgga gcatacagggt
120
tcatacggatc gtggcttggt atgagactta tagagcgtgg ctacacggtt cgagccactg
180
ttcgcgaccc agataacatg aagaagggtga agcatttggt ggaactgccg ggtgcaaaaa
240
gcaaatgtgc tctttggaag gctgatcttg ataaagaggg gagttttgat gaagcaatta
300
aagggtgcac aggagttttt catgttgcta caccaatgga ttttgaatcc aaggaccctg
360
agaatgaagt gataaagcct acaataaatg gattaataga catactgaaa gcatacgaaa
420
aggcaaaaaac agttaaaaaa ttggttttca catcatcggc tggaactgtg gacgttactg
480
aacatccaaa gtctattatt gatgaaacat gctggagtga cgttgacttt tgccgtagag
540
tcaagatgac cggttggatg tattttgttt caaagaccct agcagagcaa gaagcttgga
600
agtattttaa agagcacacaac atagattttg
630

<210> 180
<211> 579
<212> DNA
<213> Trifolium repens

<220>
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<222> (7)..(8)
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<220>
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<222> (11)..(11)
<223> Any nucleotide

<220>

<221> misc_feature
<222> (17)..(17)
<223> Any nucleotide

<220>
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<222> (20)..(20)
<223> Any nucleotide

<400> 180
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agtgaataa tacatgggtt ccgaatcgga aatagtttgt gttaccggag cttcagggtt
120

catcgggtcg tggcttggtta tgagacttat ggagcgcggc tacacgggtc gagccactgt
180

tgcgagacca gataacatga agaaggtgaa gcatttgatg gaactgccgg gtgcaaaaag
240

caaatgtgtc ctttggaagg ctgatcttga taaagagggg agttttgatg aagcaattaa
300

aggggtgcaca ggagtttttc atgttgctac accaatggat ttggaatcca aggaccotga
360

gaacgaagtg ataaagccta caataaatgg actaatagac atactgagag catgtgaaaa
420

ggcaaaaaca attagaagat tggttttcac atcatcagct ggaactgtgg acgtaactga
480

acactcaaaa tcaattgttg atgaaacatg ttggagtgac gttgactttt gccgtagagt
540

caaaatgacc ggttggtatg attttgttc aaagaccct
579

<210> 181
<211> 604
<212> DNA
<213> Trifolium repens

<220>
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<222> (12)..(12)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (17)..(17)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (20)..(20)
<223> Any nucleotide

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<222> (34)..(34)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (52)..(53)
<223> Any nucleotides

<220>
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<222> (55)..(57)
<223> Any nucleotides

<400> 181
gtcttcggtt cnatttnagn ctatattgaa aagnaataaa agagtagaga annnnntga
60
agtgaataca tacatgggtt ccgaatcaga aatagtttgt gttaccggag cttcaggttt
120
catcgggatcg tggcttggtta tgagacttat agagcgtggc tacacggttc gagccaccgt
180
tcgcagacca gataacatga agaaggtgaa gcatttgggt gaactgccgg gtgcaaaaaag
240
caaattgtct ctttgaagg ctgatcttga taaagagggg agttttgatg aagcaattaa
300
aggggtgcaca ggagtttttc atgttgctac accaatggat tttgaatcca aggaccctga
360
gaatgaagtg ataaagccta caataaatgg attaatagac atactgaaag catgcgaaaa
420
ggcaaaaaa gttagaaaat tggttttcac atcatcggct ggaactgtgg acgttactga
480
acatccaaag tctattattg atgaaacatg ctggagtgcac gttgactttt gccgtagagt
540
caagtagacc ggttggatgt attttgtttc aaagacccta gcagagcaag aagcttgga
600
gtat
604

<210> 182
<211> 586
<212> DNA
<213> Trifolium repens

<220>
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<222> (10)..(10)
<223> Any nucleotide

<400> 182
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gaaaatatac atgggttctg aatcggaat agtttgtgtt accggagctt caggtttcat
120

cgggtcgtgg ctgttatga gacttatgga gcgtggctac actgttcgag ccaccgttcg
180

tgaccagat aacatgaaga aggtgaagca ttgctggaa ctgccgggtg caaaaagcaa
240

attgtctctt tggaaggctg atcttgataa agaggggagt ttgatgaag caattaaagg
300

gtgcacagga gtttttcatg ttgtacacc aatggatttt gaatccaagg accctgagaa
360

tgaagtata aagcctacaa taaacggatt aatagacata ctgaaagcat gcgaaaaggc
420

aaaaacagtt agaaaattgg ttttcacatc atcggctgga actgtggacg ttaactgaaca
480

tccaaagtct attattgatg aaacatgctg gagtgcgctt gacttttgcc gtagagtgaa
540

aatgaccggg tggatgtatt ttgtttcaaa gaccctagca gagcag
586

<210> 183

<211> 586

<212> DNA

<213> *Trifolium repens*

<220>

<221> misc_feature

<222> (2)..(2)

<223> Any nucleotide

<220>

<221> misc_feature

<222> (11)..(11)

<223> Any nucleotide

<400> 183

gnagagaagt nacctggagt gaaaatatac atgggttctg aatcggaat agtttgtgtt
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accggagctt caggtttcat cgggtcgtgg ctgttatga gacttatgga gcgtggctac
120

actgttcgag ccaccgttcg tgaccagat aacatgaaga aggtgaagca ttgctggaa
180

ctgccgggtg caaaaagcaa attgtctctt tggaaggctg atcttgataa agaggggagt
240

ttgatgaag caattaaagg gtgcacagga gtttttcatg ttgtacacc aatggatttt
300

gagtccaagg accctgagaa tgaagtata aagcctacaa taaacggatt aatagacata
360

ctgaaagcat gcgaaaaggg aaaaacagtt agaaaattgg ttttcacatc atcggttgga
420

actgtggagc ttactgaaca tccaaagtct attattgatg aaacatgctg gagtgacgtt
480

gacttttgcc gtgagtgcaa aatgaccggg tggatgtatt ttgtttcaaa gaccctagca
540

gagcaagaag cttggaagta ttcgaaagag cacaacatga actttg
586

<210> 184

<211> 570

<212> DNA

<213> *Trifolium repens*

<220>

<221> misc_feature

<222> (10)..(11)

<223> Any nucleotides

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<222> (23)..(23)

<223> Any nucleotide

<400> 184

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60

gaactgtgga cgttactgaa catccaaagt ctattattga tgaacatgc tggagtgcg
120

ttgacttttg cgttagagtc aaaatgaccg gttggatgta ttttgttca aagaccctag
180

cagagcaaga agcttggaag tattcgaaag agcacaacat agactttgtc tccatcatc
240

cacctcttgt tgttggtccc ttcttatgg cctcaatgcc acctagtcta atcactgctc
300

ttctctttat cacaggaaat gaggccatt actcaatcat aaagcaaggg caatacgctc
360

atttagatga cctttgtctt gctcatatat ttctgtatga gaatccaaa gctcaaggga
420

gatacatttg ctgttcacat gaagcaacca ttcacaaagt tgcaaaactt attaaagaaa
480

aatacccaga gttcaatgtc ccaacaaaat tcaatgatat cccagatgaa ttggaaatta
540

ttaaaatttc taaaaagaag atcacagact
570

<210> 185

<211> 833

<212> DNA

<213> *Trifolium repens*

<220>
 <221> misc_feature
 <222> (3)..(3)
 <223> Any nucleotide

<220>
 <221> misc_feature
 <222> (34)..(34)
 <223> Any nucleotide

<400> 185
 ggcataaaaa actgcactag tgtgtataag ttntntagtg aaaaaagagt gtgtaaat
 60

acatcatggc tagtatcaaa caaattggaa acaagaaagc atgtgtgatt ggtggcactg
 120

gttttgttgc atctatgttg atcaaacagt tacttgaaaa gggttatgct gttaatacta
 180

ctgttagaga ccagatagtg cctaagaaaa tatctcacct agtggcactg caaagtttg
 240

gggaactgaa tctatttaga gcagacttaa cagttgaaga agattttgat gctcctatag
 300

caggatgtga gcttgttttt caacttgcta cacctgtgaa ctttgcttct caagatcctg
 360

agaatgacat gataaagcca gcaatcaaag gtgtgttgaa tgtgttgaaa gcaagtgcaa
 420

gagcaaaaga agtcaaaaga gttatcttaa catcttcggc agccgcggtg actataaatg
 480

aactcaaaagg gacaggtcat gttatggatg aaaccaactg gtcagatgtt gaattttctga
 540

acactgcaaa gccacccact tggggttatc ctgcttcaaa aatgctagct gaaaaggctg
 600

catggaaatt tgtgaagaa aatgacattg atctaatac tgtgatacct agtttaacaa
 660

ctggtccttc tctcacacca gatatcccat ctagtgttgg cttggcaatg tctotaataa
 720

caggcaatga tttcctcata aatgctctga aaggaaatgca atttctgtcg ggttcgttat
 780

ccatcactca tgttgaggat atttgccgag ctcatatatt tctggcagag aag
 833

<210> 186
 <211> 256
 <212> PRT
 <213> Trifolium repens

<400> 186

Met Ala Ser Ile Lys Gln Ile Gly Asn Lys Lys Ala Cys Val Ile Gly
 1 5 10 15

Gly Thr Gly Phe Val Ala Ser Met Leu Ile Lys Gln Leu Leu Glu Lys
20 25 30

Gly Tyr Ala Val Asn Thr Thr Val Arg Asp Pro Asp Ser Pro Lys Lys
35 40 45

Ile Ser His Leu Val Ala Leu Gln Ser Leu Gly Glu Leu Asn Leu Phe
50 55 60

Arg Ala Asp Leu Thr Val Glu Glu Asp Phe Asp Ala Pro Ile Ala Gly
65 70 75 80

Cys Glu Leu Val Phe Gln Leu Ala Thr Pro Val Asn Phe Ala Ser Gln
85 90 95

Asp Pro Glu Asn Asp Met Ile Lys Pro Ala Ile Lys Gly Val Leu Asn
100 105 110

Val Leu Lys Ala Ser Ala Arg Ala Lys Glu Val Lys Arg Val Ile Leu
115 120 125

Thr Ser Ser Ala Ala Val Thr Ile Asn Glu Leu Lys Gly Thr Gly
130 135 140

His Val Met Asp Glu Thr Asn Trp Ser Asp Val Glu Phe Leu Asn Thr
145 150 155 160

Ala Lys Pro Pro Thr Trp Gly Tyr Pro Ala Ser Lys Met Leu Ala Glu
165 170 175

Lys Ala Ala Trp Lys Phe Ala Glu Glu Asn Asp Ile Asp Leu Ile Thr
180 185 190

Val Ile Pro Ser Leu Thr Thr Gly Pro Ser Leu Thr Pro Asp Ile Pro
195 200 205

Ser Ser Val Gly Leu Ala Met Ser Leu Ile Thr Gly Asn Asp Phe Leu
210 215 220

Ile Asn Ala Leu Lys Gly Met Gln Phe Leu Ser Gly Ser Leu Ser Ile
225 230 235 240

Thr His Val Glu Asp Ile Cys Arg Ala His Ile Phe Leu Ala Glu Lys
245 250 255

<210> 187

<211> 576

<212> DNA

<213> Trifolium repens

<220>
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<222> (3)..(3)
<223> Any nucleotide

<220>
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<222> (34)..(34)
<223> Any nucleotide

<400> 187
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acatcatggc tagtatcaaa caaattggaa acaagaaagc atgtgtgatt ggtggcactg
120

gttttggc atctatgttg atcaaacagt tacttgaaaa gggttatgct gttaatacta
180

ctgcttagaga ccagatagt cctaagaaaa tatctcacct agtggcactg caaagtttgg
240

gggaactgaa tctatttaga gcagacttaa cagtggaaga agattttgat gctcctatag
300

caggatgtga gcttggtttt caacttgcta cacctgtgaa ctttgcttct caagatcctg
360

agaaatgacat gataaagcca gcaatcaaag gtgtgttgaa tgtgttgaaa gcaagtgcaa
420

gagcaaaaga agtcaaaaga gttatcttaa catcttcggc agccgcgggt actataaatg
480

aactcaaaag gacaggtcat gttatggatg aaaccaactg gtcagatggt gaattttotga
540

acactgcaaa gccacccact tggggttatc ctgctt
576

<210> 188
<211> 580
<212> DNA
<213> *Trifolium repens*

<220>
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<222> (3)..(3)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (5)..(5)
<223> Any nucleotide

<220>
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<222> (34)..(35)
<223> Any nucleotides

<220>
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<222> (580)..(580)
<223> Any nucleotide

<400> 188
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acatcatggc tagtatcaaa caaattggaa acaagaaagc atgtgtgatt ggtggcactg
120
gttttggttc atctatgttg atcaaacagt tacttgaaaa gggttatgct gttaatacta
180
ctgtagaga cccagatagt cctaagaaaa tatctcacct agtggcactg caaagtttgg
240
gggaactgaa tctatttaga gcagacttaa cagttgaaga agattttgat gctcctatag
300
caggatgtga gcttgttttt caacttgcta cacctgtgaa ctttgcttct caagatcctg
360
agaatgacat gataaagcca gcaatcaaa gtgtgttgaa tgtgttgaaa gcaagtgcaa
420
gagcaaaaga agtcaaaaga gttatcttaa catcttcggc agcccggtg actataaatg
480
aactcaaaagg gacaggtcat gttatggatg aaaccaactg gtcagatggt gaatttctga
540
acactgcaaa gccaccact tggggttatc ctgcttcaan
580

<210> 189
<211> 578
<212> DNA
<213> *Trifolium repens*

<220>
<221> misc_feature
<222> (14)..(14)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (29)..(30)
<223> Any nucleotides

<400> 189
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atggctagta tcaacaaaat tggaaacaag aaagcatgtg tgattgggtg cactggtttt
120
gttgcatcta tgttgatcaa acagtactt gaaaagggtt atgctgttaa tactactgtt
180

agagacccag atagtccaa gaaaatatct cacctagtgg cactgcaaaag tttgggggaa
240

ctgaatctat ttagagcaga cttaacagtt gaagaagatt ttgatgctcc tatagcagga
300

tgtgagcttg tttttcaact tgctacacct gtgaactttg cttctcaaga tcttgagaat
360

gacatgataa agccagcaat caaagggtgtg ttgaatgtgt tgaaagcaag tgcaagagca
420

aaagaagtca aaagagttat cttaacatct tggcagccg cgggtgactat aaatgaactc
480

aaagggacag gtcattgtat ggaatgaaac aactggctcg atgttgaaatt tctgaacact
540

gcaaaagccac ccactggggg ttatcctgct tcaaaaaat
578

<210> 190

<211> 619

<212> DNA

<213> *Trifolium repens*

<400> 190

taaaaactgc actagtgtgt ataagtttct tggatgaaaa agagtttgta aattaacatc
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atggcttagta tcaaaacaaat tggaaacaag aaagcatgtg tgattggtgg cactggtttt
120

gttgcattcta tgttgatcaa gcagttactt gaaaagggtt atgtgtgtaa tactaccgtt
180

agagacccag atagccctaa gaaaatatct cacctagtgg cactgcaaaag tttgggggaa
240

ctgaatctat ttagagcaga cttaacagtt gaagaagatt ttgatgctcc tatagcagga
300

tgtgaacttg tttttcaact tgctacacct gtgaactttg cttctcaaga tcttgagaat
360

gacatgataa agccagcaat caaagggtgtg ttgaatgtgt tgaaagcaat tgcaagagca
420

aaagaagtta aaagagttat cttaacatct tggcagccg cgggtgactat aaatgaactc
480

aaagggacag gtcattgtat ggaatgaaac aactggctcg atgttgaaatt tctcaacact
540

gcaaaaccac ccactggggg ttatcctgct tcaaaaaatgc tagctgaaaa ggctgcatgg
600

aaatttgctg aagaaaatg
619

<210> 191

<211> 619

<212> DNA

<213> Trifolium repens

<220>

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<223> Any nucleotide

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<221> misc_feature

<222> (614)..(614)

<223> Any nucleotide

<400> 191

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60

tatcaaacaa attggaaaca agaaagcatg tgtgattggt ggcactgggt ttgttgcac
120

tatgttgatc aagcagttac ttgaaaaggg ttatgctggt aatactaccg ttagagaccc
180

agatagccct aagaaaatat ctcacctagt ggcactgcaa agtttggggg aactgaatct
240

atttagagca gacttaacag ttgaagaaga ttttgatgct cctatagcag gatgtgaact
300

tggtttttcaa ctgtctacac ctgtgaactt tgctttctcaa gatcctgaga atgacatgat
360

aaagccagca atcaaagggtg tggtgaatgt gttgaaagca attgcaagag caaaagaagt
420

taaaagagtt atcttaacat cttcggcagc cgcggtgact ataaatgaac tcaaaggggac
480

aggtcactgt atggatgaaa ccaactggtc tgatgttgaa tttctcaaca ctgcaaaac
540

accacactgg gggtatcctg cctcaaaaaa gctagctgaa aaggctgcat ggaaatttgc
600

tgaagaaaaa gacnttgat
619

<210> 192
<211> 586
<212> DNA
<213> *Trifolium repens*

<220>
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<222> (2)..(2)
<223> Any nucleotide

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<222> (4)..(4)
<223> Any nucleotide

<220>
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<222> (23)..(23)
<223> Any nucleotide

<400> 192
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60

gcaggatgtg agcttggttt tcaacttgct acacctgtga cctttgttc tcaagatcct
120

gagaatgaca tgataaagcc agcaatcaaa ggtgtgttga atgtgttgaa agcaagtgca
180

agagcaaaag aagtcaaaag agttatctta acatcttcgg cagccgcggt gactataaat
240

gaactcaaag ggacaggtca tgttatggat gaaaccaact ggtcagggtg tgaatttctg
300

aaactgtcaa agccacccac ttgggggttat cctgcttcaa aaatgctagc tgaagggtc
360

gcatggaaat ttgctgaaga aaatgacatt gatctaatac ctgtgatacc tagtttaaca
420

actggctcct ctctcacacc agatatccca tctagtgttg gcttggcaat gtctctaata
480

acaggcaatg atttcctcat aaatgctctg aaaggaatgc aatttctgtc gggttcgtta
540

tccatcactc atgttgagga tatttgcoga gctcatatat ttctgg
586

<210> 193
<211> 567
<212> DNA
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<220>
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<223> Any nucleotide

<400> 193
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gctacacctg tgacctttgc ttctcaagat cctgagaatg acatgataaa gccagcaact
120
aaaggtgtgt tgaatgtgtt gaaagcaagt gcaagagcaa aagaagctaa aagagttatc
180
ttaacatctt cggcagocgc ggtgactata aatgaactca aagggacagg tcattgtatg
240
gatgaacca actggtcaga tgttgaattt ctgaacctg caaagccacc cacttggggg
300
tatcctgctt caaaaatgct agctgaaaag gctgcatgga aatttgctga agaaaatgac
360
attgatctaa tcactgtgat acctagttaa acaactggtc cttctctcac accagatata
420
ccatctagtg ttggcttggc aatgtctcta ataacaggca atgatttctc cataaatgct
480
ctgaaaggaa tgcaatttct gtcgggttcg ttatccatca ctcatgttga ggatatttgc
540
cgagctcata tatttctggc agagaag
567

<210> 194
<211> 597
<212> DNA
<213> *Trifolium repens*

<400> 194
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aaagagatgg atgtcttggg tccacgtttt gatagcatat ttgaaaaaat gattgttgaa
120
cgtaagaaga aggaagtgga ggggaaagaa aatgaaagta aggattttct gcagtttttg
180
ttgaatttga aggatgaggg tgattctaag actccattca caattacca tgtaaggct
240
ctactcatgg acatggttgt ggggtgatca gacacatcct ccaacacaat tgagtttgca
300
ttggcagaaa tgatgaacaa ccagaagta atgaggaagg ttcaagagga attagaagat
360
gtagtgtggga aagataactt agtagaagag tctcacattc ataagctacc ctacttgcac
420

210/390

gcagtgatga aagaaacact tcgtttacac ccagcacttc cacttttagt ccctcactgt
480

ccaagtga aa ccaccaatgt tggaggctac acaattccaa agggatctcg tgtgtttgtg
540

aacgtttggg ctattcatag agacccttcc atttgggaga aaccactaga atttgat
597

<210> 195

<211> 199

<212> PRT

<213> *Trifolium repens*

<400> 195

Gly Thr Asn Leu Ser Asp Phe Phe Pro Gly Leu Ala Arg Phe Asp Leu
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Gln Gly Val Val Lys Glu Met Asp Val Leu Val Pro Arg Phe Asp Ser
20 25 30

Ile Phe Glu Lys Met Ile Gly Glu Arg Lys Lys Lys Glu Val Glu Gly
35 40 45

Lys Glu Asn Glu Ser Lys Asp Phe Leu Gln Phe Leu Leu Asn Leu Lys
50 55 60

Asp Glu Gly Asp Ser Lys Thr Pro Phe Thr Ile Thr His Val Lys Ala
65 70 75 80

Leu Leu Met Asp Met Val Val Gly Gly Ser Asp Thr Ser Ser Asn Thr
85 90 95

Ile Glu Phe Ala Leu Ala Glu Met Met Asn Asn Pro Glu Val Met Arg
100 105 110

Lys Val Gln Glu Glu Leu Glu Asp Val Val Gly Lys Asp Asn Leu Val
115 120 125

Glu Glu Ser His Ile His Lys Leu Pro Tyr Leu His Ala Val Met Lys
130 135 140

Glu Thr Leu Arg Leu His Pro Ala Leu Pro Leu Leu Val Pro His Cys
145 150 155 160

Pro Ser Glu Thr Thr Asn Val Gly Gly Tyr Thr Ile Pro Lys Gly Ser
165 170 175

Arg Val Phe Val Asn Val Trp Ala Ile His Arg Asp Pro Ser Ile Trp
180 185 190

Glu Lys Pro Leu Glu Phe Asp

195

<210> 196
<211> 700
<212> DNA
<213> *Trifolium repens*

<220>
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<222> (2)..(2)
<223> Any nucleotide

<220>
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<222> (10)..(10)
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<222> (22)..(22)
<223> Any nucleotide

<220>
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<222> (698)..(698)
<223> Any nucleotide

<400> 196
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atcactcaat accaaacott cctttacaaa gaactttcta tatccttttt cattttcttg
120

ataacccatt tcatcataag ttttctcttc aaaaaaaatc tcaaaaaact tccaccaggc
180

ccaaaagggt ttccagttgt tgggtgcactc ccactaatgg gatccatgcc tcatgttacc
240

ctattcaaaa tgtcacaaaa atatggtccc ataattgtacc taaaaatggg atcaataaac
300

atgggtgtag catcaactcc ttcttcagcc aaagcatttc tcaaaacact tgacctaaat
360

ttctcaata gaccgccgaa cgctggcgca actcacctag cttatgattc acaagacttg
420

gttttgcgag actatggatc taggtggaaa ttacttagga aactaagtaa cttgcacatg
480

ctcggcgcaa aagccctcga aaattggtcg aaagtctctg agattgaaat gggtcacatg
540

attcgtacaa tgtacgattg tagcaagaaa gacgaatcgg ttgtgtgtgc cgaaatgttg
600

acatatgcta tggccaatat gataggtcaa gttatattga gtctgcgcgt gttcagagaca
660

aaaggttagtg actcaaatga atttaaggat atgggttgntg
700

<210> 197
<211> 216
<212> PRT
<213> Trifolium repens

<220>
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<222> (216)..(216)
<223> Any amino acid

<400> 197

Met Val Met Ile Thr Gln Tyr Gln Thr Phe Leu Tyr Lys Glu Leu Ser
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Ile Ser Phe Phe Ile Phe Leu Ile Thr His Phe Ile Ile Ser Phe Leu
20 25 30

Phe Lys Lys Asn Leu Lys Lys Leu Pro Pro Gly Pro Lys Gly Phe Pro
35 40 45

Val Val Gly Ala Leu Pro Leu Met Gly Ser Met Pro His Val Thr Leu
50 55 60

Phe Lys Met Ser Gln Lys Tyr Gly Pro Ile Met Tyr Leu Lys Met Gly
65 70 75 80

Ser Asn Asn Met Val Val Ala Ser Thr Pro Ser Ser Ala Lys Ala Phe
85 90 95

Leu Lys Thr Leu Asp Leu Asn Phe Ser Asn Arg Pro Pro Asn Ala Gly
100 105 110

Ala Thr His Leu Ala Tyr Asp Ser Gln Asp Leu Val Phe Ala Asp Tyr
115 120 125

Gly Ser Arg Trp Lys Leu Leu Arg Lys Leu Ser Asn Leu His Met Leu
130 135 140

Gly Gly Lys Ala Leu Glu Asn Trp Ser Lys Val Arg Glu Ile Glu Met
145 150 155 160

Gly His Met Ile Arg Thr Met Tyr Asp Cys Ser Lys Lys Asp Glu Ser
165 170 175

Val Val Val Ala Glu Met Leu Thr Tyr Ala Met Ala Asn Met Ile Gly
180 185 190

Gln Val Ile Leu Ser Arg Arg Val Phe Glu Thr Lys Gly Ser Asp Ser

195

200

205

Asn Glu Phe Lys Asp Met Val Xaa
210 215

<210> 198
<211> 584
<212> DNA
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<222> (10)..(10)
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<223> Any nucleotide

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atcactcaat accaaacctt ccttttcaaa gaactttcta tctccttttt cattttcttg
120

ataaccgggt tcatcataag ttttctcttc aaaaaaaatc tcaaaaaact tccaccaggc
180

ccaaagggtt ttccagttgt tgggtgacct ccactaatgg gatccatgcc tcatgttacc
240

ctattcaaaa tgtcacaaaa atatgggtccc ataattgtacc taaaaatggg atcaaatagc
300

atggttgtag catcaactcc ttcttcagcc aaagcatttc tcaaaacact tgacctaaat
360

ttctccaata gacogccgaa cgctggcgcg actocactag cttatgattc acaagacttg
420

gttttcgccc actatggatc taggtggaaa ttacttagga aactaagtaa cttgcacatg
480

ctcggcgcaa aagccctcga agattggtcg aaagttcgtg agattgaaat gggtcacatg
540

attcgtacaa tgtatgattg tagcaagaaa gacgaatccg ttgt
584

<210> 199
<211> 694
<212> DNA
<213> *Trifolium repens*

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<222> (2)..(2)
<223> Any nucleotide

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<222> (16)..(16)
<223> Any nucleotide

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<222> (20)..(21)
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<222> (692)..(692)
<223> Any nucleotide

<400> 199
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60

caacacacaaa ctttccttta caaagaactt tctatattct ttttcatttt cttgataaac
120

catttcacat ttagttttct cttcaaaaaa aatctcaaaa aactccacc aggcccaaaa
180

ggttttccag ttgttggtgc actcccacta atgggatcca tgcctcatgt tacctatttc
240

aaaaatgtcac aaaaatatgg tcctataatg tacctaaaaa tgggatcaaa taacatgggt
300

gtagcatcaa ctcttcttc agccaaagca tttctcaaaa cacttgacct aaatttctcc
360

aataggccgg cgaacgctgg cgcaactcac ctagcttatg atccacaaga cttgggttttc
420

gccgactatg gatctagggt gaaattactt aggaactaa gtaacttgca catgctcggc
480

ggaaaagccc ttgaaaattg gtcgaaagt cgtgagattg aaatgggtca catgattcgt
540

acaatgtacg attgtagcaa gaaagacgaa tccgttggtg tggccgaaat gttgacatat
600

gctatggcca atatgatagg tcaagttata ttgagtcgtc gcgtgttcga gacaaaagg
660

agtgactcaa atgaatttaa ggatatgggt gntg
694

<210> 200
<211> 580
<212> DNA

<213> Trifolium repens

<220>

<221> misc_feature

<222> (2)..(2)

<223> Any nucleotide

<220>

<221> misc_feature

<222> (14)..(14)

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<222> (16)..(16)

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<222> (44)..(44)

<223> Any nucleotide

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<221> misc_feature

<222> (55)..(56)

<223> Any nucleotides

<400> 200

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60

ataccaaaac ttcccttttca aagaactttc tatctccttt ttcattttct tgataaccgc
120

tttcatcata agtcttctct tcaaaaaaaa tctcaaaaaa cttccaccag gcccaaaggg
180

ttttccagtt gttggtgcac tcccactaat gggatccatg cctcatgtta cctatttcaa
240

aatgtcacia aaatatggtc ccataatgta cctaaaaaat ggatcaaata acatggttgt
300

agcatcaact ccttcttcag ccaaagcatt tctcaaaaca cttgacctaa atttctccaa
360

tagaccgcgc aacgctggcg cgactcacct agcttatgat tcacaagact tgggttttcgc
420

cgactatgga tctagggtga aattgcttag gaaactaagt aactgcaca tgctcggcgg
480

aaaagccctc gaagattggc cgaaagttcg cgagattgag atgggtcaca tgattcgtac
540

aatgtacgat tgtagcaaga aagacgaata tgttgttgtg
580

<210> 201

<211> 574

<212> DNA
<213> *Trifolium repens*

<220>
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<222> (8)..(8)
<223> Any nucleotide

<220>
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<222> (12)..(12)
<223> Any nucleotide

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<223> Any nucleotide

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<223> Any nucleotide

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<222> (569)..(569)
<223> Any nucleotide

<220>
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<222> (572)..(572)
<223> Any nucleotide

<400> 201
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60

caaaccttcc tttaacaaga actttctata tcctttttca ttttcttgat aaccacatttc
120

atcattagtgt ttctcttcaa aaaaaatctc aaaaaacttc caccaggccc aaaagggtttt
180

ccagttgttg gtgcactccc actaatggga tccatgcctc atgttacccct attcaaaatg
240

tcacaaaaat atggtcctat aatgtaccta aaatgggat caaataacat gggtgtagca
300

tcaactcctt cttcagccaa agcattttctc aaacacttg acctaaattt ctccaatagg
360

ccggcgaaac ctggcgcaac tcacctagct tatgatccac aagacttggt ttteggcgac
420

tatggatcta ggtggaatt acttaggaaa ctaagtaact tgcacatgct cggcggaaaa
480

gcccttgaaa attggtcgaa agttcgtgag attgaaatgg gtcacatgat tcgtacaatg
540

tacgattgta gcaagaaga cgaatccgnt gntg
574

<210> 202
<211> 1261
<212> DNA
<213> *Trifolium repens*

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<222> (7)..(7)
<223> Any nucleotide

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<222> (43)..(43)
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<222> (92)..(93)
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<222> (96)..(96)
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<222> (957)..(957)
<223> Any nucleotide

<400> 202
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60

accacaaca ccaaaacoga gtcggtttcc tnntcnaaca tggcaccaag ccaaaactta
120

agttatctct cacaacaaaa cactcttgag tcaagtttgc ttagggaaga agatgagcgt
180

ccaaaagttg cctacaataa cttcagcaac gagattccaa tcatttctct tgctggaatt
240

gatgaggttg atggtcgtag aacagagata tgtaacaaga ttgttgaagc ttgtgagaat

300

tggggtattt ttcagggtgt tgatcatggt gttgatacaa aacttgtttc tgagatgacc
360

cgttttgcta gagagttttt tgccttgcca ccggaagaga agtccgggtt tgacatgtcc
420

ggtggtaaaa aggggtggtt cattgtctct agtcatctcc aaggagaagc agtgaaggat
480

tgagagagac tagtgacata ttttctac ccaattaaac aaagagatta ttcaagggtg
540

ccagacaagc cagaaggatg gaaagaggta acagaaaaat acagtgaaaa cctaataaat
600

ttagcttgca aactattgga agttttatca gaagcaatgg gtttagaaaa agaagctcta
660

acaaaagcat gtgttgatat ggatcaaaaa gttgttataa attattaccc aaaatgocct
720

gaacctgacc tcacacttgg ccttaaacgt cacactgacc ctggcacaat tactcttttg
780

cttcaagatc aagttggtgg ccttcaagct accaaagata atggtaagac gtggattaca
840

gttcaaccag ttgaagggtc tttgttgtt aatcttggag accatgggtc ctatctaagt
900

aatggacggt tcaaaaatgc tgaccaccaa gcagtgggtga attcgaaact cagccgntta
960

tcaatagcaa catctcaaaa tccagctccc gatgcaactg tatacccttt gaagattaga
1020

gagggtgaaa aatctgtgtt ggaagaacca atcacttttg ctgaaatgta tagaaggaag
1080

atgaccaaag accttgaaat tgctaggatg aagaagttgg ctaaggaaca acaacttagg
1140

gacttgagg agaaacaagac taaatatgag gccaaacctt tgaatgagat cttgtcttaa
1200

ttaattatgc ttaatttaaa taattaataa atttttagact taatttacat ataataattt
1260

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1261

<210> 203

<211> 366

<212> PRT

<213> Trifolium repens

<220>

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<222> (286)..(286)

<223> Any amino acid

<400> 203

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Asn Asn Phe Ser Asn Glu Ile Pro Ile Ile Ser Leu Ala Gly Ile Asp
35 40 45

Glu Val Asp Gly Arg Arg Thr Glu Ile Cys Asn Lys Ile Val Glu Ala
50 55 60

Cys Glu Asn Trp Gly Ile Phe Gln Val Val Asp His Gly Val Asp Thr
65 70 75 80

Lys Leu Val Ser Glu Met Thr Arg Phe Ala Arg Glu Phe Phe Ala Leu
85 90 95

Pro Pro Glu Glu Lys Leu Arg Phe Asp Met Ser Gly Gly Lys Lys Gly
100 105 110

Gly Phe Ile Val Ser Ser His Leu Gln Gly Glu Ala Val Lys Asp Trp
115 120 125

Arg Glu Leu Val Thr Tyr Phe Ser Tyr Pro Ile Lys Gln Arg Asp Tyr
130 135 140

Ser Arg Trp Pro Asp Lys Pro Glu Gly Trp Lys Glu Val Thr Glu Lys
145 150 155 160

Tyr Ser Glu Asn Leu Met Asn Leu Ala Cys Lys Leu Leu Glu Val Leu
165 170 175

Ser Glu Ala Met Gly Leu Glu Lys Glu Ala Leu Thr Lys Ala Cys Val
180 185 190

Asp Met Asp Gln Lys Val Val Ile Asn Tyr Tyr Pro Lys Cys Pro Glu
195 200 205

Pro Asp Leu Thr Leu Gly Leu Lys Arg His Thr Asp Pro Gly Thr Ile
210 215 220

Thr Leu Leu Leu Gln Asp Gln Val Gly Gly Leu Gln Ala Thr Lys Asp
225 230 235 240

Asn Gly Lys Thr Trp Ile Thr Val Gln Pro Val Glu Gly Ala Phe Val
245 250 255

Val Asn Leu Gly Asp His Gly His Tyr Leu Ser Asn Gly Arg Phe Lys

260
 Asn Ala Asp His Gln Ala Val Val Asn Ser Asn Tyr Ser Xaa Leu Ser
 275 280 285
 Ile Ala Thr Phe Gln Asn Pro Ala Pro Asp Ala Thr Val Tyr Pro Leu
 290 295 300
 Lys Ile Arg Glu Gly Glu Lys Ser Val Leu Glu Glu Pro Ile Thr Phe
 305 310 315 320
 Ala Glu Met Tyr Arg Arg Lys Met Thr Lys Asp Leu Glu Ile Ala Arg
 325 330 335
 Met Lys Lys Leu Ala Lys Glu Gln Gln Leu Arg Asp Leu Glu Glu Asn
 340 345 350
 Lys Thr Lys Tyr Glu Ala Lys Pro Leu Asn Glu Ile Phe Ala
 355 360 365

<210> 204
 <211> 585
 <212> DNA
 <213> *Trifolium repens*

<220>
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 120
 tctcacaaca aaacactctc gagtcaagtt tcgttaggga agaagatgag cgtccaaaaa
 180
 ttgcctacaa taacttcagc aacgagattc caatcatttc tcttgctgga attgatgagg
 240
 ttgatggtcg tagaacagag atatgtaaca agattgttga agcttggtgag aattggggta
 300
 tttttcaggt tgttgatcat ggtgttgata caaaacttgt tcttgagatg acccggtttg
 360
 cttagagagtt ttttgetttg ccaccggaag agaagctccg gtttgacatg tccggtggtg
 420
 aaaagggtgg ttctcattgc tctagtcac ttcaaggaga agcagtgga gattggagag
 480
 agctagtgc atatttttca taccgaatta aacaaagaga ttattcaagg tggccagaca
 540

221/390

agccagaagg atggaaagag gtaacagaaa aatacagtga aaacct
586

<210> 205
<211> 597
<212> DNA
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<220>
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<222> (5)..(5)
<223> Any nucleotide

<220>
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<222> (7)..(7)
<223> Any nucleotide

<220>
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<222> (31)..(31)
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120

acaaaagact cttgagtcaa gtttcgttag ggaagaagat gagcgtccaa aagttgccta
180

caataacttc agcaacgaga ttccaatcat ttctcttgct ggaattgatg aggttgatgg
240

tcgcagaaca gagatatgta acaagattgt tgaagcttgt gagaattggg gtatttttca
300

ggttgttgat catggtgttg atacaaagct tgtttctgag atgactcgtt ttgctagaga
360

gttttttgct ttgccgccgg aagagaagct ccggtttgac atgtccgggt gtaaaaaggg
420

tggtttcatt gtctctagtc atctccaagg agaagcagtg aaagattgga gagagctagt
480

gacatatttt tcatacccaa ttaacaaaag agattattca aggtggccag acaagccaga
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120
gttatctctc acaacaaaaac actctogagt caagtttcgt tagggaagaa gatgagcgtc
180
caaaagttgc ctacaataac ttoagcaacg agattccaat catttctott gotggaattg
240
atgagggtta tggctgtaga acagagatat gtaacaagat tgttgaagct tgtgagaatt
300
ggggatatttt tcagggttgtt gatcatgggtg ttgatacaaa acttgtttct gagatgacct
360
gttttgctag agagtttttt gctttgccac cggaagagaa gctccggttt gacatgtccg
420
gttgtaaaaa ggggtggttc attgtctcta gtcatcttca aggagaagca gtgaaggatt
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ggagagagct agtgacatat ttttcatacc caattaaaca aagagattat tcaagggtggc

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tagct
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ttatctctca caacaaaaca ctctcgagtc aagtttcgtt agggagaag atgagcgtcc
180
aaaagttgcc tacaataact tcagcaacga gattecaatc atttctcttg ctggaattga
240
tgaggttgat ggtcgtagaa cagagatatg taacaagatt gttgaagctt gtgagaattg
300
gggtattttt caggttggtg atcatggtgt tgatacaaaa cttgtttctg agatgacccg
360
ttttgctaga gagttttttg ctttgccacc ggaagagaag ctccggttg acatgtccgg
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tggtaaaaag ggtggmttna ttgtctgtan tngtntccna ggacaacnng ngnaggattg
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120

agggaagaag atgagcgtcc aaaagttgcc tacaataact tcagcaacga gattccaatc
180

atttctcttg ctggaattga tgaggttgat ggctgtagaa cagagatatg taacaagatt
240

gttgaagctt gtgagaattg gggtattttt caggttgttg atcatggtgt tgatacaaaa
300

cttgtttctg agatgaccog ttttgctaga gagttttttg ctttgccacc ggaagagaag
360

ctccggtttg acatgtccgg tggtaaaaag ggtggtttca ttgtctctag tcattctcaa
420

ggagaagcag tgaaggattg gagagagcta gtgacatatt tttcataccc aattaaacaa
480

agagattatt caaggtggcc agacaagcca gaaggatgga aagaggtaac agaaaaatac
540

agtgaaaacc taatgaattt agcttgcaaa ctattggaag ttttatcaga agcaatgggt
600

ttagaaaaag aagctctaac aaaagcatgt gttgatatgg atcaaaaagt tgttataaat
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120
aagatgagcg tccaaaagtt gcctacaata acttcagcaa cgagattcca atcattttctc
180
ttgctggaat tgatgagggt gatggtcgta gaacagagat atgtaacaag attgttgaag
240
cttgtgagaa ttgggggtatt tttcagggtg ttgatcatgg tgttgataca aaactgttt
300
ctgagtgac cggttttgct agagagtttt ttgctttgcc accggaagag aagctccgg
360
ttgacatgtc cgggtgtaaa aagggtggtt tcattgtctc tagtcatctc caaggagaag
420
cagtgaagga ttggagagag ctagtgacat atttttcata ccaattaaa caaagagatt
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573

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120

agaagatgag cgtccaaaag ttgcctacaa taacttcagc aacgagattc caatcatttc
180

tcttgctgga attgatgagg ttgatggtcg tagaacagag atatgtaaca agattgttga
240

agcttgtgag aattggggta ttttccaggt tgttgatcat ggtgttgata caaaacttgt
300

ttctgagatg acccgttttg ctgagagatt ttttgctttg ccaccggaag agaagctccg
360

gtttgacatg tccggtggta aaaagggtgg ttctattgtc tctagtcac tccaaggaga
420

agcagtgaa gattggagag agctagtgc atatttttca tacccaatta aacaaagaga
480

ttattcaagg tggccagaca agccagaagg atggaaagag gtaacagaaa aatacagtga
540

aaacctaagt aatttagctt gcaaacattt ggaagnttta tcagaagcaa tgggtttaga
600

aaaagaagct ctaacaaang catgtgttga tatggatcaa aaagttgtta taaattatta
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<210> 211
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120

gaagatgagc gtccaaaagt tgctacaat aacttcagca acgagattcc aatcatttct
180

cttgctgaa ttgatgaggt tgatggctcg agaacagaga tatgtaacaa gattgttgaa
240

gcttgatgaga attggggtat ttttcaggtt gttgatcatg gtgttgatac aaaacttggt
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tctgagatga cccgttttgc tagagagttt tttgctttgc caccggaaga gaagctccgg
360

tttgatcatg ccggtggtaa aaagggtggt ttcattgtct ctagtcatct ccaaggagaa
420

230/390

gcagtgaagg attggagaga gctagtgaca tatttttcat acccaattaa acaagagat
480

tattcaaggt ggccagacaa gccagaagga tggaaagagg taacagaaaa atacagtga
540

aacctaatga atttagcttg caaactattg gaagttttat cagaagcaat gggtttagaa
600

aaagaagctc taacaaaagc atgtgttgat atggatcaaa aagttgttat aaattattac
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cccaaatgcc ctgaacctga cctcacactt ggcccttaaac gtcacactga ccttggcaca
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120

agatgaccgt ccaaaagttg cctacaatac cttcagcacc gagattccaa tcntttctct
180

tgctggaatt gatgaggttg atggccgaaa aacanaaatn tttaaccaaga ttggngggggc
240

ttgtnaaaat tggggtnntt ttcaggttgg tgatcatggg gtnnaacaaa acttgtttcc
300

canaaanccc ntthtntaa anagtttttt gctttncccc cggaanaaaa cctccggtt
360

nacttnnccg ggggnaaaaa aggggggggt ttnttngnc nttaagnccc nccccaggg
420

anaanccan nnaaggnttt ggaanannn nnn
453

<210> 213
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120
agaagatgag cgtccaaaag ttgctacaa taacttcagc aacgagattc caatcatttc
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tttgctgga attgatgagg ttgatggncn cacancacac atctgncca nattgctgga
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acctngcgan agncgccctn cctcnen
267

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120

gagcgtccaa aagttgccta caataacttc agcaacgaga ttccaatcat ttctcttgct
180

ggaattgatg aggttgatgg tcgtagaaca gagatatgta acaagattgt tgaagcttgt
240

gagaattggg gtatttttca ggttggtgat catgggtgtg atacaaaact tgtttctgag
300

atgaccggtt ttgctagaga gttttttgct ttgccaccgg aagagaagct ccggtttgac
360

atgtccgggtg gtaaaaagggt tggtttcatt gtctctagtc atcttcaagg agaagcagtg
420

aaggattgga gagagctagt gacatatattt tcatacccaa ttaaacaaag agattattca
480

aggtagggcag acaagccaga aggtgggaaa gaggtaacag aaaaatacag tgaanaaccta
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120

aagttgccta caataacttc agcaacgaga ttccaatcat ttctcttgct ggaattgatg
180

aggttgatgg tcgcagaaca gagatatgta acaagattgt tgaagcttgt gagaattggg
240

gtatttttca ggttggtgat catgggtgtg atacaaagct tgtttctgag atgactcgtt
300

ttgctagaga gttttttgct ttgccgccgg aagagaagct ccggtttgac atgtccgggtg

360

gtaaaaaggg tggtttcatt gtctctagtc atctccaagg agaagcagtg aaagattgga
420

gggagctagt gacatatttt tcatacccaa ttaaacaagg agattattca aggtggccag
480

acaagccaga aggatggaaa gaagtaacag aaaaatacag tgaaaccta atgaatttag
540

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120
gcgtccaaaa gttgcttaca ataacttcag caacgagatt ccaatcattt ctcttgctgg
180
aattgatgag gttgatggtc gtagaacaga gatatgtaac aagattgttg aagcttgtaga
240
gaattggggt atttttcagg ttgttgatca tgggtgtgat acaaaacttg tttctgagat
300
gacccgtttt gctagagagt tttttgcttt gccaccggaa gagaagctoc ggtttgacat
360
gtncgggtggt aaaaagggtg gtttcattgn ctctagtcac ctncaggan aagcannгаа
420
ngattggaga gagctngnga catatttttn
450

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<221> misc_feature

<222> (644)..(644)

<223> Any nucleotide

<400> 217

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120

gatgagcgtc caaaagttgc ctacaataac ttcagcaacg agattccaat catttctctt
180

gctggaattg atgaggttga tggctgtaga acagagatat gtaacaagat tgttgaagct
240

tgtgagaatt ggggtatctt tcagggtggt gatcatggtg ttgatacaaa acttgttctt
300

gagatgaccg gttttgctag agagtttttt gctttgccac cggaagagaa gctccggttt
360

gacatgtccg gtggtaaaaa ggggtggttc attgtctcta gtcattctca aggagaagca
420

gtgaaggatt ggagagagct agtgacatat ttttcatacc caattaaaca aagagattat
480

tcaaggtggc cagacaagcc agaaggatgg aaagaggtaa cagaaaaata cagtgaatac
540

ctaatagaatt tagcttgcaa actattggaa gttttatcag aagcaatggg tttagaaaaa
600

gaagctctaa caaaagcatg tgttgatatg gatcaaaaag ttgntataaa ttattaccga
660

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681

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120

aagatgagcg tccaaaaggt gcctacaata acttcagcaa cgagattcca atcattttctc
180

ttgctggaat tgatgaggtt gatggtcgaa gaacagagat atgtaacaag attgttgaag
240

cttgtgagaa ttgggggtatt tttcagggtg ttgatcatgg tgttgataca aaacttgttt
300

ctgagatgac ccgttttctc agagagtttt ttgctttgcc accggaagag aagctccggt
360

ttgacatgtc cggtgggtaaa aagggtggtt tcattgtctc tagtcatctc caaggagaa
420

cagtgaagga ttggagagag ctagtacat atttttcata cccaattaaa caaagagatt
480

attcaaggtg gccagacaag ccagaaggat ggaaagaggt aacagaaaaa tacagtga

540

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562

<210> 219
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120

tgagcgtcca aaagttgcct acaataactt cagcaacgag attccaatca tttctcttgc
180

tggaattgat gaggttgatg gtcgtagaac agagatatgt aacaagattg ttgaagcttg
240

tgagaattgg ggtatttttc aggttggtga tcatggtggt gatacaaaac ttgtttctga
300

gatgaccctt tttgctagag agttttttgc tttgccaccg gaagagaagc tccggtttga
360

catgtccgggt ggtaaaaagg gtgggttcat tgtctctagt catctccaag gagaagcagt
420

gaaggattgg agagagctag tgacatatct ttcataccca attaaacaaa gagattatct
480

aagggtggcca gacaagccag aaggatggaa agaggtaaca gaaaatata gtgaaaacct
540

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agctctaaca
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<222> (593)..(593)

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120

gatgagcgtc caaaagttgc ctacaataac ttcagcaacg agattccaat catttctctt
180

gctggaattg atgaggttga tggtcgtaga acagagatat gtaacaagat tgttgaagct
240

tgtgagaatt ggggtatttt tcaggttggt gatcatggtg ttgatacaaa acttgtttct
300

gagatgaccc gttttgctag agagtttttt gctttgccac cggaagagaa gtcocggttt
360

gacatgtcog gtggtaaaaa ggggtggttc attgtctcta gtcattctca aggagaagca
420

gtgaaggatt ggagagagct agtgacatat ttttcatacc caattaaaca aagagattat
480

tcaaggtggc cagacaagcc agaaggatgg aaagaggtaa cagaaaaata cagtgaanaa
540

ctaataaatt tagcttgcaa gctattggaa gttttatcag aagcaatggg ttn
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120
atgagcgtcc aaaagttgcc tacaataact tcagcaacga gattccaatc atttctcttg
180
ctggaattga tgaggttgat ggnnnnnggna ccnggnnatg tggnnagagg acgnnn
236

<210> 222
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120

ccaaaagtgg cctacaataa cttcagcaac nagattccaa tcatttctct tgotggaatt
180

gatgaggttg atggtcgnag aacanagata tgtaacaaga ttgttgaagc ttgtgagaat
240

tggggtattt ttcangttgt tgatcatggn gtn
273

<210> 223
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120

gagcgtccaa aagttgccta caataacttc agcaacgaga ttccaatcat ttctcttgct
180

ggaattgatg aggttgatgg tcgcagaaca gagatatgta acaagattgt tgaagcttgt
240

gagaattggg gtatttttca ggttggtgat catggtgttg atacaaagct tgtttctgag
300

atgactcggt ttgctagaga gttttttgct ttgcccgagg aagagaagct cgggtttgac
360

atgtccgggt gtaaaaaggg tggtttcatt gtctctagtc atctccaagg agaagcagtg
420

aaagattgga gagagctagt gacatatttt tcatacccaa ttaaacaag agattattca
480

aggtggccag acaagccaga aggatggaaa gaagtaacag aaaaatacag tgaaaaccta
540

atgaatttag cttgcaagct attggaagtt tt
572

<210> 224

<211> 575

<212> DNA

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120

gagcgtccaa aagttgccta caataacttc agcaacgaga ttccaatcat ttctcttgct
180

ggaattgatg aggttgatgg tcgtagaaca gagatatgta acaagattgt tgaagcttgt
240

gagaattggg gtatttttca ggttggtgat catgggtgtg atacaaaact tgtttctgag
300

atgaccgcgt ttgctagaga gttttttgct ttgccaccgg aagagaagct cgggtttgac
360

atgtccgggt gtaaaaaggg tggtttcatt gtctctagtc atctccaagg agaagcagtg

420

aaggattgga gagagctagt gacatatattt tcatacccaa ttaaacaag agattattca
480

aggtaggcag acaagccaga aggatggaaa gaggtaacag aaaatacag tgaaaaccta
540

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<223> Any nucleotide

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taagtattct ctccacaaca aacctctctg agtcaagttt cgttagggaa gaagatgagc
120

gtccaaaagt tgccataaat aacttcagca acgagattcc aatcatttct cttgctggaa
180

ttgatgaggt tgatggctct agaacagaga tatgtaacaa gattgttgaa gcttgtgaga
240

attgggggtat ttttcaggtt gttgatcatg gtgttgatag aaaacttggt tctgagatga
300

cccgttttgc tagagagttt tttgctttgc caccggaaga gaagctccgg tttgacatgt
360

ccggtggtaa aaagggtggt ttcattgtct ctagtcatct ccaaggagaa gcagtgaagg
420

attggagaga gctagtgaac tatttttcat acccaattaa acaagagat taltcaaggt
480

ggccagacaa gccagaagga tggaaagagg taacagaaaa atacagtga aacctaatga
540

atttagcttg caaactattg gaagttttat cagaagcaat gggtttagaa aaagag
596

<210> 226
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120
caaaagttgc ctacaataac ttcagcaacg agattccaat catttctctt gctggaattg
180
atgaggttga tggctgtaga acagagatat gtaacaagat tgttgaagct tgtgagaatt
240
ggggtatctt tcaggttggt gatcatggtg ttgatacaaa acttgtttct gagatgaccc
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gttttgctag agagtttttt gctttgccac cggaagagaa gtcocggttt gacatgtccg
360
gtggtaaaaa ggggtggttc attgtctcta gtcatctcca aggagaagca gtgaaggatt
420
ggagagagct agtgacatat ttttcatacc caattaaaca aagagattat tcaaggtggc
480
cagacaagcc agaaggatgg aaagaggtaa cagaaaaata cagtgaanaa ctaatgaatt
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caaaagcatg tg
612

<210> 227
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120
aaagttgect acaataactt cagcaacgag attccaatca ttctcttgc tggaattgat
180
gaggttgatg gtcgtagaac agagatatgt aacaagattg ttgaagcttg tgagaattgg
240
ggtatttttc aggttggtga tcatgggtgt gatacaaaac ttgtttctga gatgaccggt
300
tttgctagag agttttttgc ttgcccgcg gaagagaagc tccggtttga catgtccggt
360
ggtaaaaagg gtggtttcat tgtctctagt catctccaag gagaagcagt gaaggattgg
420
agagagctag tgacatat ttcatacca attaaacaaa gagattatto aagggtggca
480
gacaagccag aaggatggaa agaggtaaca gaaaaatata gtgaaaacct aatgc
535

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120

aaaagttgcc tacataaact tcagcaacga gattccaato atttctcttg ctggaattga
180

tgaggttgat ggctgtagaa cagagatatg taacaagatt gttgaagctt gtgagaattg
240

gggtattttt cagggtgttg atcatgggtg tgatacaaaa cttgtttctg agatgacccg
300

ttttgctaga gagttttttg ctttgccacc ggaagagaag ctcgggttg acatgtccgg
360

tggtaaaaag ggtggtttca ttgtctctag toatctccaa ggagaagcag tgaaggattg
420

gagagagcta gtgacatatt ttccataccc aattaaacaa agagattatt caaggtggcc
480

agacaagcca gaaggatgga aagaggtaac agaaaaatac agtgaaaacc taatgaattt
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agcttgcaaa ctattggan
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<210> 229

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<213> *Trifolium repens*

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120

caaaagttgc ctacaataac ttcagcaacg agattccaat catttctctt gctggaattg
180

atgaggttga tggctgcaga acagagatat gtaacaagat tgttgaagct tgtgagaatt
240

ggggtatttt tcagggtgtt gatcatgggt ttgatacaaa gcttgttctt gagatgaact
300

gttttgctag agagtttttt gctttgccgc cggaagagaa gctccgggtt gacatgtccg
360

tggttaaaaa ggggtggttc attgtctcta gtcctctcca aggagaagca gtgaaagatt
420

ggagagagct agtgacatat ttttcatacc caattaaaca aagagattat tcaaggtggc
480

cagacaagcc agaaggatgg aaagaagtaa cagaaaaata cagtgaanaa ctaatgaatt
540

tagcttgcaa gctattggaa gtttt
565

<210> 230
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120

gtccaaaagt tgccataaat aacttcagca acgagattcc aatcattttct cttgctggaa

180

ttgatggagt tgatggtcga agaacagaga tatgtaacaa gattgttgaa gcttgtgaga
240

attggggat ttttcagggt gttgatcatg gtgttgatac aaaacttggt tctgagatga
300

ccggttttgc tagagagttt ttgcttttgc caccggaaga gaagctccgg tttgacatgt
360

ccggtggtaa aaaggggtgt ttcattgtct ctatgcatct ccaaggagaa gcagtgaagg
420

attggagaga gctagtgaca tatttttcat acccaattaa acaaagagat tattcaagggt
480

ggccagacaa gccagaagga tggaaagagg taacagaaaa atacagtga aacctaata
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<210> 231
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gtacancaaa caccanaaac gagnccgttt cctmtcnaa catggcacca agccaaactc
120

tacaaaagt tgcctacaat aacttcagca acgagattcc aatcatttct cttgctggaa
180

ttgatgaggt tgaatggctcg agaacagaga tatgtaacaa gattgttgaa gcttgtgaga
240

attgggggat ttttcaggtt gttgatcatg gtgttgatac aaaacttggt tctgagatga
300

cccgttttgc tagagagttt ttgctttgc caccggaaga gaagctccgg ttgacatgt
360

ccggtggtaa aaaggggggt ttcattgtct ctagtcatct tcaaggagaa gcagtgaagg
420

attggagaga gctagtgaca tatttttcat acccaattaa acaagagat tattcaaggt
480

ggccagacaa gccagaagga tggaaagagg taacagaaaa atacagttaa aacctaatga
540

atthagcttg caagctattg gaagttttat cagaagcaat gggttttagaa aaagaagctc
600

taacaaaaag
609

<210> 232
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120

cctacaataa cttcagcaac gagattccaa tcattttctct tgctggaatt gatgagggtg
180

atggtcgtag aacagagata tgtaacaaga ttgttgaagc ttgtgagaat tggggtattt
240

ttcaggttgt tgatcatggg gttgatataa aacttggttc tgagatgacc cgttttgcta
300

gagagttttt tgctttgccg cgggaagaga agctccggtt tgacatgtcc ggtggtaaaa
360

aggggtggtt cattgtctct agtcattccc aaggagaagc agtgaaggat tggagagagc
420

tagtgacata tttttcatac ccaattaaac aaagagatta ttcaagggtg ccagacaagc
480

cagaaggatg gaaagaggta acagaaaaat acagtgaata cctaataaat ttacgttgca
540

agctattgga agttttatca gaagcaatgg gtttagaaaa agaagctcta acaaaaag
597

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<211> 418

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120

agttgcctac aataacttca gcaacgagat tccaatcatt tctcttgctg gaattgatga
180

ggttgatggt cgtagaacag agatatgtaa caagattggt gaagcttggt agaattgggg
240

tatttttcag gttgttgatc atggtgttga taaaaaactt gtttctgaga tgaccggttt

300

tgctagagag ttttttgctt tgccacogga agagaagctc cggtttgaca tgtncggtgg
360

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<211> 570

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<400> 234

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120

caaaagtgtc ctacaataac ttcagcaacg agattccaat cttttctctt gctggaattg
180

atgagggtga tggctgtaga acagagatat gtaacaagat tgttgaagct tgtgagaatt
240

gggggtattt tcagggtgtt gatcatgggtg ttgatacaaa acttgtttct gagatgacct
300

gttttgcctag agagtttttt gctttgccac cggaagagaa gctccggttt gacatgtccg
360

gtggtaaaaa ggggtggttc attgtctcta gtcattctcca aggagaagca gtgaaggatt
420

ggagagagct agtgacatat ttttcatacc caattaaaca aagagattat tcaagggtgc
480

cagacaagcc agaaggatgg aaagaggtaa cagaaaaata cagtgaatac ctaatgaatt
540

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570

<210> 235

<211> 608

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120
aagttgccta caataacttc agcaacgaga ttccaatcat ttctcttgct ggaattgatg
180
aggttgatgg tcgtagaaca gagatatgta acaagattgt tgaagcttgt gagaattggg
240
gtatttttca ggttgtagat catgggtgtg atacaaaact tgtttctgag atgaccogtt
300
ttgctagaga gttttttgct ttgccaccgg aagagaagct ccggtttgac atgtccggtg
360
gtaaaaaggg tggtttcatt gtctctagtc atctccaagg agaagcagtg aaggattgga
420
gagagctagt gacatatatt tcatacccaa ttaataaaag agattattca aggtggccag
480
acaagccaga aggatggaaa gaggtaacag aaaaatacag tgaaaaccta atgaatttag
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cttgcaaaact attggaagtt ttatcagaag caatgggttt agaaaaagaa gctctaacaa
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aagcatgt
608

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120

tgcttacaat aacttcagca acgagattcc aatcatttct cttgctggaa ttgatgaggt
180

tgatgggtgc agaacagaga tatgtaacaa gattgttgaa gottgtgaga attggggtat
240

ttttcaggtt gttgatcatg gtgttgatac aaagcttggt tctgagatga ctcgttttgc
300

tagagagttt tttgctttgc cgccggaaga gaagctocgg tttgacatgt ccggtggtaa
360

aaagggtggt ttcattgtct ctagtcgtct ccaaggagaa gcagtgaaag attggagaga
420

gctagtgaac tatttttcat acccaattaa acaagagat tattcaaggt ggccagacaa
480

gccagaagga tggaaagaag taacanaaaa atacagtga aaacctaatga atttancctg
540

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600

nt
602

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tcccacaaaa cactcttgag tcagtttcgt tagggaagaa gatgagcgtc caaaagttgc
120

ctacaataac ttcagcaacg agattccaat cattnctctt gctggaattg atgaggttga
180

tggctgcaga acagagatat gtaacaagat tgttgaagct tgtgagaatt ggggtatatt
240

tcaggttggt gatcatgggt ttgatacaaa ncttgtttct gagatgacct gttttgctag
300

agagtttttt gctntgccac cggaagagaa gctccggttt gacatgtccg gtggtaaaaa
360

gggtgggttc attgtctcta gtcactnca agganaagca ntgaaggatt ggagagagct
420

agtacatat ttttcatacc caattaaca aagagattat tcaagggtgc cagacaagcc
480

agaaggatgg aaagaggtna cagaaaaata cagcgaaaac ctaatgaatt tanctn
536

<210> 238
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<400> 238

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ctctcacaac aaaagactct tgagtcnagt ttcgttaggg aagaagatga gcgtccaaaa
120

gttgcttaca ataacttcag caacgagatt ccaatcattt ctcttgctgg aattgatgag
180

gttgatggtc gcagaacaga gatatgtaac aagattgttg aagcttgatga gaattggggg
240

atttttcagg ttgttgatca tgggtgtgat acaaagcttg tttctgagat gactcgttt
300

gctagagagt tttttgcttt gccgccggaa gagaagctcc ggtttgacat gtcgggtgg
360

aaaaagggtg gtttcattgt ctctagtcac ctccaaggag aagcagtga agattggagg
420

gagctagtga catatttttc ataccgaatt aaacaaagag attattcaag gtggccagac
480

aagccagaag gatggaaaaga agtaacagaa aaatacagtg aaaacctaata gaatttagct
540

tgcaagctat tggaagtttt atcagaagca at
572

<210> 239

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120

ttgcctacaa taacttcagc aacgagattc caatcatttc tcttgctgga attgatgagg
180

ttgatggctg aagaacagag atatgtaaca agattgttga agcttgtgag aattggggta
240

tttttcaggt tgttgatcat ggtgttgata caaaacttgt tttctgagatg acccggtttg

300

ctagagagtt ttttgccttg ccaccggaag agaagctccg gtttgacatg tccggtggta
360

aaaagggtgg tticattgtc tctagtcac tcacaggaga agcagtgaag gattggagag
420

agctagtgc atatttttca tacccaatta aacaaagaga ttattcaagg tggccagaca
480

agccagaagg atggaaagag gtaacagaaa aatacagtga aaacctaatg aatttagctt
540

gcaaactatt ggaagtttta tcagaagcaa tgg
573

<210> 240
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60

ctcacaacaa aagactcttg agtcaagttt cgtaggggaa gaagatgagc gtccaaaagt
120

265/390

tgcttacaat aacttcagca acgagattcc aatcatttct cttgctggaa ttgatgaggt
180

tgatgggtgc agaacagaga tatgtaacaa gattgttgaa gcttgtgaga attgggggtat
240

ttttcaggtt gttgatcatg gtgttgatac aaagcttggt tctgagatga ctctgtttgc
300

tagagagttt ttgtctttgc cgccggaaga gaagctcgg tttgacatgt ccggtggtaa
360

aaaggggtgt ttcatgtgtc ctatgcatct ccaaggagaa gcagtgaag attggagggga
420

gctatgaca tatttttcat acccaattaa acaagagat tattcaaggt ggccagacaa
480

gccagaagga tggaaagaag taacagaaaa atacagtga aacotaatga atttagcttg
540

caagctattg gaagttttat cagaagcaat ggg
573

<210> 241

<211> 584

<212> DNA

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120
tgccatacaat aacttcagca acgagattcc aatcatttct cttgctggaa ttgatgaggt
180
tgatggtcgc agaacagaga tatgtaacaa gattgttgaa gcttgtgaga attggggatat
240
ttttcagggtt gttgatcatg gtgttgatgc aaagcttggt tctgagatga ctgcttttgc
300
tagagagttt tttgctttgc cgccggaaga gaagctccgg tttgacatgt ccggtggtaa
360
aaagggtggt ttcattgtct ctagtcatct ccaaggagaa gcagtgaaag attggagaga
420
gctagtgaca tatttttcat acccaattaa acaaagagat tattcaaggt gccagacaa
480
gccagaagga tggaagaag taacagaaaa atacagttaa aacctaata atttagcttg
540
caagctattg gaagttttat cagaagcaat gggattagaa aaag
584

<210> 242
<211> 529
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120

tgtatgaggtt gatggtcgca gaacagagat atgtaacaag attgttgaag cttgtgagaa
180

ttgggggtatt ttccaggttg ctgatcatgg tgttgataca aagcttggtt ctgagatgac
240

tcgttttgc agagagtttt ttgctttgcc gccggaagag aagctccggt ttgacatgac
300

cggtggtaaa aagggtggtt tcattgtctc tnnatcatctc caaggagaag cagnгааага
360

ttggaganag ctatgtgacat attntcata ccaattaaa caaagagatt atncaagggtg
420

gtcanacnag ccagaaggat ggaaagaagt aacagaaaaa tacagtгaaа acctaатгаа

480

tttacctngc aagctattgg aagttttata ataancnatg gnattaaga
529

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120

ggaagagaag ctccggtttg acatgtccgg tggtaaaaag ggtgggttca ttgtctctag
180

tcctctccaa ggagaagcag tgaaggattg gagagagcta gtgacatatt tttcataccc
240

aattaaacaa agagattatt caaggtggcc agacaagcca gaaggatgga aagaggtaac
300

agaaaaatac agtgaatacc taatgaattt agcttgcaaa ctattggaag ttttatcaga
360

agcaatgggt ttgaaaaaag aagctctaac aaaagcatgt gttgatattg atcaaaaagt
420

tggtataaat tattacccaa aatgccctga acctgacctc acacttggcc ttaaacgtca
480

270/390

cactgacctt ggcacaatta ctcttttgct tcaagatcaa gttggtggct tccaagctac
540

caagataat ggtaagacgt ggattacagt tcaaccagtt gaagggtgctt ttgttggttaa
600

tcttgagac catggtcact atctaagtaa tggacggctc aaaaatgctg accatcaagc
660

agtggatgaat tcgaactaca gccgnttacc aatagcaa
698

<210> 244
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ttaaagccca cactgacctt ggnacaatta ctcttttgct tcaagatcaa gttggtggcc
120

ttcaagctac caaagataat ggtaagacgt ggattacagt tcaaccagtt gaagggtgctt
180

ttgttggttaa tcttgagac catggtcatt atctaagtaa tggacggctc aaaaatgctg
240

accaccaagc agtggatgaat tcgaactaca gccgtttacc aatagcaaca ttccaaaatc
300

cagctcccca tgcaactgta taccctttag agattagaga gggtgaaaaa tctgtgttgg
360

aagaaccaat cacttttgct gaaatgtata gaaggaagat gaccaaagac cttgaattg
420

ctaggatgaa gaagttggct aaggaacaac aacttaggga cttggaggag aacaagacta
480

aatatgagggc caaacctttg aatgagatct ttgcttaatt aattagtctt aatttaaata
540

attaataaat tttagactta atttacetat aataatttt
579

<210> 245
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<212> DNA
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<222> (30)..(30)
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60

aagtaaaata ccataacaca ataatatgaa taccataatc ttgaatcata caaacaacct
120

tggatcaaac aaaacaacaa ccatgggtga tctagaaaca gaaccaagtt caccatttat
180

tcaatcccca gaacacagac caaaatcctc aataatcatt gctgaaggta tccctctaata
240

tgatctcact cctataaact acaaagatga aatcatcacc aacctacttt ccattgaaga
300

cttagtcaaa gaaataggca aagcatgtaa agaattgggt ttctttcaag tgattaatca
360

caaagttcct ttggataaac gtgaaggat tgaagaatct tcaagaagt tttttgaact
420

tagtttggag gaaaaactta aggtgagaag agatgaagtt aatttgcttg gttattttga
480

agctgagcat acaaaaaatg tatgggactg gaaggaaatt tatgatttta atgtgcaaca
540

accaactttt ataccacctt cggatgacca aagttttcag tttcaatggg aaaatcgatg
600

g
601

<210> 246
 <211> 172
 <212> PRT
 <213> *Trifolium repens*

<400> 246

Met Asn Thr Ile Ile Leu Asn His Thr Asn Asn Leu Gly Ser Asn Lys
 1 5 10 15

Thr Thr Thr Met Val Asp Leu Glu Thr Glu Pro Ser Ser Pro Phe Ile
 20 25 30

Gln Ser Pro Glu His Arg Pro Lys Ser Ser Ile Ile Ile Ala Glu Gly
 35 40 45

Ile Pro Leu Ile Asp Leu Thr Pro Ile Asn Tyr Lys Asp Glu Ile Ile
 50 55 60

Thr Asn Pro Leu Ser Ile Glu Asp Leu Val Lys Glu Ile Gly Lys Ala
 65 70 75 80

Cys Lys Glu Trp Gly Phe Phe Gln Val Ile Asn His Lys Val Pro Leu
 85 90 95

Asp Lys Arg Glu Arg Ile Glu Glu Ser Ser Lys Lys Phe Phe Glu Leu
 100 105 110

Ser Leu Glu Glu Lys Leu Lys Val Arg Arg Asp Glu Val Asn Leu Leu
 115 120 125

Gly Tyr Phe Glu Ala Glu His Thr Lys Asn Val Arg Asp Trp Lys Glu
 130 135 140

Ile Tyr Asp Phe Asn Val Gln Gln Pro Thr Phe Ile Pro Pro Ser Asp
 145 150 155 160

Asp Gln Ser Phe Gln Phe Gln Trp Glu Asn Arg Trp
 165 170

<210> 247
 <211> 585
 <212> DNA
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<220>
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<400> 247
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cagctttctt caaatccaga aaataggcca aaactttcca taatccaagc tgaaggaatt
120

cctgtaatca atctctcccc attaattcac cacacagttc aagactcctc tgccattgaa
180

agcttagtca aagaaaatagg aaatgcttgc aaggaatggg gtttcttcca agtaacaaac
240

catggtgtcc ctctaatact aaggctcaga ctcgaggaag ctaccaaagt tttctttgca
300

cagagtttgg aggagaagag gaagcttacc gtagatgata acagtttgcc tgggttatcat
360

gatacagagc acaccaagaa tgtcagagac tggaaagaag tgtttgattt tttatccaaa
420

gaccccaactt tgattcctct gaattctgat gaacatgatg atcgagtcac tcaatggact
480

aatccatccc ctcaatatcc tccaaacttc aaagttattt tggaagagta tattaaagag
540

atggaaaaagc taggctttaa gttgctagag cttatagctt tgagc
585

<210> 248

<211> 187

<212> PRT

<213> *Trifolium repens*

<400> 248

Met Leu Val Tyr Gln Glu Arg Trp Glu Arg Trp Ile Gln Leu Ser Ser
1 5 10 15

Asn Pro Glu Asn Arg Pro Lys Leu Ser Ile Ile Gln Ala Glu Gly Ile
20 25 30

Pro Val Ile Asn Leu Ser Pro Leu Ile His His Thr Val Gln Asp Ser
35 40 45

Ser Ala Ile Glu Ser Leu Val Lys Glu Ile Gly Asn Ala Cys Lys Glu
50 55 60

Trp Gly Phe Phe Gln Val Thr Asn His Gly Val Pro Leu Asn Leu Arg
65 70 75 80

Leu Arg Leu Glu Glu Ala Thr Lys Val Phe Phe Ala Gln Ser Leu Glu
85 90 95

Glu Lys Arg Lys Leu Thr Val Asp Asp Asn Ser Leu Pro Gly Tyr His
100 105 110

Asp Thr Glu His Thr Lys Asn Val Arg Asp Trp Lys Glu Val Phe Asp
115 120 125

Phe Leu Ser Lys Asp Pro Thr Leu Ile Pro Leu Asn Ser Asp Glu His
 130 135 140

Asp Asp Arg Val Thr Gln Trp Thr Asn Pro Ser Pro Gln Tyr Pro Pro
 145 150 155 160

Asn Phe Lys Val Ile Leu Glu Glu Tyr Ile Lys Glu Met Glu Lys Leu
 165 170 175

Gly Phe Lys Leu Leu Glu Leu Ile Ala Leu Ser
 180 185

<210> 249
 <211> 604
 <212> DNA
 <213> *Trifolium repens*

<400> 249
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atggcgttag ctggagtttt caatattggt gattttgttc ctgctttgga atgggttagat
 120

attcaagggtg tacaaggaat aatgaagaaa ttacataaaa gatttgatgc atttttaact
 180

agcattattg aagatcacat gatttccaag agtgagaagc ataatagactt attgagtacg
 240

ttgttatcac taaaagaaaa agttgatgag gatggtgaca aacttaatga tactgagatc
 300

aaagcattac tcttgaacat gttcacagct ggaacagaca catcatcaag cacaacagag
 360

tgggctattg ctgaactaat aaaaaatcca aaactaatga ttctgtgtca aaatgagttg
 420

gacactgttg tgggcccaga caagcttgta actgaacaag acttgcccca tcttcttacc
 480

ttagaggctg taataaagga gacatttcgt ctccatccat caacccctct tctctccca
 540

cgtgttgcaa caaatagttg tgaaatcctc gactatcaca ttcccaaagg tgcaactctc
 600

ttgg
 604

<210> 250
 <211> 201
 <212> PRT
 <213> *Trifolium repens*

<400> 250

Gly Asn Gly Gly Gly Glu Cys Asp Pro Arg Ala Asp Glu Leu Val Met
 1 5 10 15

Val Val Glu Leu Met Ala Leu Ala Gly Val Phe Asn Ile Gly Asp Phe
 20 25 30
 Val Pro Ala Leu Glu Trp Leu Asp Ile Gln Gly Val Gln Gly Lys Met
 35 40 45
 Lys Lys Leu His Lys Arg Phe Asp Ala Phe Leu Thr Ser Ile Ile Glu
 50 55 60
 Asp His Met Ile Ser Lys Ser Glu Lys His Asn Asp Leu Leu Ser Thr
 65 70 75 80
 Leu Leu Ser Leu Lys Glu Lys Val Asp Glu Asp Gly Asp Lys Leu Asn
 85 90 95
 Asp Thr Glu Ile Lys Ala Leu Leu Leu Asn Met Phe Thr Ala Gly Thr
 100 105 110
 Asp Thr Ser Ser Ser Thr Thr Glu Trp Ala Ile Ala Glu Leu Ile Lys
 115 120 125
 Asn Pro Lys Leu Met Ile Arg Val Gln Asn Glu Leu Asp Thr Val Val
 130 135 140
 Gly Arg Asp Lys Leu Val Thr Glu Gln Asp Leu Ala His Leu Pro Tyr
 145 150 155 160
 Leu Glu Ala Val Ile Lys Glu Thr Phe Arg Leu His Pro Ser Thr Pro
 165 170 175
 Leu Ser Leu Pro Arg Val Ala Thr Asn Ser Cys Glu Ile Leu Asp Tyr
 180 185 190
 His Ile Pro Lys Gly Ala Thr Leu Leu
 195 200
 <210> 251
 <211> 581
 <212> DNA
 <213> Trifolium repens
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 60
 ttatggcggt agctggagtt ttcaatattg gtgattttgt tcttgctttg gaatgggttag
 120
 atattcaagg tgtacaagga aaaatgaaga aattacataa aagatttgat gcatttttaa
 180
 ctgacattat tgaagatcac atgatttcca agagtgaagaa gcataatgac ttattgagta

240

cggtgttattc actaaaagaa aaagttgatg aggatgggtga caaacttaat gatactgaga
300

tcaaagcatt actcttgaac atgttcacag ctggaacaga cacatcatca agcacaacag
360

agtgggctat tgctgaacta ataaaaaatc caaaactaat gattcgtgtt caaaatgagt
420

tggacactgt tgtgggccga gacaagcttg taactgaaca agacttggcc catcttcctt
480

acttagaggc tgtaataaag gagacatttc gtctccatcc atcaaccctt cttctctctc
540

cacgtgttgc aacaaatagt tgtgaaatcc togactatca c
581

<210> 252

<211> 603

<212> DNA

<213> *Trifolium repens*

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<400> 252

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60

tggcgttagc tggagttttc aatattgggt attttgttcc tgctttggaa tgggttagata
120

ttcaagggtgt acaaggaaaa atgaagaat tacataaaag atttgatgca tttttaacta
180

gcattattga agatcacatg atttccaaga gtgagaagca taatgactta ttgagtacgt
240

tgttatcact aaaagaaaaa gttgatgagg atggtgacaa acttaatatgat actgagatca
300

aagcattact cttgaacatg ttcacagctg gaacagacac atcatcaagc acaacagagt
360

gggctattgc tgaactaata aaaaatccaa aactaatgat tcgtgttcaa aatgagttgg
420

acactgttgt gggccgagac aagcttgtaa ctgaacaaga cttggcccat cttccttact
480

tagaggctgt aataaaggag acatttcgtc tccatccatc aacctctctt tctctcccat
540

gtgttgcaac aaatagtgtg gaaatcctcg actatcacat tcccaaagggt gcaactctct
600

tgg

603

<210> 253
<211> 621
<212> DNA
<213> *Trifolium repens*

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ctccctaaaa attctatagc taccacatca ncacaacata acannaatta agaaatattn
 120

ttatntactat tttaagatat ggaagtagta gcagcagcaa tcacaaaaaa caatggcaag
 180

attgattcat ttgtcttgaa tcatgctaata gctaataaca tgaaagttaa tgggtgctgat
 240

cctttgaatt ggggtgtggc tgctgaggca atgaaggga gtcacttgga tgaggtgaag
 300

cgtaggtgg aggaataccg gaaaccggtt gtccgtcttg gtggcgagac actgacgatt
 360

tctcaggtgg ctgccattgc tgcacacgat ggtgcaacgg tggagctatc ggaatctgct
 420

agagccggcg ttaaggcgag cagtactggt gttatggaga gtatgaacaa aggtacagac
 480

agttatggtg tcaactacag gttcggcgct acotcgacc gccgaaccaa acaaggtggt
 540

gctttgcaga aagagctcat aaggtntttt gaatgcagga atatttggaa atgggaacntg
 600

agacaaagcc acacactacc c
 621

<210> 254
 <211> 159
 <212> PRT
 <213> Trifolium repens

<400> 254

Met Glu Val Val Ala Ala Ala Ile Thr Lys Asn Asn Gly Lys Ile Asp
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Ser Phe Cys Leu Asn His Ala Asn Ala Asn Asn Met Lys Val Asn Gly
 20 25 30

Ala Asp Pro Leu Asn Trp Gly Val Ala Ala Glu Ala Met Lys Gly Ser
 35 40 45

His Leu Asp Glu Val Lys Arg Met Val Glu Glu Tyr Arg Lys Pro Val
50 55 60
Val Arg Leu Gly Gly Glu Thr Leu Thr Ile Ser Gln Val Ala Ala Ile
65 70 75 80
Ala Ala His Asp Gly Ala Thr Val Glu Leu Ser Glu Ser Ala Arg Ala
85 90 95
Gly Val Lys Ala Ser Ser Asp Trp Val Met Glu Ser Met Asn Lys Gly
100 105 110
Thr Asp Ser Tyr Gly Val Thr Thr Gly Phe Gly Ala Thr Ser His Arg
115 120 125
Arg Thr Lys Gln Gly Gly Ala Leu Gln Lys Glu Leu Ile Arg Phe Glu
130 135 140
Cys Arg Asn Ile Trp Lys Trp Asn Arg Gln Ser His Thr Leu Pro
145 150 155

<210> 255
<211> 582
<212> DNA
<213> Trifolium repens

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<222> (549)..(549)

<223> Any nucleotide

<400> 255

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60

ctccctaaaa attctatagc taccacatca ncacaacata acannaatta agaaatattn
120

tatntactat ttttaagatat ggaagtagta gcancagcaa tcacaaaaaa caatggcgaag
180

attgattcat tttgcttgaa tcatgctaata gctaataaca tgaaagttaa tgggtgctgat
240

cctttgaatt ggggtgtggc tgctgaggca atgaaggga gtcacttgga tgagggtgaag
300

cgtatggttg aggaataccg gaaaccggtt gtccgtcttg tggcgagac gctgacgatt
360

tctcaggttg ctgccattgc tgcacacgat ggtgcaacgg tgganctatc ggaatctgct
420

agagccggcg ttaaggcgag cagtgactgg gttatggaga gcatgaacaa aggtacagac
480

agttatggtg tctactacgg gttcggcgct acctcncacc gccgaaccaa acaaggtggt
540

gctttgcana aagagctcat aagctaattt gcttgtgtca at
582

<210> 256
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60

ctccctaaaa attctatagc taccacatca ncacaacata acannaatta agaatattn
120

tatntactat nttaagatat ggaagtagta gcagcagcaa tcacaaaaaa caatggcaag
180

attgattcoat ttgtgctgaa tcatgctaata gctaataaca tgaaagtgaat tgggtgctgat
240

cctttgaatt ggggtgtggc tgcgtgaggca atgaaggga gtcacttgga tgaggtgaag
300

cgtatgggtgg aggaataccg gaaaccggtt gtccgtcttg gtggcgagac actaaccatt
360

tctcagggtgg ctgcccattgc tgcacacgat ggtgcaacgg tggagctatc ggaatctgct
420

agagccggcg ttaaggcaag cagtgactgg gttatggaga gtatgaacaa aggtaccgac
480

agctacgggtg tcccaacagg gtccggcgct acctcgacac gccgaaccaa acaaggtggt

540

gctttgcaga aagagctcat aaggtnntttt gaatgctgga atatttgga atggaacntg
600

agtcnaagcc acacactacc c
621

<210> 257
<211> 600
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120
tttaagnnat ggaagtagta gcagcagcaa tcacaaaaaa caacggaaag attgattcat
180
ttgcttgtaa tcattgcta gctaataaca tgaaagttaa tgggtctgat cctttgaatt
240
ggggtgtggc tgctgaggca atgaaaggaa gtcacttgga tgagggtgaag tgtatggtgg
300
aggagtatcg aaaaccgggt gtccgtcttg gtggcgagac actgacgatt tctcaagtgg
360
ctgccattgc tgcacacgat ggtgcgacgg tggagctatc ggaatctgct agagccggcg
420
ttaaggcgag cagtgactgg gttatggaaa gtatgaacaa aggtactgac agttatggtg
480
tcactacagg gttcgcgct acctcgacc gccgaaccaa acaagggtgt gctttgcaga
540
aagagctcat aaggtnnttt gaatgcagga atatttgtaa atggaacttg anacaaatcc
600

<210> 258
<211> 693
<212> DNA
<213> *Trifolium repens*

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<400> 258

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60

cttatttccc cccacacaaac ataacnaata catntctctc tcctctcacc acaattatta
120

ctttctacac acccccctct caactattat taactaacat aatggaggga attaccaatg
180

gccatgctga agcaactttt tgcgtgacca aaagtgttgg tgatccactc aactgggggtg
240

cagccgcgga gtcgttgatg gggagtcatt tggatgaggt gaagcgtatg gtggaggaat
300

accgtaatcc attgggtaaa attggcggcg agacgcttac cattgctcag gtggctggaa
360

ttgcttctca tgatagtggg gtgagggtgg agctgtctga gtccgccagg gccggcggtta
420

aggcgagtag tgattgggtg atggacagca tgaacaatgg gactgatagt tatgggtgta
480

ccaccgggtt cgggccccc tctcaccgga gaaccaagca ggggtgtgcc ttgcagaagg
540

agctaattag gtttttgaat gctggaatat ttggcaatgg tacagaatct aactgtacac
600

taccacacac agcaaccaga gctgcaatgc ttgtgagaat caacactctt cttcaagagg
660

aatatttctt gaatggcctt tgtaaatttt tgg
693

<210> 259

<211> 177

<212> PRT

<213> *Trifolium repens*

<400> 259

286/390

Met Glu Gly Ile Thr Asn Gly His Ala Glu Ala Thr Phe Cys Val Thr
 1 5 10 15

Lys Ser Val Gly Asp Pro Leu Asn Trp Gly Ala Ala Ala Glu Ser Leu
 20 25 30

Met Gly Ser His Leu Asp Glu Val Lys Arg Met Val Glu Glu Tyr Arg
 35 40 45

Asn Pro Leu Val Lys Ile Gly Gly Glu Thr Leu Thr Ile Ala Gln Val
 50 55 60

Ala Gly Ile Ala Ser His Asp Ser Gly Val Arg Val Glu Leu Ser Glu
 65 70 75 80

Ser Ala Arg Ala Gly Val Lys Ala Ser Ser Asp Trp Val Met Asp Ser
 85 90 95

Met Asn Asn Gly Thr Asp Ser Tyr Gly Val Thr Thr Gly Phe Gly Ala
 100 105 110

Thr Ser His Arg Arg Thr Lys Gln Gly Gly Ala Leu Gln Lys Glu Leu
 115 120 125

Ile Arg Phe Leu Asn Ala Gly Ile Phe Gly Asn Gly Thr Glu Ser Asn
 130 135 140

Cys Thr Leu Pro His Thr Ala Thr Arg Ala Ala Met Leu Val Arg Ile
 145 150 155 160

Asn Thr Leu Leu Gln Glu Glu Tyr Phe Leu Asn Gly Leu Cys Lys Phe
 165 170 175

Leu

<210> 260
 <211> 592
 <212> DNA
 <213> Trifolium repens

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120

ttaactangc ataatggagg gaattaccaa tggccagctg ctttcaaaaa aaaaccaatg
180

gccatgctga aacaactttt tgcgtgacca aaagtgttgg tgatccactc aactggggtg
240

cagccgcgga gtcgttgacg ggtagtcatt tggatgaggt gaagcgtatg gtggaggagt
300

accgtaatcc gttggttaaa attggcggcg agacgcttac cattgctcag gtggctggaa
360

tgtcttctca tgatagtggg gtgagggtgg agctgtccga gtccgcaagg gccggcgtaa
420

aggcgagtag tgattgggtg atggatagca tgaacaatgg gactgatagt tacggtgtta
480

ccaccggttt tgggtgccacc tctcaccgga gaaccaagca ggggtgtgccc ttgcagaagg
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agcctaattag gtttttgaat gctggaatat ttggcaatgg tacagaatct an
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taatggaggg aattaccaat ggccatgctg aagcaacttt ttgctgacg aaaagtgttg
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gtgatccact caactggggg gcagccgctg agtcgttgat ggggagtcac ttggatgagg
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ccattgtcga ggtggctgga attgcttctc atgatatggt tgtgagggtg gagctgtctg
360
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420
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480
aaggtggtgc cttgcagaag gagctaatta gggttttgaa tgctggaata tttggcaatg
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120

taatggaggg aattactaat ggccatgctg aagcaacttt ttgcgtnacc aaaagtgttg
180

gtgatccact caactggggg gcagccggg agtcgntgat ggggagtnat ttggatgagg
240

tgaancgtat ggtggaggaa tacgtaatc cattgggttaa aattggcgcc gagacgctta
300

ccattgtcca ggtggctgga attgcttctc atgatagnn tgtgagggg gagctgtctg
360

agtnccgagc ggccggcggt aangcgagta gtgattgnt gatggacagn atgaacaatg
420

ggactgatag ttatggngtn accaccggt tcggcgccac ctctcaccgg agaaccaagc
480

aggggtggtgc cttgcaaaaag gagctaatta tgtttttgaa tgcagggaata tttggcaatg
540

gtacagaatc taactgtaca cttnacaca cagcaaccan agntgcattg ctttggtgca
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120

atggaggggaa ttactaatgg ccatgctgaa gcaacttttt gcgtgaccaa aagtgttggt
180

gattccactca actgggggtgc agccgcggag tcgttgatgg ggagtcattt ggatgaggtg
240

aagcgtatgg tggaggaata ccgtaatcca ttggttaaaa ttggcggcga gacgcttacc
300

attgctcagg tggctggaat tgcttctcat gatagtgggtg tgaggggtgga gctgtctgag
360

tcgccaggg ccggcggttaa ggcgagtagt gattgggtga tggacagcat gaacaatggg
420

actgatagtt atgggtgttac caccggttcc ggccgccacct ctcaccggag aaccaagcag
480

ggtggtgcct tgcagaagga gctaattagg tttttgaatg ctggaatatt tggcaatggt
540

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120

atggaggaggaa ttaccaatgg ccatgctgaa gcaacttttt gcgtgaccaa aagtgttggt
180

gatccactca actgggggtgc agccgcggag tcgttgatgg ggagtcattt ggatgaggtg
240

aagcgtatgg tggaggaata ccgtaatcca ttggttaaaa ttggcggcga gaogcttacc
300

attgctcagg tggctggaat tgcttctcat gatagtgggtg tgagggtgga gctgtctgag
360

tccgccaggg ccggcgtaa ggccagtagt ggttggtgga tggacagcat gaacaatggg
420

actgatagtt atgggtgttac cactggttcc ggccgccacct ctcaccggag aaccaagcag
480

ggtggtgcct tgcagaagga gctaattagg tttttgaatg ccggaatatt tggcaatggt
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acagaatcta actgtacact accacacaca gcaaccagag ctgcaatgct tgtgagaatc
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aacactcttc ttcaag

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120

tggagggaat taccaatggc catgctgaaa caactttttg cgtgaccaa agtggtggtg
180

atccactcaa ctgggggtgca gccgcggagt cgttgacggg gagtcatttg gatgaggtga
240

agcgtatggt ggaggagtac cgtaatcgt tggctaaaaat tggcggcgag acgcttacca
300

ttgctcaggt ggctggaatt gcttctcatg atagtggtgt gaggggtggag ctgnncgagt
360

ccgcaagggc cggcgtaaag gcgagtactg attgggtgat gnataacatg aacaatggga
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120

tggaggggaat taccaatggc catgctgaag caactttttg cgtgaccaa agtgttggtg
180

atccactcaa ctgggggtgca gccgcggagt cgttgatggg gagtcatttg gatgagggtg
240

agcgtatggt ggaggaatac cgtaatccat tgggttaaat tggcggcgag acgcttacca
300

ttgtcagggt ggctggaatt gcttctcatg atagtgggtg gagggtgag ctgtctgagt
360

cggccagggc cggcgtaag gcgagtagtg gttgggtgat ggacagcatg aacaatggga
420

ctgatagtta tgggtgttacc actgggttcg gcgccacctc tcaccggaga accaagcagg
480

gtgggtgcctt gcagaaggag ctaattaggt ttttgaatgc cggaatatct ggcaatggta
540

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567

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120

tttgctgac caaaagtgtt ggtgatccac tcaactgggg tgcagccgag gagtcgtcga
180

cggggagtc tttggatgag gtgaagcgta tgggtggagga gtaccgtaac ccgttggtta
240

aaattggcgg cgagacgctt accattgttc aggtggctgg aattgctctt catgatagtg
300

gtgtgagggg ggagctgtcc gactccgcaa gggccggcgt taaggcgagt agtgattggg
360

tgatggatag catgaacaat gggactgata gttacgggtg taccaccggt tttggtgcca
420

cctctcaccg gagaaccaag cagggtgggt ccttcagaaa ggagctaatt aggtttttga
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<211> 579

<212> DNA

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120

cgatgtttca aggaacaagg ccattcatgg tggtaacttt caaggaacac ctattggagt
180

ttcaattgat aacacaogtt tagctcttgc ttcaattggt aaactcatgt ttgctcaatt
240

ctctgaactt gttaatgatt tttaacaaa cgggttgccct tgaatcttta ctgctagtag
300

gaaccggagc ttggactatg gtttcaaggg atcggaatgt gccatggctt cgtattgttc
360

cgagttacaa tatcttgcta atcctgtcac caccatgttc caaagtgcg agcaacacaa
420

ccaagatggt aactctttgg gtttgatttc atctagaaaa acaaatgaag ctattgagat

480

tctcaagctc atgtcttcca cttcttgat tgcattatgt caagcaatcg acctaaaggca
540

cttgaggagaa aatctcagga acaccgtcaa gaacacggt
579

<210> 269

<211> 192

<212> PRT

<213> *Trifolium repens*

<400> 269

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Ile Glu Val Ile Arg Phe Ser Thr Lys Ser Ile Glu Arg Glu Ile Asn
20 25 30

Ser Val Asn Asp Asn Pro Leu Ile Asp Val Ser Arg Asn Lys Ala Ile
35 40 45

His Gly Gly Asn Phe Gln Gly Thr Pro Ile Gly Val Ser Met Asp Asn
50 55 60

Thr Arg Leu Ala Leu Ala Ser Ile Gly Lys Leu Met Phe Ala Gln Phe
65 70 75 80

Ser Glu Leu Val Asn Asp Phe Tyr Asn Asn Gly Leu Pro Ser Asn Leu
85 90 95

Thr Ala Ser Arg Asn Pro Ser Leu Asp Tyr Gly Phe Lys Gly Ser Glu
100 105 110

Ile Ala Met Ala Ser Tyr Cys Ser Glu Leu Gln Tyr Leu Ala Asn Pro
115 120 125

Val Thr Thr His Val Gln Ser Ala Glu Gln His Asn Gln Asp Val Asn
130 135 140

Ser Leu Gly Leu Ile Ser Ser Arg Lys Thr Asn Glu Ala Ile Glu Ile
145 150 155 160

Leu Lys Leu Met Ser Ser Thr Phe Leu Ile Ala Leu Cys Gln Ala Ile
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Asp Leu Arg His Leu Glu Glu Asn Leu Arg Asn Thr Val Lys Asn Thr
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120
caattggctg gaatcaatac cgagttcttt gaattacaac caaaagaagg tcttgcactt
180
gttaatggaa ctgctgttgg ttctggttta gcttctattg ttctttttga ggctaacata
240
ttggcggtgt tgtctgaagt tctatcgga attttcgctg aagtattgca aggggaagccc
300
gaatttactg atcatttgac acataagttg aagcaccacc ctggccaat tgaggctgct
360
gctattatgg aacacatttt ggatgggagt gcttatgtta aagacgcgaa gaagttgcat
420
gagatggacc ctttacagaa gccaaagcaa gatagatatg cacttagaac ttcaccacaa
480
tggcttggtc ctttgattga agtgattaga ttttcaacca agtcaattga gagagagatc
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Leu Leu Thr Gly Arg Xaa Asn Ser Lys Ala His Gly Pro Thr Gly Glu
 20 25 30

Val Leu Asn Ala Lys Glu Ala Phe Gln Leu Ala Gly Ile Asn Thr Glu
 35 40 45

Phe Phe Glu Leu Gln Pro Lys Glu Gly Leu Ala Leu Val Asn Gly Thr
 50 55 60

Ala Val Gly Ser Gly Leu Ala Ser Ile Val Leu Phe Glu Ala Asn Ile
 65 70 75 80

Leu Ala Val Leu Ser Glu Val Leu Ser Ala Ile Phe Ala Glu Val Met
 85 90 95

Gln Gly Lys Pro Glu Phe Thr Asp His Leu Thr His Lys Leu Lys His
 100 105 110

His Pro Gly Gln Ile Glu Ala Ala Ala Ile Met Glu His Ile Leu Asp
 115 120 125

Gly Ser Ala Tyr Val Lys Asp Ala Lys Lys Leu His Glu Met Asp Pro
 130 135 140

Leu Gln Lys Pro Lys Gln Asp Arg Tyr Ala Leu Arg Thr Ser Pro Gln
 145 150 155 160

Trp Leu Gly Pro Leu Ile Glu Val Ile Arg Phe Ser Thr Lys Ser Ile
 165 170 175

Glu Arg Glu Ile Asn Ser Val Asn Asp Asn Pro Leu Ile Asp Val Ser
180 185 190

Arg Asn Lys Ala Leu
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120

ctattaagat atggaagtag tagcagcagc aatcacaaaa aacaacggca agattgatcc
180

attttgcttg aatcatgcta atgctaataa catgaaagtg aatgatgctg atcctttgaa
240

ttggggtgtg gctgctgagg caatgaaggg aagtcaactg gatgaggtga aacgtatggt
300

ggaggagtag cggaagcgca ttgtccgtct tggtagcgag acgctgaaga tttctcaggt
360

ggctgccatt gctgcacacg atgggtcgat gggtgagctg tcggaatctg ctagagccgg
420

cgttaaggca agcagtgatt gggttatgga gagtatgaac aaaggtactg acagttatgg
480

tgtcaccaca gggttcggcg ctacctcnca ccgcgaac aaacaaggtg gtgctttaca
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gaaagggctc ataaggtttt tgaatgctgg aatatttgna aatgnaactg an
592

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Ser Phe Cys Leu Asn His Ala Asn Ala Asn Asn Met Lys Val Asn Asp
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Ala Asp Pro Leu Asn Trp Gly Val Ala Ala Glu Ala Met Lys Gly Ser
35 40 45

His Leu Asp Glu Val Lys Arg Met Val Glu Glu Tyr Arg Lys Pro Ile
50 55 60

Val Arg Leu Gly Gly Glu Thr Leu Thr Ile Ser Gln Val Ala Ala Ile
65 70 75 80

Ala Ala His Asp Gly Ala Met Val Glu Leu Ser Glu Ser Ala Arg Ala
85 90 95

Gly Val Lys Ala Ser Ser Asp Trp Val Met Glu Ser Met Asn Lys Gly
100 105 110

Thr Asp Ser Tyr Gly Val Thr Thr Gly Phe Gly Ala Thr Xaa His Arg
115 120 125

Arg Thr Lys Gln Gly Gly Ala Leu Gln Lys Gly Leu Ile Arg Phe Leu
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Asn Ala Gly Ile Phe Xaa Asn Xaa Thr Xaa
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120

accaatggcc atgctgaaac aacttttagc gtgacaaaa gtgnngnga tccactcaac
180

tggcgnngcag ccgcgagtc gtcgacgggg agtcatttgg atgagggtgaa gcgatatggng
240

gaggagtacc gtaatccgnt ggtaaaaatt ggcggcgaga cgcttaccat tgctnnggta
300

nttggaattg cttctcatga tagtgagtg aggggtggagc tgtccgagtt cgcaaggccc
360

ggcgtaagg cgagtagtga ttgngtgatg gatagcatga acaatgggac tgatagttac
420

ggtgttacca ccgcntttgg tgccacctgt caccggagaa ccaagccang gtgggtgcctt
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gcagaaggag ctaaattnng gtgttttgaa ngctggnaat antttggcnn tgggtcagaa
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Thr Gly Ser His Leu Asp Glu Val Lys Arg Met Xaa Glu Glu Tyr Arg
 35 40 45

Asn Pro Xaa Val Lys Ile Gly Gly Glu Thr Leu Thr Ile Ala Xaa Val
 50 55 60

Xaa Gly Ile Ala Ser His Asp Ser Gly Val Arg Val Glu Leu Ser Glu
 65 70 75 80

Phe Ala Arg Ala Gly Val Lys Ala Ser Ser Asp Xaa Val Met Asp Ser
 85 90 95

Met Asn Asn Gly Thr Asp Ser Tyr Gly Val Thr Thr Xaa Phe Gly Ala
 100 105 110

Thr Cys His Arg Arg Thr Lys Pro Xaa Trp Cys Leu Ala Glu Gly Ala
 115 120 125

Lys Xaa Xaa Cys Phe Glu Xaa Trp Xaa Xaa Phe Gly Xaa Gly Ser Glu
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Ile Xaa Thr Cys Xaa Leu Thr Thr
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120

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180

tgctcgngn

188

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120

ttatcgtgac caaaagtgtt ggtgatccac tcaactgggg tgcagccgcg gagtgcgcga
180

cgggggagtca tttggatgag gtgaagcgta tggnggagga gtaccgtaac ccgntgggta
240

aaattggcgg cgagacgctt accattgctn nggtantcgg aattgcttct catgatagtg
300

gagtggaggt ggagctgtcc gagttcgcaa gggccggcgt taaggcgagt agtgattgng
360

tgatggatag catgaacaat gggactgata gttacggtgt taccaccgcn ttgggtgccca
420

cctgtcaccg gagaaccaag ccanggtggt gccttcgaga aggagctaaa ttnnngtggtt
480

ttgaangctg gnaatanctt ggcnnctggt cagaaatctn aacttgtnca cttaccacac
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541

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120

atcaagagtc ttcttgaaaa tggatactct gttaatacca ctattagagc tgatccagaa
180

cgtaagaggg atgtaagctt cctaacaaat ctacccggcg catccgaag gctacatttc
240

ttcaacgccg atctagacga ccagagaggt ttcaacgaag caattgaagg ttgtgtcggg
300

atatccaca cgccttcacc aatcgatttc gccgtgagtg agccagaaga aatagtgaca
360

aaaaaagacag tggatggagc attaggaatt ttaaaagcat gtgtgaattc aaagacagtg
420

aagagattta tttaacttc aagnggttct gctgtttcat tcaatggaaa aaacaagat
480

gnntnggatg agagtgattg gagtgatgtt gatttgctta gaagtgttaa accatttggt
540

tggagttatg gngtgttcaa gactttggct gagaaagcag tgcttgaatt tgggtcnacaa
600

aatgggattg atgtgtttac ttgtattctt cctttttattg ttggagggtt tgtttgtccc
660

aagcttctctg attctgttga gaaagctctt gttttggtag taggcaaaaa ggaacaaatt
720

ggtattataa gtttcacat ggtacatgta gatgatgtgg cttaggcaca tatctatcta
780

cttgagaatc ctgttccagg aggtagatat aattgttcac cattctttgt atctattgaa
840

gaaagtgcac agcttctctc agccaaatat ccagaatato aaatactatc agtagatgag
900

ttgaaggaaa ttaaaggggc aagattgcc aatttgaact cgaagaagct cgtggacgct
960

ggttttgagt ttaagtatat tgtcgatgat atgttcgatg atgcgattca atgctgcaag
1020

gaaaaaggct atctctaagc atgtatttga aaattccatg aagttgagaa aacaataatg
1080

tgccataaat caatgatggc taatgagatg tacaagtta tgcattaagt tattttgtgat
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 Asn Thr Thr Ile Arg Ala Asp Pro Glu Arg Lys Arg Asp Val Ser Phe
 35 40 45
 Leu Thr Asn Leu Pro Gly Ala Ser Glu Arg Leu His Phe Phe Asn Ala
 50 55 60
 Asp Leu Asp Asp Pro Glu Ser Phe Asn Glu Ala Ile Glu Gly Cys Val
 65 70 75 80
 Gly Ile Phe His Thr Ala Ser Pro Ile Asp Phe Ala Val Ser Glu Pro
 85 90 95
 Glu Glu Ile Val Thr Lys Arg Thr Val Asp Gly Ala Leu Gly Ile Leu
 100 105 110
 Lys Ala Cys Val Asn Ser Lys Thr Val Lys Arg Phe Ile Tyr Thr Ser
 115 120 125
 Xaa Gly Ser Ala Val Ser Phe Asn Gly Lys Asn Lys Asp Xaa Xaa Asp
 130 135 140
 Glu Ser Asp Trp Ser Asp Val Asp Leu Leu Arg Ser Val Lys Pro Phe
 145 150 155 160
 Gly Trp Ser Tyr Xaa Val Phe Lys Thr Leu Ala Glu Lys Ala Val Leu
 165 170 175
 Glu Phe Gly Xaa Gln Asn Gly Ile Asp Val Val Thr Leu Ile Leu Pro
 180 185 190
 Phe Ile Val Gly Gly Phe Val Cys Pro Lys Leu Pro Asp Ser Val Glu
 195 200 205
 Lys Ala Leu Val Leu Val Leu Gly Lys Lys Glu Gln Ile Gly Ile Ile
 210 215 220
 Ser Phe His Met Val His Val Asp Asp Val Ala Arg Ala His Ile Tyr
 225 230 235 240
 Leu Leu Glu Asn Pro Val Pro Gly Gly Arg Tyr Asn Cys Ser Pro Phe
 245 250 255
 Phe Val Ser Ile Glu Glu Met Ser Gln Leu Leu Ser Ala Lys Tyr Pro
 260 265 270
 Glu Tyr Gln Ile Leu Ser Val Asp Glu Leu Lys Glu Ile Lys Gly Ala
 275 280 285

Arg Leu Pro Asp Leu Asn Ser Lys Lys Leu Val Asp Ala Gly Phe Glu
290 295 300

Phe Lys Tyr Ser Val Asp Asp Met Phe Asp Asp Ala Ile Gln Cys Cys
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120
atcaagagtc ttcttgaaaa tggatactct gttaatacca ctattagagc tgatccagaa
180
cgtaagaggg atgtaagctt cctaacaaat ctaccggcg catccgaaag gctacatttc
240
ttcaacggcg atctagacga cccagagagt ttcaacgaag caattgaagg ttgtgtcggg
300
atatccaca ccgcttcacc aatcgatttc gccgtgagtg agccagaaga aatagtgaca
360
aaaagaacag tggatggagc attaggaatt ttaaaagcat gtgtgaattc aaagacagtg
420
aagagattta ttacacttc aagnggttct gctgtttcat tcaatgnaaa aancaagat
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120

aagactcttc ttgaaatgg atactctggt aataccacta ttagagctga tccagaacgt
180

aaggggatg taagcttcct aacaaatcta cccggcgcat ccgaaaggct acatttcttc
240

aacgccgatc tagacgacct agagagtttc aacgaagcaa ttgaaggttg tgtcgggata
300

ttccacacc cttaccaat cgatttcgcc gtgagtgcgc cagaagaaat agtgacaaaa
360

agaacagtgg atggagcatt aggaatttta aaagcatgtg tgaattcaaa gacagtgaag
420

agatttattt acacttcaag tggttctgct gtttcattca atggaaaaaa caaagatgtt
480

ttggatgaga gtgattggag tgatgttgat ttgottagaa gtgttaaacc atttggttgg
540

agttatggtg tnttcaagac ttggctgag aaagcagtcg ttgaatttgg tcaacaaaa
600

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601

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120

attctgttga gaaagctctt gttttggtac taggcaaaaa ggaacaaatt ggtattataa
180

gtttccacat ggtacatgtg gatgatgtgg cttagacaca tatctatcta cttgagaatc
240

ctgttccagg aggttagatat aattgttcac cattctttgt atctattgaa gaaatgtcac
300

agctctcttc agccaaatat ccagaatata aaatactata ttagatgag ttgaaggaaa
360

ttaaaggggc aagggttgcca gatttgaact cgaagaagct cgtggacgct gggtttgagt
420

ttaagtatat tgcgatgat atgttcgatg atgcgattca atgctgcaag gaaaaaggct
480

atctctaagc atgtgtttga aaattccatg aagttgagaa aacaatactg tgcctaaaa
540

caatgatggc taatgatgat tacaagtta tgcattaagt tatttgtgat caatcaata
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120

agaaagctct tgttttggtg ctaggcaaaa aggaacaaat tgggtattata agttccaca
180

tggtacatgt ggatgatgtg gctagagcac atatctatct acttgagaat cctgttccag
240

gaggtagata taattgttca ccattctttg tatctattga agaaatgtca cagcttcttt
300

cagccaaata tccagaatat caaatactat ctgtagatga gttgaaggaa attaaagggg

360

caagggttgc agatttgaac tcgaagaagc tcgtggacgc tggttttgag ttttaagtata
420

gtgtcgatga tatgttcgat gatgcgattc aatgctgcaa ggaaaaaggc tatctctaag
480

catgtgtttg aaaattccat gaagttgaga aaacaatact gtgcctaaaa tcaatgatgg
540

ctaattgagat gtacaagttt atgcattaag ttatttgtga tcaatcaaat aatgaaataa
600

tc

602

<210> 284
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120

aggcaaaaaag gaacaaattg gtattataag ttccacatg gtacatgtag atgatgtggc
180

tagagcacat atctatctac ttgagaatcc tgttccagga ggtagatata attgttcacc
240

attcttttga tctattgaag aaatgtcaca gcttctctca gccaaatc cagaatatca
300

aatactatca gtagatgagt tgaaggaaat taaagggtgca agattgccag atttgaactc
360

gaagaagctc gtggacgctg gttttgagtt taagtatagt gtcgatgata tgtttgatga
420

tgcgattcaa tgcgtcaagg aaaaaggcta tctctaagca tgtatttgaa aattccatga
480

agttgagaaa acaataatgt gcctaaaatc aatgatggct aatgatagtg acaagtttat
540

gcattaagtt atttgtgac aatcaataa tgaan
575

<210> 285
<211> 604
<212> DNA
<213> *Trifolium repens*

<220>
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<222> (1)..(2)
<223> Any nucleotides

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<222> (14)..(15)
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<222> (56)..(56)
<223> Any nucleotide

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120

aggcaaaaag gaacaaattg gtattataag tttccacatg gtacatgtag atgatgtggc
180

tagagccatc atctatctac ttgagaatcc tgttccagga ggtagatata attgttcacc
240

attcttttga tctattgaag aaatgtcaca gcttctctca gccaaatc cagaatatca
300

aatactatca gtagatgagt tgaaggaaat taaagggtgca agattgccag atttgaactc
360

gaagaagctc gtggacgctg gttttgagtt taagtatagt gtcgatgata tgtttgatga
420

tgcgattcaa tgcgtcaagg aaaaaggcta tctctaagca tgtatttgaa aattccatga
480

agttgagaaa acaataatgt gcctaaaatc aatgatggct aatgagatgt acaagtttat
540

gcattaagtt atttgtgac aatcaataa tgaataatc tgttcatttt tccgaaaaaa
600

aaaa
604

<210> 286
<211> 695
<212> DNA
<213> *Lolium perenne*

<400> 286
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120

agtcagagac ccaggcaatc agaagaaggt agcacacctc tggaaacttag caggggcca
180

ggaaagtggt gagcttgta aagctgacct cttggaagaa gggagcttcg atgatgctgt
240

gatggcctgt gaggtgtct tccacactgc atcacctatc atcaccaaat ctgataccaa
300

ggaaagaaat cttgattctg caattaacg cactcctaac gtgctgagat cgtgcaagaa
360

gaatcctttt ctcaaaaggg ttgttctcac gtcatcatcg tcaaccgtga ggctgaggg
420

tgaagctgaa ttcccacca acgtgttgct ggatgaacaa tcatggagct ccgtggagtt
480

ctgtgaaagt atccaggtat ggtatggtgt cgcgaagatc cttgctgaga aatcagcttg
540

ggagttcgcc aagagaaca acatcgacct agtggtgtgt cttccaacgt tcgtgattgg
600

acctaacttc tcgcttgaat taggaccac tggttttagat gtccttggtc tatttaaagg
660

agagacagag aagttcacca tgtttkggaa ggatg
695

<210> 287
<211> 231
<212> PRT
<213> *Lolium perenne*

<400> 287

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Gly Ala Ser Gly Phe Val Ala Ser Trp Leu Val Lys Arg Leu Leu Glu

20	25	30
Ser Gly Tyr Asn Val Leu Gly Thr Val Arg Asp Pro Gly Asn Gln Lys 35 40 45		
Lys Val Ala His Leu Trp Asn Leu Ala Gly Ala Lys Glu Arg Leu Glu 50 55 60		
Leu Val Lys Ala Asp Leu Leu Glu Glu Gly Ser Phe Asp Asp Ala Val 65 70 75 80		
Met Ala Cys Glu Gly Val Phe His Thr Ala Ser Pro Ile Ile Thr Lys 85 90 95		
Ser Asp Thr Lys Glu Glu Met Leu Asp Ser Ala Ile Asn Gly Thr Leu 100 105 110		
Asn Val Leu Arg Ser Cys Lys Lys Asn Pro Phe Leu Lys Arg Val Val 115 120 125		
Leu Thr Ser Ser Ser Ser Thr Val Arg Leu Arg Asp Glu Ala Glu Phe 130 135 140		
Pro Pro Asn Val Leu Leu Asp Glu Thr Ser Trp Ser Ser Val Glu Phe 145 150 155 160		
Cys Glu Ser Ile Gln Val Trp Tyr Gly Val Ala Lys Ile Leu Ala Glu 165 170 175		
Lys Ser Ala Trp Glu Phe Ala Lys Glu Asn Asn Ile Asp Leu Val Ala 180 185 190		
Val Leu Pro Thr Phe Val Ile Gly Pro Asn Leu Ser Ser Glu Leu Gly 195 200 205		
Pro Thr Val Leu Asp Val Leu Gly Leu Phe Lys Gly Glu Thr Glu Lys 210 215 220		
Phe Thr Met Phe Gly Lys Asp 225 230		

<210> 288
 <211> 667
 <212> DNA
 <213> Lolium perenne

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 <222> (19)..(19)
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120
caggcaatca gaagaaggta gcacacctctt ggaacttagc agggggccaag gaaaggttgg
180
agcttgtcaa agctgacctc ttggaagaag ggagcttcga tgatgctgtg atggcctgtg
240
aggggtgtctt ccacactgca tcacctatca tcaccaaatc tgataccaag gaagaaatgc
300
ttgattctgc aattaacggc actctaaacg tgcctgagatc gtgcaagaag aatccttttc
360
tcaaaagggg tgttctcacg tcatcatcgt caaccgtgag gctgagggat gaagctgaat
420
tcccaccaa cgtgttgctg gatgaaacat catggagctc cgtggagttc tgtgaaagta
480
tccaggtatg gtatggtgtc gcgaagatcc ttgctgagaa atcagcttgg gagttcgcca
540
aggagacaac catcgaccta gtggctgttc ttccaacgtt cgtgattgga cctaactctc
600
cgtctgaatt aggaccact gtttttagatg tccttggctt atttaaagga gagacagaga
660
agttcac
667

<210> 289
<211> 688
<212> DNA
<213> *Lolium perenne*

<220>
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<222> (23)..(23)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (651)..(651)
<223> Any nucleotide

<400> 289
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120
gaccaggga atcagaagaa ggtagcacac ctctggaact tagcaggggc caaggaaagg
180
ttggagcttg tcaaaagctga cctcttgga gaaggagact tcgatgatgc tgtgatggcc

240

tgtgagggtg tcttccacac tgcacacct atcatcacca aatctgatac caaggaagaa
300

atgcttgatt ctgcaattaa cggcactcta aacgtgtga gatcgtgcaa gaagaatcct
360

ttctcaaaa gggttgttct cactgcatca tcgtcaaccg tgaggctgag ggatgaagct
420

gaattccac ccaacgtgtt gctggatgaa acatcatgga gtcctgtgga gttctgtgaa
480

agtatccagg tatggtatgg tgtcgcgaag atcctgtctg agaaatcagc ttgggagttc
540

gccaaaggaga acaacatcga cctagtggtc gttcttccaa cgctcgtgat tggacctaata
600

ctctcgtctg aattaggacc cactgtttta gatgtccttg gcttatttaa nggagagaca
660

gagaagttca ccatgttttg gaaggatg
688

<210> 290
<211> 425
<212> DNA
<213> *Lolium perenne*

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<222> (62)..(62)
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<222> (352)..(352)
<223> Any nucleotide

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<222> (423)..(423)
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120
gaagaaggta gcacacctct ggaacttagc agggggccaag gaaagggttg agcttgtaa
180

agctgacctc ttggaagaag ggagcttcga tgatgctgtg atggcctgtg aggggtgtctt
240

ccacactgca tcacctatca tcaccaaato tgataccaag gaagaaatgc ttgattctgc
300

aattaacggc actctaaacg ngctgagatc gngcaagaag aatncttttc tnaaaagggg
360

tgntctcagc tcatcatcgc caccocngan gctganggat gaanctgant tccccccaa
420

cgngn
425

<210> 291

<211> 691

<212> DNA

<213> *Lolium perenne*

<220>

<221> misc_feature

<222> (691)..(691)

<223> Any nucleotide

<400> 291

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120

cagagaccga ggcaatcaga agaaggtagc acacctctgg agcttagcag gggccaagga
180

aaggctggag cttgtcagag ctgacctctt ggaagaagg agcttcgatg atgcgctgat
240

ggcctgtgag ggtgtcttcc acactgcac acctatcat accaaatctg ataccaagga
300

agaaatgctt gattctgcaa taaacggcac tctaaacgtg ctgagatcgt gcaagaagaa
360

tccttttctc aaaagggttg ttctcacgtc atcatcgtca accgtgaggc tgagggatga
420

agctgaatto ccaaccaacg tgttgctgga tgaaacatca tggagctcgg tggagtcttg
480

tgaaagtate caggatgggt acggtgtcgc aaagatcctt gccagagaaat cagcctggga
540

gtttgccaaq gagaacaaca tcgacctagt ggctgttctt ccaacattcg tgattggacc
600

taatctctcg tctgaattag gaccocactgt tttagatgtc cttggcttat ttaaaggaga
660

gacagagaag ttcacatgt ttgggaagga n
691

<210> 292

<211> 365
<212> DNA
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<400> 292
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120

gtcagagacc caggcaatca gaagaaggta gcacacctct ggagcttagc aggggccaag
180

gaaaggctgg agcttgtcag agctgacctc ttggaagaag ggagcttcga tgatgcogtg
240

atggcctgtg aggggtgtctt ccacactgca tcacctatca tcaccaaatc tgataccaag
300

gaagaaatgc ttgattctgc aataaacggc nctctaaacg tgcgtgnnacc cgggtnaaaa
360

aaan
365

<210> 293
<211> 524
<212> DNA
<213> Lolium perenne

<220>
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<222> (169)..(169)
<223> Any nucleotide

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120
aagtgcgaag acgacggcaa gcccatggcg aagccgtaca agttctccna ccagaggctc
180
agggacctgg gattaaaatt cactcgcgtg gcggaaagtt tgtacgagac cgtgacgtgc
240
ctgcaaaaaa atggccacct gcctctgccc gctcccatgg cgccaaagcg tgcataccta
300
taatactaca aagacacggc cggtatcgac aagccaagaa acagaggatt ctcccgaggt
360
tcacatggga attgtgtatt tcacaaagtt tgaattctta ttttttttat tatgaagaaa
420
tacggaaaaa caatactgta taccagaggc aagtgttaaca atgtaaatag tcgtgtaaat
480
cttgttcaag aatgaatgat aaagtatttt ttgcaaaaaa aaaa
524

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<210> 294
<211> 100
<212> PRT
<213> Lolium perenne

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<222> (57)..(57)
<223> Any amino acid

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<400> 294

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Val Leu Ala Tyr Glu Arg Pro Asp Ala Arg Gly Arg Tyr Leu Cys Ile
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Gly Ala Val Leu His Arg Ala His Phe Leu Lys Leu Leu Lys Asp Leu
20          25          30

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```

Phe Pro Gln Tyr Ser Phe Thr Ala Lys Cys Glu Asp Asp Gly Lys Pro
35          40          45

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Met Ala Lys Pro Tyr Lys Phe Ser Xaa Gln Arg Leu Arg Asp Leu Gly
50          55          60

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```

Leu Lys Phe Thr Pro Leu Ala Glu Ser Leu Tyr Glu Thr Val Thr Cys
65          70          75          80

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Leu Gln Lys Asn Gly His Leu Pro Leu Pro Ala Pro Met Ala Pro Lys
85          90          95

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Arg Ala Tyr Leu
100

<210> 295
<211> 524
<212> DNA
<213> Lolium perenne

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<222> (306)..(306)
<223> Any nucleotide

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<222> (482)..(482)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (519)..(519)
<223> Any nucleotide

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120

aagtcgcaag acgacggcaa gcccatggcg aagccgtaca agttctccaa ccagaggctc
180

agggacctgg gattaaaaatt cactccgctg gcggaaaagtt tgtacgagac cgtgacgtgc
240

ctgcaaaaaa atgccacact gcctctgccc gctcccgctg cgccaaaagcg tgcatactta
300

taatantacc aagacacggc cgggatcgac aagccaagaa acagaggatt ctcccagggt
360

tcaccatgga attgtgtatt tcagaaagtt tgaattctta ttttttttat tatgaaggaa
420

tacggataac caatactgta taccagaggc aagtgttaaca atgtaaatag tcgtgtaaat
480

cntgttcaag attgaatgat aaagtatttt ttgcaaaaana aaaa
524

<210> 296
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<212> DNA
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<223> Any nucleotide

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<222> (25)..(26)

<223> Any nucleotides

<400> 296

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gcggaaagtt tgtacgagac cgtgacgtgc ctgcaaaaaa atggccacct gcctctgcc
120

gtctccatgg cgccaaagcg tgcataccta taatactaca aagacacggc cgggatcgac
180

aagccaagaa acagaggatt ctcccagggt tcaccatgga attgtgtatt tcacaaagtt
240

tgaattctta ttttttttat tatgaagaaa tacggaaaac caatactgta taccagaggg
300

aagtgttaaca atgtaaatag tcgtgtaaat ctgtgtcaag aatgaatgat aaagtatttt
360

ttgcaaaaaa aaaa
374

<210> 297

<211> 363

<212> DNA

<213> Lolium perenne

<220>

<221> misc_feature

<222> (7)..(8)

<223> Any nucleotides

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<222> (363)..(363)

<223> Any nucleotide

<400> 297

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gtacgagacc gtgacgtgcc tgcaaaaaaa tggccacctg cctctgcccg ctccatggcc
120

gccaaagcgt gcatacctat aatactacaa agacacggcc gggatcgaca agccaagaaa
180

cagaggatcc tcccagggtt caccatggaa ttgtgtattt cacaagttt gaattcttat
240

tttttttatt atgaagaaat acggaaaaac aatactgtat accagaggca agtgaataca
300

tgtaaatagt cgtgtaaatc ttgttcaaga atgaatgata aagtattttt tgcaaaaaaa

360

aan
363<210> 298
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<223> Any nucleotide<400> 298
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180cgcccgagcc tcgccaatgt cgaccacgag tcggcgcgcg gcattccgct catcgacctg
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600gcgctggcgc tgaggctcct ggaggcgata tcggagagcc tagggctgga gagaggccac
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720

cgcgagccgg agctcaccta cggctcgcca gggcacacgg accccaacgc cctcaccatc
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840

gccgtccacc cagcggccaa cgccctggtc atcaacctag gcgaccagct acaggcgctg
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agcaacggcg cgtacaagag cgtgtggcac cgggcagtgg tgaacgcgga gcaggagcgt
960

ctgtcggtgg catcttttct gtgccctgtc aacagcgcggt ttatctgccc cgcgccgagg
1020

ctcgtcgggc acgggggagga ccccgcttac cggagctaca cctacgacga gtactacaag
1080

aggtttttgga gcaggaaact ggatcaggag cactgcctcg agctcttcag gagtcagcac
1140

tgatgcttga accttgagbt actagctagc tctctttaac agtgcaaatc catggcccaa
1200

gagggccccc attgcatggt tacttatggt gtttgaaactg gtattgctta agtgcccta
1260

aacattgcta cattctactn ctatcttgtc cgtttaaaat tataagatgg cctaaccctt
1320

ttcttaattg tatgcatnct gaacatatat aagtgtgtgt gttcagacag tttagtctgc
1380

a
1381

<210> 299
<211> 346
<212> FRT
<213> Lolium perenne

<400> 299

Met Ser Asn Pro Leu Leu Ser Asp Arg Val Ala Arg Ser Lys Lys Val
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Pro Ser Ser His Val Arg Ala Val Gly Asp Arg Pro Asp Leu Ala Asn
20 25 30

Val Asp His Glu Ser Gly Ala Gly Ile Pro Leu Ile Asp Leu Lys Gln
35 40 45

Leu Glu Gly Pro Gly Arg Arg Val Val Glu Ala Ile Gly Ser Ala
50 55 60

Cys Glu Asn Asp Gly Phe Phe Met Val Thr Asn His Gly Ile Pro Glu
65 70 75 80

Ala Val Val Glu Gly Met Leu Ser Val Ala Arg Glu Phe Phe His Leu
85 90 95

Pro Glu Ser Glu Arg Leu Lys Cys Tyr Ser Asp Asp Pro Lys Lys Ala
 100 105 110

Val Arg Leu Ser Thr Ser Phe Asn Val Arg Thr Glu Lys Val Ser Asn
 115 120 125

Trp Arg Asp Phe Leu Arg Leu His Cys Tyr Pro Leu Glu Ser Phe Val
 130 135 140

Asp Gln Trp Pro Ser Asn Pro Pro Ala Phe Arg Gln Val Val Gly Thr
 145 150 155 160

Tyr Ser Thr Glu Ala Arg Ala Leu Ala Leu Arg Leu Leu Glu Ala Ile
 165 170 175

Ser Glu Ser Leu Gly Leu Glu Arg Gly His Met Val Lys Ala Met Gly
 180 185 190

Arg His Ala Gln His Met Ala Val Asn Tyr Tyr Pro Pro Cys Pro Gln
 195 200 205

Pro Glu Leu Thr Tyr Gly Leu Pro Gly His Thr Asp Pro Asn Ala Leu
 210 215 220

Thr Ile Leu Leu Met Asp Pro His Val Ser Gly Leu Gln Val Leu Arg
 225 230 235 240

Asp Gly Ala Lys Trp Ile Ala Val His Pro Arg Pro Asn Ala Leu Val
 245 250 255

Ile Asn Leu Gly Asp Gln Leu Gln Ala Leu Ser Asn Gly Ala Tyr Lys
 260 265 270

Ser Val Trp His Arg Ala Val Val Asn Ala Glu Gln Glu Arg Leu Ser
 275 280 285

Val Ala Ser Phe Leu Cys Pro Cys Asn Ser Ala Val Ile Cys Pro Ala
 290 295 300

Pro Arg Leu Val Gly Asp Gly Glu Asp Pro Val Tyr Arg Ser Tyr Thr
 305 310 315 320

Tyr Asp Glu Tyr Tyr Lys Arg Phe Trp Ser Arg Asn Leu Asp Gln Glu
 325 330 335

His Cys Leu Glu Leu Phe Arg Ser Gln His
 340 345

<210> 300
<211> 755
<212> DNA
<213> *Lolium perenne*

<220>
<221> misc_feature
<222> (5)..(5)
<223> Any nucleotide

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120

agtgatcggg tggcacgctc caagaaagtc ccatctagcc acgttagagc ggtgggagac
180

cgccacagacc tcgccaatgt cgaccacgag tcgggcggcg gcattcgcct catcgacctg
240

aagcagctcg aagggtccagg gcgcccgcagg gtctctgagg ccatcggtctc cgcgtgcgag
300

aacgatgggt ttttcatggt gacgaatcat ggcattccag aggcggtcgt ggaggggatg
360

ctgagcgtgg cgaggggagt ctccacctg ccggagtcgg agcgggtcaa gtgctactcc
420

gacgacccca agaaggcggt ccggctgtcg acgagcttca acgtgcgcac ggagaagggtg
480

agcaactggc gcgacttctc ccggctgcat tgctaccctc ttgagagctt cgtcgaccag
540

tggccgtcga acccgcccg cttcaggcaa gtctcgcca cctactcgac ggaagcgaga
600

gcgctggcgc tgaggctcct ggaggcgata tcggagagcc tagggctgga gagaggccac
660

atggtgaagg ccatggggcg gcaacgcgag cacatggcgg tgaactacta cccgccgtgc
720

ccgcagccgg agctcaccta cggctctgcca gggca
755

<210> 301
<211> 780
<212> DNA
<213> *Lolium perenne*

<220>
<221> misc_feature
<222> (21)..(21)
<223> Any nucleotide

<220>
<221> misc_feature
<222> (778)..(778)

<223> Any nucleotide

<400> 301

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120

tgatcgggtg gcaacgtcca agaaagtccc atctagccac gttagagcgg tgggagaccg
180

ccgacacctc gccaatgtcg accacgagtc cggcgcgggc attcgcgtca tcgacctgaa
240

gcagctcgaa ggtccagggc gccgcagggt cgtcgaggcc atcgggtccg cgtgcgagaa
300

cgatgggttt ttcatgtgta cgaatcatgg catcccagag gcggtcgtgg aggggatgct
360

gagcgtggcg agggagtctt tccacctgcc ggagtcggag cggctcaagt gctactccga
420

cgaccccaag aaggcgggtc ggctgtcgac gagcttcaac gtgcgcacgg agaaggtgag
480

caactggcgc gacttctctc ggctgcattg ctacctctt gagagcttcg tcgaccagtg
540

gccgtcgaac ccgcccgctc tcaggcaagt cgtcggcacc tactcgacgg aagcgagagc
600

gctggcgctg aggcctctgg aggcgatatc ggagagccta gggctggaga gaggccacat
660

ggtgaaggcc atggggcggc acgcgcagca catggcggtg aactactacc cgccgtgccc
720

gcagccggag ctacactacg gtctgccagg gcacacggac cccaatgcc tcaccatnct
780

<210> 302

<211> 793

<212> DNA

<213> Lolium perenne

<220>

<221> misc_feature

<222> (64)..(64)

<223> Any nucleotide

<220>

<221> misc_feature

<222> (692)..(692)

<223> Any nucleotide

<220>

<221> misc_feature

<222> (750)..(750)

<223> Any nucleotide

<400> 302
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120
taccgcgggt gccccgagcc ggacctcacc tacggcctgc ccaagcacac ggaccccaac
180
gccctcacca tectctcat ggatccccac gtctcgggcc tcagggtcct cagggaaggc
240
gccaaagtga tcgcgtcca cccacgcccc aacgccttg tcataacct aggcgaccag
300
ctacaggcgc tgagcaacgg cgcgtacaag agcgtgtggc accgggcagt ggtgaacgag
360
gagcaggagc gtctgtcggg ggcatcttct ctgtgccgt gcaacagcgc ggttatctgc
420
cccgcgccga ggctcgtcgg cgacggggag gacccgtct accggagcta cacctacgac
480
gagtactaca agaggttttg gagcaggaac ctggatcagg agcactgcct cgagctcttc
540
aggagtcagc actgatgctt gaaccttgag ttactagcta gctctctta acagtcaaa
600
tccatggccc aagagggccc cgattgcatg gttactatg ttgtttgaac tggatttgc
660
taagtgccta ataacattgc tacattctac tncatcttg tccgtttaaa attataagat
720
ggcctaacct ttttcttaat tgtatgcatt ctgaacatat ttaagtgtgt gtgttcagac
780
agtttagtct gca
793

<210> 303
<211> 1395
<212> DNA
<213> *Lolium perenne*

<400> 303
gaattcgatt aagcagtggt aacaacgcag agtacgggg gactctcaga acacactgtg
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taaccacggt agcagtggt aagactagca gaaagtacgg acatcagcta accattcttc
120
aactagaata agcatggctc cggcgatgac caaccctctc ctacgtgac gggtggcacg
180
ctccaagaaa gtcccatcta gccacgttag agcggtgagg gaccgccag acctcgccaa
240
tgtcgaccac gagtcggcg cgggcattcc gctcatcgac ctgaagcagc tcgaaggctc
300

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aggcgccgcg agggctcgtcg agggccatcgg ctcccgctgc gagaacgatg ggtttttcat
360
ggtgacgaat catggcatcc cagaggcggg cgtggagggg atgctgagcg tggcgaggga
420
gtttttccac ctgccggagt cggagcggct caagtgtac tccgacgacc ccaagaaggc
480
ggtcgggctg tcgacgagct tcaactgtcg cacggagaag gtgagcaact ggcgcgactt
540
cctccggctg cattgtctacc ctcttgagag ctctcgtcgc cagtggccgt cgaaccgcgc
500
cgcccttcagg caagtctgtcg gcacctactc gaagggaagcg agagcgctgg cgctgaggct
560
cctggaggcg atatcggaga gcctagggct ggagagaggc cactgggtga aggccatggg
720
gcggcacgcg cagcacatgg cgggtaacta ctaccgccg tgcccgcagc cggagctcac
780
ctacggtctg ccaggggcaca aggaccccaa tgccatcacg ctccctctcg aggacggcgt
840
ctccggcctg caggctccagc gcgacggccg gtgggtggcc gtcaaccocg tgcccaacgc
900
cctcgctcatc aacatcggcg atcagttaca ggcgctgagc aacgaccgat acaagagcgt
960
gaaccacaga gtgatcgtca acagcgcgag cgagaggatt tcggtgccga cgtttctactg
1020
ccgctcgccg gacacgggtg tcgcgccggc cgacgcgctg gtggacgacg cccaccctcg
1080
ggcctaccag cccttcacgt accaggagta ctaaggaggag ttctggaaga tgggccttca
1140
gtcagcaagt tgcctcgaca ggttcgcagc gatcgagtga tggacaagac gtgggcccgtt
1200
gttatctcct gggccatgag cgttgccgca gccgatgtgt cgccatatgg tggagacggt
1260
tcctccctcc ggaagaaaaa aataaaacag agtgagagacc actagaaccg tcagatagca
1320
tcccaaaaaa aaaaaaaaaa aaaaaaaaaa aaagtactc tgcgttggtta ccactgctta
1380
atcactagtg aattc
1395

<210> 304
<211> 348
<212> PRT
<213> Lolium perenne

<400> 304
Met Ala Pro Ala Met Ser Asn Pro Leu Leu Ser Asp Arg Val Ala Arg

```

1	5	10	15
Ser Lys Lys Val Pro Ser Ser His Val Arg Ala Val Gly Asp Arg Pro	20	25	30
Asp Leu Ala Asn Val Asp His Glu Ser Gly Ala Gly Ile Pro Leu Ile	35	40	45
Asp Leu Lys Gln Leu Glu Gly Pro Gly Arg Arg Arg Val Val Glu Ala	50	55	60
Ile Gly Ser Ala Cys Glu Asn Asp Gly Phe Phe Met Val Thr Asn His	65	70	75
Gly Ile Pro Glu Ala Val Val Glu Gly Met Leu Ser Val Ala Arg Glu	85	90	95
Phe Phe His Leu Pro Glu Ser Glu Arg Leu Lys Cys Tyr Ser Asp Asp	100	105	110
Pro Lys Lys Ala Val Arg Leu Ser Thr Ser Phe Asn Val Arg Thr Glu	115	120	125
Lys Val Ser Asn Trp Arg Asp Phe Leu Arg Leu His Cys Tyr Pro Leu	130	135	140
Glu Ser Phe Val Asp Gln Trp Pro Ser Asn Pro Pro Ala Phe Arg Gln	145	150	155
Val Val Gly Thr Tyr Ser Thr Glu Ala Arg Ala Leu Ala Leu Arg Leu	165	170	175
Leu Glu Ala Ile Ser Glu Ser Leu Gly Leu Glu Arg Gly His Met Val	180	185	190
Lys Ala Met Gly Arg His Ala Gln His Met Ala Val Asn Tyr Tyr Pro	195	200	205
Pro Cys Pro Gln Pro Glu Leu Thr Tyr Gly Leu Pro Gly His Lys Asp	210	215	220
Pro Asn Ala Ile Thr Leu Leu Leu Gln Asp Gly Val Ser Gly Leu Gln	225	230	235
Val Gln Arg Asp Gly Arg Trp Val Ala Val Asn Pro Val Pro Asn Ala	245	250	255
Leu Val Ile Asn Ile Gly Asp Gln Leu Gln Ala Leu Ser Asn Asp Arg	260	265	270

Tyr Lys Ser Val Asn His Arg Val Ile Val Asn Ser Ala Ser Glu Arg
 275 280 285

Ile Ser Val Pro Thr Phe Tyr Cys Pro Ser Pro Asp Thr Val Val Ala
 290 295 300

Pro Ala Asp Ala Leu Val Asp Asp Ala His Pro Arg Ala Tyr Gln Pro
 305 310 315 320

Phe Thr Tyr Gln Glu Tyr Tyr Glu Glu Phe Trp Lys Met Gly Leu Gln
 325 330 335

Ser Ala Ser Cys Leu Asp Arg Phe Arg Arg Ile Glu
 340 345

<210> 305
 <211> 1309
 <212> DNA
 <213> *Trifolium repens*

<400> 305
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tataagtttc ttggtgaaaa aagagtttgt aaattaacat catggctagt atcaaacaaa
 120

ttggaaacaa gaaagcatgt gtgattggtg gcactgggtt tgttgcatct atgttgatca
 180

agcagttact tgaaaagggt tatgctgtta atactaccgt tagagaccca gatagcccta
 240

agaaaaatc tcacctagt gcactgcaaa gtttggggga actgaatcta tttagagcag
 300

acttaacagt tgaagaagt ttgatgctc ctatagcagg atgtgaactt gtttttcaac
 360

ttgtacacc tgtgaacttt gcttctcaag atcctgagaa tgacatgata aagccagcaa
 420

tcaaagggtg gttgaatgtg ttgaaagcaa ttgcaagagc aaaagaagtt aaaagagtta
 480

tcttaacatc ttccgcagcc gcggtgacta taaatgaact caaagggaca ggtcatgtta
 540

tggatgaaac caactggtct gatgttgaat ttctcaacac tgcaaaacca cccactggg
 600

gttatctctc ctcaaaaatg ctagtgtgaa aggctgcatg gaaatttgcg gaagaaaatg
 660

acattgatct aatcactgtg atacctagtt taacaactgg tccttctctc acaccagata
 720

tcccatctag tgttggtctg gcaatgtctc taataacagg caatgatctt ctcataaatg
 780

ctttgaaagg aatgcagttt ctgtcgggtt cgttatcoat cactcatggt gaggatattt
 840
 gccgagctca tatatttctt gcagagaaag aatcagcttc tggtagatac atttgctgtg
 900
 ctcaacaatc tagtggtccc gagcttgcaa agttttctcaa caaacgatat cctcagtata
 960
 aagttccaac tgaatttgat gattgcccc gcaaggcaaa gttgataatc tcttctgaaa
 1020
 agcttatcaa agaagggttc agtttcaagc atggtattgc cgaacttttc gaccagactg
 1080
 tcgagtattt taagactaag ggggcactga agaattagat tttgatattt ctaattcaat
 1140
 agcaactctc aagcttggtta tgtgtttgtg aagtctcagag tgaatatca aatgaataag
 1200
 tggagagagc acaataagag gagagcacia taattttgga aaaaaaaaaa aaaaaaaaaa
 1260
 aaaaaaaaag actctgcggt gttaccactg cttaatcact agtgaattc
 1309

<210> 306
 <211> 338
 <212> PRT
 <213> Trifolium repens

<400> 306

Met	Ala	Ser	Ile	Lys	Gln	Ile	Gly	Asn	Lys	Lys	Ala	Cys	Val	Ile	Gly
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Gly	Thr	Gly	Phe	Val	Ala	Ser	Met	Leu	Ile	Lys	Gln	Leu	Leu	Glu	Lys
			20					25						30	

Gly	Tyr	Ala	Val	Asn	Thr	Thr	Val	Arg	Asp	Pro	Asp	Ser	Pro	Lys	Lys
			35				40					45			

Ile	Ser	His	Leu	Val	Ala	Leu	Gln	Ser	Leu	Gly	Glu	Leu	Asn	Leu	Phe
	50					55					60				

Arg	Ala	Asp	Leu	Thr	Val	Glu	Glu	Asp	Phe	Asp	Ala	Pro	Ile	Ala	Gly
65					70				75					80	

Cys	Glu	Leu	Val	Phe	Gln	Leu	Ala	Thr	Pro	Val	Asn	Phe	Ala	Ser	Gln
				85				90						95	

Asp	Pro	Glu	Asn	Asp	Met	Ile	Lys	Pro	Ala	Ile	Lys	Gly	Val	Leu	Asn
			100					105					110		

Val	Leu	Lys	Ala	Ile	Ala	Arg	Ala	Lys	Glu	Val	Lys	Arg	Val	Ile	Leu
		115					120					125			

Thr Ser Ser Ala Ala Ala Val Thr Ile Asn Glu Leu Lys Gly Thr Gly
130 135 140

His Val Met Asp Glu Thr Asn Trp Ser Asp Val Glu Phe Leu Asn Thr
145 150 155 160

Ala Lys Pro Pro Thr Trp Gly Tyr Pro Ala Ser Lys Met Leu Ala Glu
165 170 175

Lys Ala Ala Trp Lys Phe Ala Glu Glu Asn Asp Ile Asp Leu Ile Thr
180 185 190

Val Ile Pro Ser Leu Thr Thr Gly Pro Ser Leu Thr Pro Asp Ile Pro
195 200 205

Ser Ser Val Gly Leu Ala Met Ser Leu Ile Thr Gly Asn Asp Phe Leu
210 215 220

Ile Asn Ala Leu Lys Gly Met Gln Phe Leu Ser Gly Ser Leu Ser Ile
225 230 235 240

Thr His Val Glu Asp Ile Cys Arg Ala His Ile Phe Leu Ala Glu Lys
245 250 255

Glu Ser Ala Ser Gly Arg Tyr Ile Cys Cys Ala His Asn Thr Ser Val
260 265 270

Pro Glu Leu Ala Lys Phe Leu Asn Lys Arg Tyr Pro Gln Tyr Lys Val
275 280 285

Pro Thr Glu Phe Asp Asp Cys Pro Ser Lys Ala Lys Leu Ile Ile Ser
290 295 300

Ser Glu Lys Leu Ile Lys Glu Gly Phe Ser Phe Lys His Gly Ile Ala
305 310 315 320

Glu Thr Phe Asp Gln Thr Val Glu Tyr Phe Lys Thr Lys Gly Ala Leu
325 330 335

Lys Asn

<210> 307
<211> 1005
<212> DNA
<213> Trifolium repens

<400> 307
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tcccaataaa aaaagatctg aaacaacata gtcaccccat tttttaacat taaactaaaa
 120
 atatgtcggc catcaccgca atccaagtcg agaacttga atttcggct gtgggtactt
 180
 ctccggccac cggttaagtc tattttcttg gtggtgcagg ggagagaggt ttgactattg
 240
 aaggaaactt catcaagttc actgccatag gagtatattt ggaagatgta gcagtggctt
 300
 cacttgccac taaatggaag ggtaaatcct ctgaggagtt gcttgagact cttgactttc
 360
 atagagacat catttcagga ccccttgaaa agttgattcg aggatcgaag attagggaaat
 420
 tgagtgggtc tgagtactca aggaagggtta atgaaaactg cgtggcacac ttaaaatctg
 480
 ttgggactta tggagatgct gaagctgaag ctatgcacaa atttgttgaa gccttcaagc
 540
 ctattaattt tccacctggt gcctctgttt ttacagga atcacctgat ggaatattag
 600
 ggcttagttt ctctcaagat gcaagtatac cagaaaagga ggctgcagta atagagaaca
 660
 aggcagcttc atcggcagtg ttagaacta tgattggtga acatgctgtt tctcctgatt
 720
 taaagcggtg ttgggtgca agattacctg cctgtgtgaa cgagggtact ttcaagattg
 780
 aatgaaaact gattattatt atctccaaa gcattgcagc acaagattga gtcatttatg
 840
 agcatggaca tttttatgtc cacacatgtt taacttttgt atctctcttt agattctcat
 900
 caatatcaat aatactaata tgaacgaag tcaaaaaaaaa aaaaaaaaaa aaaaaaaaaa
 960
 aaaagtactc tgcgttggtta ccactgctta atcactagtg aattc
 1005

<210> 308
 <211> 220
 <212> PRT
 <213> Trifolium repens

<400> 308

Met Ser Ala Ile Thr Ala Ile Gln Val Glu Asn Leu Glu Phe Pro Ala
 1 5 10 15

Val Val Thr Ser Pro Ala Thr Gly Lys Ser Tyr Phe Leu Gly Gly Ala
 20 25 30

Gly Glu Arg Gly Leu Thr Ile Glu Gly Asn Phe Ile Lys Phe Thr Ala
 35 40 45

Ile Gly Val Tyr Leu Glu Asp Val Ala Val Ala Ser Leu Ala Thr Lys
50 55 60

Trp Lys Gly Lys Ser Ser Glu Glu Leu Leu Glu Thr Leu Asp Phe Tyr
65 70 75 80

Arg Asp Ile Ile Ser Gly Pro Phe Glu Lys Leu Ile Arg Gly Ser Lys
85 90 95

Ile Arg Glu Leu Ser Gly Pro Glu Tyr Ser Arg Lys Val Asn Glu Asn
100 105 110

Cys Val Ala His Leu Lys Ser Val Gly Thr Tyr Gly Asp Ala Glu Ala
115 120 125

Glu Ala Met Gln Lys Phe Val Glu Ala Phe Lys Pro Ile Asn Phe Pro
130 135 140

Pro Gly Ala Ser Val Phe Tyr Arg Gln Ser Pro Asp Gly Ile Leu Gly
145 150 155 160

Leu Ser Phe Ser Gln Asp Ala Ser Ile Pro Glu Lys Glu Ala Ala Val
165 170 175

Ile Glu Asn Lys Ala Ala Ser Ser Ala Val Leu Glu Thr Met Ile Gly
180 185 190

Glu His Ala Val Ser Pro Asp Leu Lys Arg Cys Leu Ala Ala Arg Leu
195 200 205

Pro Ala Leu Leu Asn Glu Gly Thr Phe Lys Ile Glu
210 215 220

<210> 309

<211> 1105

<212> DNA

<213> *Trifolium repens*

<400> 309

gaattcacta gtgattaagc agtggtaaca acgcagagta cgcggggaca ttacaactca
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caacaccttc tccattacca tctatcttct actaagtcca acgagatcaa tggcacttcc
120

ttctgtcacc gctttgaata tcgagaacaa tctattccct cctaccgtca caccaccggg
180

atccaccaac aattttcttc tcggcgggtgc aggagagcgg ggtcttcaaa ttcaagacaa
240

atttgtcaaa ttcaccgcta ttggtgttta tctacaggac attgctgttc cttacctcgc
300

cactaaatgg aagggtlaaga ctgctcaaga gctaaccgaa actgttcctt tcttcaggga
360

cactcgttaca ggtccatttg agaaatttat gcagggtgaca atgatcttgc cattgactgg
420

gcaacaatac tcagagaaaag tgtcagaaaa ttgtgtagct atttggaagt ctcttgggag
480

ttataccgac gaagaagcca aagcaattga gaagtttggt tctgtcttca aagatgaaac
540

attcccacca ggctcctcta tccttttcac agtattaccc aaaggattag gatcactaac
600

gataagtttc tctaaagatg gatccattcc agagaccgag tctgcagtta tagagaataa
660

gctaactctca caagctgtgc ttgagtcgat gataggggag caggtgtct cccctgcagc
720

aaaacagagt ttggccacca ggttatccga gttattcaac gaggttggtg atgctagcaa
780

ctgattatat caacaaaaag aaaatgaaag tcctttctgc aataaagacc aagcggaaat
840

tttattttag gtgcactttg aaatgacctc tttggcgact tttcttgta ctaataataa
900

agagtgtggt tgtatcatgt tgtaatttta ttttagaaaa agtgaggtaa gaaaggagtc
960

cttatgttta tttcaattat tgaaaaatta tttgcatgta taattgattt caactgatgt
1020

tatttaatca cgttttttct aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa gtactctgag
1080

ttgttaccac tgcttaatcg aattc
1105

<210> 310

<211> 224

<212> PRT

<213> Trifolium repens

<400> 310

Met Ala Leu Pro Ser Val Thr Ala Leu Asn Ile Glu Asn Asn Leu Phe
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Pro Pro Thr Val Thr Pro Pro Gly Ser Thr Asn Asn Phe Phe Leu Gly
20 25 30

Gly Ala Gly Glu Arg Gly Leu Gln Ile Gln Asp Lys Phe Val Lys Phe
35 40 45

Thr Ala Ile Gly Val Tyr Leu Gln Asp Ile Ala Val Pro Tyr Leu Ala
50 55 60

Thr Lys Trp Lys Gly Lys Thr Ala Gln Glu Leu Thr Glu Thr Val Pro
65 70 75 80

Phe Phe Arg Asp Ile Val Thr Gly Pro Phe Glu Lys Phe Met Gln Val
85 90 95

Thr Met Ile Leu Pro Leu Thr Gly Gln Gln Tyr Ser Glu Lys Val Ser
100 105 110

Glu Asn Cys Val Ala Ile Trp Lys Ser Leu Gly Ile Tyr Thr Asp Glu
115 120 125

Glu Ala Lys Ala Ile Glu Lys Phe Val Ser Val Phe Lys Asp Glu Thr
130 135 140

Phe Pro Pro Gly Ser Ser Ile Leu Phe Thr Val Leu Pro Lys Gly Leu
145 150 155 160

Gly Ser Leu Thr Ile Ser Phe Ser Lys Asp Gly Ser Ile Pro Glu Thr
165 170 175

Glu Ser Ala Val Ile Glu Asn Lys Leu Leu Ser Gln Ala Val Leu Glu
180 185 190

Ser Met Ile Gly Ala His Gly Val Ser Pro Ala Ala Lys Gln Ser Leu
195 200 205

Ala Thr Arg Leu Ser Glu Leu Phe Asn Glu Val Gly Asp Ala Ser Asn
210 215 220

<210> 311

<211> 1272

<212> DNA

<213> *Trifolium repens*

<400> 311

gaattcgatt aagcagtggt aacaacgcag agtacgcggg gattcaaaca tagctcaaag
60

tgtgtaacaa atttcttaac ttaaaacatt ttcaacccaa caaaaaaaaa caagacaaa
120

aacatgggta gtgttgaaat tccaacaaag gttcttacta acagttctag tcaagtgaag
180

atgcctctgg ttggaatggg atcagcacct gatttcacat gtaagaaga cacaaaagat
240

gcaatcattg aagccatcaa acagggttat agacactttg atactgtctg tgcttatggc
300

tcagaacaag ctcttggtga aggtttgaaa gaagcaattg aacttggtct tgtoactaga
360

gaagaccttt ttgttacttc taaactttgg gtcactgaaa atcatcctca tcttgttggt

420

cctgctcttc aaaaatctct caagactctt caattggagt acttggactt gtatttgatc
480

cattggccac ttagtctca gcctggaaag ttttcatttc caattgatgt ggcagatctc
540

ttgccatttg atgtgaaggg tgtttgggaa tccatggaag aaggcttgaa acttggactc
600

actaaagcta ttggtgttag taacttctct gtcaagaaac ttcaaaatct tgtctcagtt
660

gccactgttc ttctgtctgt caatcaagtg gagatgaacc ttgcatggca acaaaagaag
720

cttagagaat tttgcaatgc aaatggaata gtgttaactg cattttcacc attgagaaaa
780

ggtgcaagca ggggacccaa tgaagttatg gaaaatgata tgcctaaaga gattgcagat
840

gtcatggaa agtctgttgc acaaatttca ttgagatggt tatatgaaca aggagtcact
900

tttgttccca agagctatga taaggaaaga atgggtcaaa atttggctat ctttgattgg
960

acattggcaa aagaagatca tgagaaaatt gatcaaatga agcagaaccg tttgatccct
1020

ggaccaacca agccaggact cagtaccta tgggatgatg aaatataaag tggaagatgt
1080

taaaagtcct ttaagctcac tcaatatcta tctattgtgt actttttgca tttgggggtt
1140

gaaattgagt caccccttgt tctgtatoga tttaaaattt aaataatcaa tttttcatta
1200

caaaaaaaaa aaaaaaaaaa aaaaaaaaaa agtactctgc gttgttacca ctgcttaact
1260

actagtgaat tc
1272

<210> 312

<211> 314

<212> PRT

<213> Trifolium repens

<400> 312

Met	Gly	Ser	Val	Glu	Ile	Pro	Thr	Lys	Val	Leu	Thr	Asn	Ser	Ser	Ser
1				5					10					15	

Gln	Val	Lys	Met	Pro	Val	Val	Gly	Met	Gly	Ser	Ala	Pro	Asp	Phe	Thr
			20					25					30		

Cys	Lys	Lys	Asp	Thr	Lys	Asp	Ala	Ile	Ile	Glu	Ala	Ile	Lys	Gln	Gly
	35						40					45			

Tyr Arg His Phe Asp Thr Ala Ala Ala Tyr Gly Ser Glu Gln Ala Leu
50 55 60

Gly Glu Gly Leu Lys Glu Ala Ile Glu Leu Gly Leu Val Thr Arg Glu
65 70 75 80

Asp Leu Phe Val Thr Ser Lys Leu Trp Val Thr Glu Asn His Pro His
85 90 95

Leu Val Val Pro Ala Leu Gln Lys Ser Leu Lys Thr Leu Gln Leu Glu
100 105 110

Tyr Leu Asp Leu Tyr Leu Ile His Trp Pro Leu Ser Ser Gln Pro Gly
115 120 125

Lys Phe Ser Phe Pro Ile Asp Val Ala Asp Leu Leu Pro Phe Asp Val
130 135 140

Lys Gly Val Trp Glu Ser Met Glu Glu Gly Leu Lys Leu Gly Leu Thr
145 150 155 160

Lys Ala Ile Gly Val Ser Asn Phe Ser Val Lys Lys Leu Gln Asn Leu
165 170 175

Val Ser Val Ala Thr Val Leu Pro Ala Val Asn Gln Val Glu Met Asn
180 185 190

Leu Ala Trp Gln Gln Lys Lys Leu Arg Glu Phe Cys Asn Ala Asn Gly
195 200 205

Ile Val Leu Thr Ala Phe Ser Pro Leu Arg Lys Gly Ala Ser Arg Gly
210 215 220

Pro Asn Glu Val Met Glu Asn Asp Met Leu Lys Glu Ile Ala Asp Ala
225 230 235 240

His Gly Lys Ser Val Ala Gln Ile Ser Leu Arg Trp Leu Tyr Glu Gln
245 250 255

Gly Val Thr Phe Val Pro Lys Ser Tyr Asp Lys Glu Arg Met Gly Gln
260 265 270

Asn Leu Ala Ile Phe Asp Trp Thr Leu Ala Lys Glu Asp His Glu Lys
275 280 285

Ile Asp Gln Ile Lys Gln Asn Arg Leu Ile Pro Gly Pro Thr Lys Pro
290 295 300

Gly Leu Ser Asp Leu Trp Asp Asp Glu Ile

305

310

<210> 313
<211> 1548
<212> DNA
<213> *Trifolium repens*

<400> 313
gaattcgatt aagcagtggg atcaacgcag agtacgoggg gacaacaact ataacttcct
60
gttattaacc aattgagttc aaattacata catagcagga actatactaa agatatcaac
120
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180
gccattggta ctgcaaatcc agcaaatcgt gttgaccaga gtacatatcc tgatttctac
240
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300
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360
cctagtcttt gtgaatacat ggacacctca ttggatgcta ggcaagacat ggtggtggtt
420
gaggtaccta gacttgggaa ggaggctgca gtgaaagcta tcaagaatg gggtcaacca
480
aagtc aaaga ttactcaact aatcttttgc accacaagtg gtgttgacat gcctggtgcc
540
gattaccaac tcacaaaact cttaggctct cgcctcatatg tgaagaggta catgatgtac
600
caacaagggt gctttgcagg tgggacgggt cttcgttttg ccaaggattt ggccgagAAC
660
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720
ccagtgaca ctcatattga cagtcttgtt ggacaagcac tattcggaga tggagctgct
780
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tggaccgcac agacaattgc tccagatagt gaagggtcca ttgatggta tcttcgtgaa
900
gctggactaa catttcatct tcttaaagat gttcctggga ttgtctcaaa gaacattgat
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1020
attgctcacc cagggtgtcc tgcaattcta gaccaagttg agataaagtt gggcttaaaa
1080
cctgaaaaaa tgaaggccac cagagatgta cttagtgaat atggtaacat gtcaagtga
1140

tgtgtattgt tcattctaga tgagatgaga aagaaatcgg ctgaaaatgg acttaaaacc
1200

acaggagaag gacttgactg ggggtgtgtg ttgggatttg ggcccggaact taccattgaa
1260

actgtttgtc tacatagtgt ggctatatga gaatgagaga ctgtgatttgt ttttattgta
1320

ttgtattgta ttactttaaa tcttggttga acctccattt taagaataaa tatggagtgc
1380

aatatggacc atcctgttaa aataatatat cgtaaatagc tattatttta gtgtctgttt
1440

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1500

aaaaaaaaa cctgcggttg ttaccactgc ttaactacta gtgaattc
1548

<210> 314
<211> 389
<212> PRT
<213> Trifolium repens

<400> 314

Met Val Ser Val Ser Glu Ile Arg Lys Ala Gln Arg Ala Glu Gly Pro
1 5 10 15

Ala Thr Ile Leu Ala Ile Gly Thr Ala Asn Pro Ala Asn Arg Val Asp
20 25 30

Gln Ser Thr Tyr Pro Asp Phe Tyr Phe Lys Ile Thr Asn Ser Glu His
35 40 45

Lys Val Glu Leu Lys Glu Lys Phe Gln Arg Met Cys Asp Lys Ser Met
50 55 60

Ile Lys Ser Arg Tyr Met Tyr Leu Thr Glu Glu Ile Leu Lys Glu Asn
65 70 75 80

Pro Ser Leu Cys Glu Tyr Met Ala Pro Ser Leu Asp Ala Arg Gln Asp
85 90 95

Met Val Val Val Glu Val Pro Arg Leu Gly Lys Glu Ala Ala Val Lys
100 105 110

Ala Ile Lys Glu Trp Gly Gln Pro Lys Ser Lys Ile Thr His Leu Ile
115 120 125

Phe Cys Thr Thr Ser Gly Val Asp Met Pro Gly Ala Asp Tyr Gln Leu
130 135 140

Thr Lys Leu Leu Gly Leu Arg Pro Tyr Val Lys Arg Tyr Met Met Tyr

145 150 155 160
 Gln Gln Gly Cys Phe Ala Gly Gly Thr Val Leu Arg Leu Ala Lys Asp
 165 170 175
 Leu Ala Glu Asn Asn Lys Gly Ala Arg Val Leu Val Val Cys Ser Glu
 180 185 190
 Val Thr Ala Val Thr Phe Arg Gly Pro Ser Asp Thr His Leu Asp Ser
 195 200 205
 Leu Val Gly Gln Ala Leu Phe Gly Asp Gly Ala Ala Ala Leu Ile Val
 210 215 220
 Gly Ser Asp Pro Val Pro Glu Ile Glu Lys Pro Ile Phe Glu Met Val
 225 230 235 240
 Trp Thr Ala Gln Thr Ile Ala Pro Asp Ser Glu Gly Ala Ile Asp Gly
 245 250 255
 His Leu Arg Glu Ala Gly Leu Thr Phe His Leu Leu Lys Asp Val Pro
 260 265 270
 Gly Ile Val Ser Lys Asn Ile Asp Lys Ala Leu Val Glu Ala Phe Gln
 275 280 285
 Pro Leu Asn Ile Ser Asp Tyr Asn Ser Ile Phe Trp Ile Ala His Pro
 290 295 300
 Gly Gly Pro Ala Ile Leu Asp Gln Val Glu Ile Lys Leu Gly Leu Lys
 305 310 315 320
 Pro Glu Lys Met Lys Ala Thr Arg Asp Val Leu Ser Glu Tyr Gly Asn
 325 330 335
 Met Ser Ser Ala Cys Val Leu Phe Ile Leu Asp Glu Met Arg Lys Lys
 340 345 350
 Ser Ala Glu Asn Gly Leu Lys Thr Thr Gly Glu Gly Leu Asp Trp Gly
 355 360 365
 Val Leu Phe Gly Phe Gly Pro Gly Leu Thr Ile Glu Thr Val Val Leu
 370 375 380
 His Ser Val Ala Ile
 385
 <210> 315
 <211> 1447
 <212> DNA

<213> Trifolium repens

<400> 315

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120
taagatatgg tgagtgtagc tgaaattcgc aaggctcaga gggctgaagg cccctgcaacc
180
attttggcca ttggcactgc aaatccacca aaccgtgttg agcagagcac atatcctgat
240
ttctacttca aaattacaaa cagtgcagc aagactgagc tcaaagagaa gttccaacgc
300
atgtgtgaca aatccatgat caagagcaga tacatgtatc taacagaaga gattttgaaa
360
gaaaatccta gtctttgtga atacatggca ccttcattgg atgctaggca agacatggtg
420
gtgggtgagg tacctagact tgggaaggag gctgcagtc aagccattaa agaattgggt
480
caaccaaaagt caaagattac tcacttaatc ttttgacca caagtggtgt tgacatgcct
540
gggtgctgatt accaactcac aaaactctta ggtcttcgcc catatgtgaa aaggatatg
600
atgtaccaac aaggttgttt tgcaggaggc acggtgcttc gtttgccaaa agatttgccc
660
gagaacaaac aagggtgctcg tgtgctagt gttgtttctg aagtcaccgc agtcacattt
720
cgcggcccca gtgatactca cttggacagt cttgttggaac aagcattgtt tggagatgga
780
gccgctgcac taattgttgg ttctgatcca gtgcctgaaa ttgagaaacc aatatttgag
840
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900
cgtgaagctg ggctaacatt tcactctctt aaagatgttc ctgggattgt atcaagaac
960
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1020
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1080
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1140
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1200
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1260

attgaaacgc ttgttcttcg tagcgtggct atataagatg tctgattgtt tttattttaa
1320

tgtattactt ttaatcttgc tgccttgaat ttogatttaa gaataataaa atatatcttt
1380

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1440

cgaattc
1447

<210> 316

<211> 389

<212> FRT

<213> Trifolium repens

<400> 316

Met Val Ser Val Ala Glu Ile Arg Lys Ala Gln Arg Ala Glu Gly Pro
1 5 10 15

Ala Thr Ile Leu Ala Ile Gly Thr Ala Asn Pro Pro Asn Arg Val Glu
20 25 30

Gln Ser Thr Tyr Pro Asp Phe Tyr Phe Lys Ile Thr Asn Ser Glu His
35 40 45

Lys Thr Glu Leu Lys Glu Lys Phe Gln Arg Met Cys Asp Lys Ser Met
50 55 60

Ile Lys Ser Arg Tyr Met Tyr Leu Thr Glu Glu Ile Leu Lys Glu Asn
65 70 75 80

Pro Ser Leu Cys Glu Tyr Met Ala Pro Ser Leu Asp Ala Arg Gln Asp
85 90 95

Met Val Val Val Glu Val Pro Arg Leu Gly Lys Glu Ala Ala Val Lys
100 105 110

Ala Ile Lys Glu Trp Gly Gln Pro Lys Ser Lys Ile Thr His Leu Ile
115 120 125

Phe Cys Thr Thr Ser Gly Val Asp Met Pro Gly Ala Asp Tyr Gln Leu
130 135 140

Thr Lys Leu Leu Gly Leu Arg Pro Tyr Val Lys Arg Tyr Met Met Tyr
145 150 155 160

Gln Gln Gly Cys Phe Ala Gly Gly Thr Val Leu Arg Leu Ala Lys Asp
165 170 175

Leu Ala Glu Asn Asn Lys Gly Ala Arg Val Leu Val Val Cys Ser Glu
180 185 190

Val Thr Ala Val Thr Phe Arg Gly Pro Ser Asp Thr His Leu Asp Ser
195 200 205

Leu Val Gly Gln Ala Leu Phe Gly Asp Gly Ala Ala Ala Leu Ile Val
210 215 220

Gly Ser Asp Pro Val Pro Glu Ile Glu Lys Pro Ile Phe Glu Met Val
225 230 235 240

Trp Thr Ala Gln Thr Ile Ala Pro Asp Ser Glu Gly Ala Ile Asp Gly
245 250 255

His Leu Arg Glu Ala Gly Leu Thr Phe His Leu Leu Lys Asp Val Pro
260 265 270

Gly Ile Val Ser Lys Asn Ile Asn Lys Ala Leu Val Glu Ala Phe Gln
275 280 285

Pro Leu Gly Ile Ser Asp Tyr Asn Ser Ile Phe Trp Ile Ala His Pro
290 295 300

Gly Gly Pro Ala Ile Leu Asp Gln Val Glu Gln Lys Leu Ala Leu Lys
305 310 315 320

Pro Glu Lys Met Arg Ala Thr Arg Glu Val Leu Ser Glu Tyr Gly Asn
325 330 335

Met Ser Ser Ala Cys Val Leu Phe Ile Leu Asp Glu Met Arg Lys Lys
340 345 350

Ser Ala Gln Asn Gly Leu Lys Thr Thr Gly Glu Gly Leu Asp Trp Gly
355 360 365

Val Leu Phe Gly Phe Gly Pro Gly Leu Thr Ile Glu Thr Val Val Leu
370 375 380

Arg Ser Val Ala Ile
385

<210> 317
<211> 2394
<212> DNA
<213> Trifolium repens

<400> 317
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aaattcactc attgcataga aaaccatata catttgatct tgcaaaagaag aaatatggga
120

gacgaaggta tagtgagagg tgtcacaaag cagacaaccc ctgggaaggc tactatatgt
180
gctcttggca aggcattccc tcaccaactt gtgatgcaag agtgtttagt tgatgggtat
240
tttagggaca ctaattgtga caatcctgaa ctaagcaga aacttgctag actttgtaag
300
acaaccacgg taaaaacaag gtatgttgtt atgaatgagg agatactaaa gaaatatcca
360
gaactgttg tcgaaggcgc ctcaactgta aaacaacgtt tagagatatg taatgaggca
420
gtaacacaaa tggcaattga agcttcccaa gtttgccata agaattgggg tagatcctta
480
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540
ctatacttgt caaaaggact aggactaac cctaaaattc aaagaacat gctctatttc
600
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660
cctggaaagta gagttttgct tgctacttog gaaactacaa ttattggatt caagccacca
720
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960
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1020
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1080
tcgcgcgaga agctgaatgc tagtagaaaa gctctaattg attatggaaa tgctagcagc
1140
aatactattg tttatgtgct ggaatatatg ctagaagagg aaaagaagt taaaaaggcg
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1260
gggattctag caaggaactt gtgtgcatga agtcttatac aattgtgatg catgacttat
1320
actcttattt ctactaatta ttatattaag caaattcaga acttttaagt aatgatttaa
1380
tgaagaatac ttatagtata ttgactttat tcactttcaa agcaagttta tgatcctaag
1440

acatggtaga acttgagcat gtggaatagt tgtaacaaaa actctaagca aatagagact
 1500
 ttatgtagta taaagcattt ccagacatga taaataatgg tacctcagaa cataaaatat
 1560
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 1620
 caacacaaaa tgtactctaa gtctaacatg agtaacacaa catgatgcct gattaagtta
 1680
 aaagaaaaga aaatctgagg gcatagatct tcaatcacac cactccagag ggaaggcgta
 1740
 gaacaagctg tccgccgaaa aactgcaat tcaataata tcattaggac aacagtgcag
 1800
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 1860
 tactaacctt ttcacataat agtaacagaa atcagctaag atgaatgtct ggacaatttc
 1920
 tgagataaga accatgacgg ccataagcca taccccaagg caaccaataa atgtccacgg
 1980
 gtatctaaca cctgttgcaa gaaatagtaa gttattagga gatgtgcggt tacgaaattc
 2040
 aagctacaca acaaaaaggag gccagaacaa cagcaatctt gtaaccagat gacaacaata
 2100
 aaatgtaaac ttaagagac cgaacacaca aacattgcaa ctcatagga attgctgcc
 2160
 tgtaactagt aggagatttg ggagctcaaa tcagtatat atgcaataac aaggatgac
 2220
 cgcttgtct attgtagcat acaacaaacg tacagtgggt ttgtccctct caaaatggca
 2280
 ggatctttac agcacaatat ttggttttgt catacttata ccataaaaaa aaaaaaaaaa
 2340
 aaaaaaaaaa aaagtactct gcgttgttac cactgcttaa tcactagtga attc
 2394

<210> 318

<211> 391

<212> PRT

<213> *Trifolium repens*

<400> 318

Met Gly Asp Glu Gly Ile Val Arg Gly Val Thr Lys Gln Thr Thr Pro
 1 5 10 15

Gly Lys Ala Thr Ile Leu Ala Leu Gly Lys Ala Phe Pro His Gln Leu
 20 25 30

Val Met Gln Glu Cys Leu Val Asp Gly Tyr Phe Arg Asp Thr Asn Cys
 35 40 45

Asp Asn Pro Glu Leu Lys Gln Lys Leu Ala Arg Leu Cys Lys Thr Thr
 50 55 60

Thr Val Lys Thr Arg Tyr Val Val Met Asn Glu Glu Ile Leu Lys Lys
 65 70 75 80

Tyr Pro Glu Leu Val Val Glu Gly Ala Ser Thr Val Lys Gln Arg Leu
 85 90 95

Glu Ile Cys Asn Glu Ala Val Thr Gln Met Ala Ile Glu Ala Ser Gln
 100 105 110

Val Cys Leu Lys Asn Trp Gly Arg Ser Leu Ser Asp Ile Thr His Val
 115 120 125

Val Tyr Val Ser Ser Ser Glu Ala Arg Leu Pro Gly Gly Asp Leu Tyr
 130 135 140

Leu Ser Lys Gly Leu Gly Leu Asn Pro Lys Ile Gln Arg Thr Met Leu
 145 150 155 160

Tyr Phe Ser Gly Cys Ser Gly Gly Val Ala Gly Leu Arg Val Ala Lys
 165 170 175

Asp Val Ala Glu Asn Asn Pro Gly Ser Arg Val Leu Leu Ala Thr Ser
 180 185 190

Glu Thr Thr Ile Ile Gly Phe Lys Pro Pro Ser Val Asp Arg Pro Tyr
 195 200 205

Asp Leu Val Gly Val Ala Leu Phe Gly Asp Gly Ala Gly Ala Met Ile
 210 215 220

Ile Gly Ser Asp Pro Val Phe Glu Thr Glu Thr Pro Leu Phe Glu Leu
 225 230 235 240

His Thr Ser Ala Gln Glu Phe Ile Pro Asp Thr Glu Lys Lys Ile Asp
 245 250 255

Gly Arg Leu Thr Glu Glu Gly Ile Ser Phe Thr Leu Ala Arg Glu Leu
 260 265 270

Pro Gln Ile Ile Glu Asp Asn Val Glu Gly Phe Cys Asn Lys Leu Ile
 275 280 285

Asp Val Val Gly Leu Glu Asn Lys Glu Tyr Asn Lys Leu Phe Trp Ala
 290 295 300

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Val His Pro Gly Gly Pro Ala Ile Leu Asn Arg Val Glu Lys Arg Leu
 305 310 315 320

Glu Leu Ser Pro Gln Lys Leu Asn Ala Ser Arg Lys Ala Leu Met Asp
 325 330 335

Tyr Gly Asn Ala Ser Ser Asn Thr Ile Val Tyr Val Leu Glu Tyr Met
 340 345 350

Leu Glu Glu Glu Lys Lys Ile Lys Lys Ala Gly Gly Gly Asp Ser Glu
 355 360 365

Trp Gly Leu Ile Leu Ala Phe Gly Pro Gly Ile Thr Phe Glu Gly Ile
 370 375 380

Leu Ala Arg Asn Leu Cys Ala
 385 390

<210> 319
 <211> 1663
 <212> DNA
 <213> Trifolium repens

<400> 319
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tttctttttt agtccttgct acgtggcttt accaaaaaac gttgctaagt catcaacctt
 120

tccaattcct taatataacc tatcagtact caccatcttt tcttctctcc tgctaacttt
 180

agactcagag aagatggtga atgttaatga gatccgccag gcacagagag ctgaaggccc
 240

tgccaccgtg ttggcaatcg gcaactgcaac tcttccaaac tgtgtcgatc agagtaacata
 300

cccagactac tacttcogca tcacaaacag tgagcacaag acagagctca aagaaaaatt
 360

ccagcgcatg tgtgacaaat ctatgattaa gaagagatac atgcatttga cagaagagat
 420

tttgaaggag aatccaagtt tatgtgagta catggcacct tcattggatg caagacaaga
 480

catggtgtggt gtggaagtac caaggctagg aaaagaggct gcaacaaaag ctatcaagga
 540

atgggggtcaa cctaagtcga agattactca cctcatcttt tgcaccacaa gtggtgtgga
 600

catgcctggc gccgactatc agottacaaa gcttttaggc cttcgtcgcg atgtgaagcg
 660

tttatgatg taccaacaag gttgtttcgc tgggtggtacg gtgcttcggt tggctaagaa
 720

360/390

cttggctgaa aacaacaaag gtgcccggtg gttgggtggt ttgtcagaga tcactgcggt
780

tactttccgt ggaccacgtg acactcatct tgatagcctt gtggggcagg cattgtttgg
840

agatggtgca gcagctgtga ttgtagggtc agaccatta ccacaagttg agaagccctt
900

gtttgaattg gtatggactg ctcaacaat ccttcagac agtgaaggag ccattgatgg
960

gcaccttcgt gaagtcgggc tgacattcca tctcctaag gatgttcctg gactcatctc
1020

aaagaacatt gagaagctc ttgttgaggc ctttcaacct ttaggtatct ctgattacaa
1080

ttctatatct tggatcgac atcctggtgg acctgcaatt ctggaccaag tggaagccaa
1140

attaagctta aagccagaga aaatgcaag ccccgccat gtgcttagcg agtatggtaa
1200

catgtcaagt gcatgtgtgt tatttatctt ggatgagatg aggagggaagt caaagaaga
1260

tggacttgcc acaacaggcg aggggctgga atgggggtga ctattcggtt ttggaccggg
1320

actcatggt gagactgtat tgctccatag tgttgccact taaattgcct agatatgcta
1380

taactatatg cttatttaat tctttgttc tgggggattt tatcttcact tacttcactg
1440

agcatttgaa taaagtttgt tttaattatt cataatgtaa tatggtgttg cttaatgtac
1500

ccatccatat aatatttgta atacatatat taatcaactt gcaatttcac gaaaaaaaaa
1560

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaggaaaaaa aaaaaaaaaa aaaaaaaaaa
1620

aagtactctg cgttgttacc actgcttaac cactagttaa ttc
1663

<210> 320

<211> 389

<212> PRT

<213> Trifolium repens

<400> 320

Met Val Asn Val Asn Glu Ile Arg Gln Ala Gln Arg Ala Glu Gly Pro
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Ala Thr Val Leu Ala Ile Gly Thr Ala Thr Pro Pro Asn Cys Val Asp
20 25 30

Gln Ser Thr Tyr Pro Asp Tyr Tyr Phe Arg Ile Thr Asn Ser Glu His
35 40 45

Lys Thr Glu Leu Lys Glu Lys Phe Gln Arg Met Cys Asp Lys Ser Met
50 55 60

Ile Lys Lys Arg Tyr Met His Leu Thr Glu Glu Ile Leu Lys Glu Asn
65 70 75 80

Pro Ser Leu Cys Glu Tyr Met Ala Pro Ser Leu Asp Ala Arg Gln Asp
85 90 95

Met Val Val Val Glu Val Pro Arg Leu Gly Lys Glu Ala Ala Thr Lys
100 105 110

Ala Ile Lys Glu Trp Gly Gln Pro Lys Ser Lys Ile Thr His Leu Ile
115 120 125

Phe Cys Thr Thr Ser Gly Val Asp Met Pro Gly Ala Asp Tyr Gln Leu
130 135 140

Thr Lys Leu Leu Gly Leu Arg Pro His Val Lys Arg Tyr Met Met Tyr
145 150 155 160

Gln Gln Gly Cys Phe Ala Gly Gly Thr Val Leu Arg Leu Ala Lys Asp
165 170 175

Leu Ala Glu Asn Asn Lys Gly Ala Arg Val Leu Val Val Cys Ser Glu
180 185 190

Ile Thr Ala Val Thr Phe Arg Gly Pro Ser Asp Thr His Leu Asp Ser
195 200 205

Leu Val Gly Gln Ala Leu Phe Gly Asp Gly Ala Ala Ala Val Ile Val
210 215 220

Gly Ser Asp Pro Leu Pro Gln Val Glu Lys Pro Leu Phe Glu Leu Val
225 230 235 240

Trp Thr Ala Gln Thr Ile Leu Pro Asp Ser Glu Gly Ala Ile Asp Gly
245 250 255

His Leu Arg Glu Val Gly Leu Thr Phe His Leu Leu Lys Asp Val Pro
260 265 270

Gly Leu Ile Ser Lys Asn Ile Glu Lys Ala Leu Val Glu Ala Phe Gln
275 280 285

Pro Leu Gly Ile Ser Asp Tyr Asn Ser Ile Phe Trp Ile Ala His Pro
290 295 300

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Gly Gly Pro Ala Ile Leu Asp Gln Val Glu Ala Lys Leu Ser Leu Lys
 305 310 315 320

Pro Glu Lys Met Gln Ala Thr Arg His Val Leu Ser Glu Tyr Gly Asn
 325 330 335

Met Ser Ser Ala Cys Val Leu Phe Ile Leu Asp Glu Met Arg Arg Lys
 340 345 350

Ser Lys Glu Asp Gly Leu Ala Thr Thr Gly Glu Gly Leu Glu Trp Gly
 355 360 365

Val Leu Phe Gly Phe Gly Pro Gly Leu Thr Val Glu Thr Val Leu Leu
 370 375 380

His Ser Val Ala Thr
 385

<210> 321
 <211> 1653
 <212> DNA
 <213> *Trifolium repens*

<400> 321
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 60

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 120

gatttgaatg gaagttcctc ggtgaatgga gcacgtgcta gacgtgctcc tactcaggga
 180

aaggcaacga tacttgcatt aggaaaggct ttccccgccc aggtcctccc tcaagagtgc
 240

ttggtggaag gattcattcg cgacactaag tgtgacgata cttatattaa ggagaaattg
 300

gagcgtcttt gcaaaaacac aactgtgaaa acaagataca cagtaatgtc aaaggagatc
 360

ttagacaact atccagagct agccatagat ggaacaccaa caataaggca aaagcttgaa
 420

atagcaaatc cagcagtagt tgaaatggca acaagagcaa gcaagattg catcaaagaa
 480

tggggaagggt cacctcaaga tatcacacac atagtctatg ttctctcgag cgaaattcgt
 540

ctaccocgggt gtgaccttta tcttgcaaat gaactcgggt taaacagcga tgtaaatcgc
 600

gtaatgctct atttctcgg ttgctacggc ggtgtcactg gcttacgtgt cgccaaagac
 660

atcgccgaaa ataaccctgg tagtaggggt ttaactcaca catccgagac cactattctc
 720

gggttttcgac caccgagtaa agctagacct tatgacctcg ttggcgctgc acttttcgggt
 780
 gatggcgccg ctgctgcaat aattggaaca gaccctatat tgaatcaaga atcacctttc
 840
 atggaattga accatgcagt ccaaaaattc ttgcctgata cacaaaatgt gattgatggt
 900
 agaatactg aagagggtat taattttaag ctggaagag accttcctca aaaaattgaa
 960
 gacaatattg aagaattttg caagaaaatt atggctaaaa gtgatgttaa ggaatttaat
 1020
 gacttatttt gggctgttca tcttggtggg ccagctatac tcaataagct agaaaaata
 1080
 ctcaaattga aaagtataa attggattgt agtaggaagg cattaatgga ttatggaat
 1140
 gttagtagca atactatatt ctatgtgatg gagtatatga gagattattt gaaggaagat
 1200
 ggaagtgaag aatggggatt aggattggct ttggaccag ggattacttt tgaaggggtt
 1260
 ctctccgta gcctttaatc ttgaaataat aatcatatg aaattacttg tcttaagatt
 1320
 gtgataggaa gatgaatatg tattggatta atattgatat ggtgttattt taagttgatt
 1380
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 aattgttcta tgatatcttc attgttgata ctgtaataat ataatatcta atttggctgg
 1560
 caaaatgaaa gatttttcac cgaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aagtactctg
 1620
 cgttggtacc actgcttaat cactagttaa ttc
 1653

<210> 322
 <211> 389
 <212> PRT
 <213> Trifolium repens

<400> 322

Met Pro Gln Gly Asp Leu Asn Gly Ser Ser Ser Val Asn Gly Ala Arg
 1 5 10 15

Ala Arg Arg Ala Pro Thr Gln Gly Lys Ala Thr Ile Leu Ala Leu Gly
 20 25 30

Lys Ala Phe Pro Ala Gln Val Leu Pro Gln Glu Cys Leu Val Glu Gly
 35 40 45

Phe Ile Arg Asp Thr Lys Cys Asp Asp Thr Tyr Ile Lys Glu Lys Leu
50 55 60

Glu Arg Leu Cys Lys Asn Thr Thr Val Lys Thr Arg Tyr Thr Val Met
65 70 75 80

Ser Lys Glu Ile Leu Asp Asn Tyr Pro Glu Leu Ala Ile Asp Gly Thr
85 90 95

Pro Thr Ile Arg Gln Lys Leu Glu Ile Ala Asn Pro Ala Val Val Glu
100 105 110

Met Ala Thr Arg Ala Ser Lys Asp Cys Ile Lys Glu Trp Gly Arg Ser
115 120 125

Pro Gln Asp Ile Thr His Ile Val Tyr Val Ser Ser Ser Glu Ile Arg
130 135 140

Leu Pro Gly Gly Asp Leu Tyr Leu Ala Asn Glu Leu Gly Leu Asn Ser
145 150 155 160

Asp Val Asn Arg Val Met Leu Tyr Phe Leu Gly Cys Tyr Gly Gly Val
165 170 175

Thr Gly Leu Arg Val Ala Lys Asp Ile Ala Glu Asn Asn Pro Gly Ser
180 185 190

Arg Val Leu Leu Thr Thr Ser Glu Thr Thr Ile Leu Gly Phe Arg Pro
195 200 205

Pro Ser Lys Ala Arg Pro Tyr Asp Leu Val Gly Ala Ala Leu Phe Gly
210 215 220

Asp Gly Ala Ala Ala Ala Ile Ile Gly Thr Asp Pro Ile Leu Asn Gln
225 230 235 240

Glu Ser Pro Phe Met Glu Leu Asn His Ala Val Gln Lys Phe Leu Pro
245 250 255

Asp Thr Gln Asn Val Ile Asp Gly Arg Ile Thr Glu Glu Gly Ile Asn
260 265 270

Phe Lys Leu Gly Arg Asp Leu Pro Gln Lys Ile Glu Asp Asn Ile Glu
275 280 285

Glu Phe Cys Lys Lys Ile Met Ala Lys Ser Asp Val Lys Glu Phe Asn
290 295 300

365/390

Asp Leu Phe Trp Ala Val His Pro Gly Gly Pro Ala Ile Leu Asn Lys
 305 310 315 320

Leu Glu Asn Ile Leu Lys Leu Lys Ser Asp Lys Leu Asp Cys Ser Arg
 325 330 335

Lys Ala Leu Met Asp Tyr Gly Asn Val Ser Ser Asn Thr Ile Phe Tyr
 340 345 350

Val Met Glu Tyr Met Arg Asp Tyr Leu Lys Glu Asp Gly Ser Glu Glu
 355 360 365

Trp Gly Leu Gly Leu Ala Phe Gly Pro Gly Ile Thr Phe Glu Gly Val
 370 375 380

Leu Leu Arg Ser Leu
 385

<210> 323
 <211> 1600
 <212> DNA
 <213> Trifolium repens

<400> 323
 gaattcacta gtgattaagc agtggtaaca acgcagagta cgcgggggaa tccacccaaa
 60

caacaccatt aataacccctc caaattctcg ttacctcacc aaatctcatt ttctattata
 120

tatcttgggt acatcttttg ttacctcaa caaaaaaatg gtgaccgtag aagagattgc
 180

taacgcccaa cggtcaaatg gccctgccac tatcttagct ttggcacag ccaactcctc
 240

taactgtgtc actcaagctg attatcctga ttactacttt cgtatcacca acagcgaaca
 300

tatgactgat cttaaggaaa aattcaagcg gatgtgtgat agatcaatga taaagaaacg
 360

ttacatgcac ctaacagaag actttctgaa ggagaatcca aatatgtgtg aatacatggc
 420

accatcacta gatgtaagac gagacatagt ggttggtgaa gtaccaaagc taggtaaaga
 480

agcagcaaaa aaagccatat gtgaatgggg acaacaaaaa tccaaaatca cacatcttgt
 540

ttctgcacc acttcgggtg ttgacatgcc gggagccgat taccaactca ccaaactttt
 600

aggcttaaaa ccttctgtca agcgtctcat gatgtatcaa caaggttgtt tcgctggcgg
 660

cacagttctc cgcttagcaa aagaccttgt tgagaataac aaaaatgcaa gagttcttgt
 720

tgtttgttct gaaattactg cggttacttt tcgtggacca tcggatactc atcttgatgc
 780
 gctcgtggga caggcgcttt ttgggtgatgg agccgcagca atgattattg gtgcggatcc
 840
 tgatttaacc gtggagcgtc cgattttcga gattgtttcg gctgctcaga ctattcttcc
 900
 tgattctgat ggcgaattg atggacatct tcgtgaagtg gggctcactt ttcatttatt
 960
 gaaagatgtt cgggggatta tttcaaagaa cattgaaaaa agtttagttg aagcttttgc
 1020
 gcctattggg attaatgatt ggaactcaat attttgggtt gcacatccag gtggaccggc
 1080
 tattttagac caggttgaag agaaactcca tcttaagag gagaaactcc ggtccacccg
 1140
 gcattgtcct agtgaatatg gaaatatgtc aagtgcattg gttttattta ttttggatga
 1200
 aatgagaaag aggtctaaag aggaagggat gattacaact ggtgaagggg tggaatgggg
 1260
 tgtgtgtgtt ggggttggac cgggtttaac tgttgaaacc gttgtgcttc atagtgttcc
 1320
 ggttcagggt tgaatttatt atacatagat tggaataaa aatttgccctg ccgagagatg
 1380
 tgaactaact ttgtaggcaa gctcaaatta aagtttgaga taatattgtg ctttagttat
 1440
 tatggtatgt aatgtaattg ttttactttt ttogaaattc atgtaatttg atatgtaaa
 1500
 taatatgttt ggggttggat ataattattt gttaactaaa aaaaaaaaaa aaaaaaaaaa
 1560
 aaaaagtact ctgcgttgtt accactgctt aatcgaattc
 1600

<210> 324

<211> 391

<212> PRT

<213> *Trifolium repens*

<400> 324

Met Val Thr Val Glu Glu Ile Arg Asn Ala Gln Arg Ser Asn Gly Pro
 1 5 10 15

Ala Thr Ile Leu Ala Phe Gly Thr Ala Thr Pro Ser Asn Cys Val Thr
 20 25 30

Gln Ala Asp Tyr Pro Asp Tyr Tyr Phe Arg Ile Thr Asn Ser Glu His
 35 40 45

Met Thr Asp Leu Lys Glu Lys Phe Lys Arg Met Cys Asp Arg Ser Met

50 55 60
 Ile Lys Lys Arg Tyr Met His Leu Thr Glu Asp Phe Leu Lys Glu Asn
 65 70 75 80
 Pro Asn Met Cys Glu Tyr Met Ala Pro Ser Leu Asp Val Arg Arg Asp
 85 90 95
 Ile Val Val Val Glu Val Pro Lys Leu Gly Lys Glu Ala Ala Lys Lys
 100 105 110
 Ala Ile Cys Glu Trp Gly Gln Pro Lys Ser Lys Ile Thr His Leu Val
 115 120 125
 Phe Cys Thr Thr Ser Gly Val Asp Met Pro Gly Ala Asp Tyr Gln Leu
 130 135 140
 Thr Lys Leu Leu Gly Leu Lys Pro Ser Val Lys Arg Leu Met Met Tyr
 145 150 155 160
 Gln Gln Gly Cys Phe Ala Gly Gly Thr Val Leu Arg Leu Ala Lys Asp
 165 170 175
 Leu Val Glu Asn Asn Lys Asn Ala Arg Val Leu Val Val Cys Ser Glu
 180 185 190
 Ile Thr Ala Val Thr Phe Arg Gly Pro Ser Asp Thr His Leu Asp Ser
 195 200 205
 Leu Val Gly Gln Ala Leu Phe Gly Asp Gly Ala Ala Ala Met Ile Ile
 210 215 220
 Gly Ala Asp Pro Asp Leu Thr Val Glu Arg Pro Ile Phe Glu Ile Val
 225 230 235 240
 Ser Ala Ala Gln Thr Ile Leu Pro Asp Ser Asp Gly Ala Ile Asp Gly
 245 250 255
 His Leu Arg Glu Val Gly Leu Thr Phe His Leu Leu Lys Asp Val Pro
 260 265 270
 Gly Ile Ile Ser Lys Asn Ile Glu Lys Ser Leu Val Glu Ala Phe Ala
 275 280 285
 Pro Ile Gly Ile Asn Asp Trp Asn Ser Ile Phe Trp Val Ala His Pro
 290 295 300
 Gly Gly Pro Ala Ile Leu Asp Gln Val Glu Glu Lys Leu His Leu Lys
 305 310 315 320

Glu Glu Lys Leu Arg Ser Thr Arg His Val Leu Ser Glu Tyr Gly Asn
 325 330 335

Met Ser Ser Ala Cys Val Leu Phe Ile Leu Asp Glu Met Arg Lys Arg
 340 345 350

Ser Lys Glu Glu Gly Met Ile Thr Thr Gly Glu Gly Leu Glu Trp Gly
 355 360 365

Val Leu Phe Gly Phe Gly Pro Gly Leu Thr Val Glu Thr Val Val Leu
 370 375 380

His Ser Val Pro Val Gln Gly
 385 390

<210> 325
 <211> 1333
 <212> DNA
 <213> Trifolium repens

<400> 325
 gaattcacta gtgattaagc agtggttaaca acgcagagta cgcgggggtg acttgatcta
 60

gcagttatca aacacaacag tcttcactt gagctctgtt tctccacatg tcgaagctag
 120

tttgcgtcac cggcggcagc ggatgcatcg gttcatggct agtccatctc cttctctccc
 180

gcgggtacac tgttcaacgc accgtccaaa atctcaatga tgagaacgaa acgaagcacc
 240

tagaagctct cgaaggagca caaactaatc tccgtctctt ccagatcgat ctccttaact
 300

acgacacaat cctcgctgct gtccgcggtt gcgtcggaat ttccacctc gcttcacctt
 360

gcactgtaga caaagttcat gatcctcaga aggagctttt ggatcctgca attaaaggga
 420

ctttgaatgt gottactgca gctaaggaag taggggtgaa gcgtgtggtt gttacctcgt
 480

ctgtctcgcc gattactcct agtctcgatt ggcctctctga tgttggttaa agagaggatt
 540

gttggactga tgttgaatat tgcaagaaaa aagagttgtg gtatcogttg tccaaacatc
 600

tggtcgagaa agctgcgtgg gatttttcca aagaaaatgg tttggatgtt gttgtggtga
 660

atcccggtag tgtgatgggt cctgttatcc caccacggca taatgcaagc atgctcatgc
 720

ttgtgagact tcttgaaggc tgcgctgaaa catttgaaga ctattttatg ggattggtcc
 780

acttcaaaga tgtagcattg gcgcataattt tgggtgatga gaacaaagaa gcatctggta
 840
 gacatgtgtg tggtagaaact atctctcact acggtgatatt tgtggcaaaa gttgctgaac
 900
 ttatccaga atatatgtgtt cctaggatgc agcgagatac gcaacctgga ttgttgagag
 960
 cgaatgatgg atcaagaag ctcatagatt tgggtttgga attcattcca atggagcaaa
 1020
 ttatcaagga tgctgtagag agtttgaaga acaaaggatt catttcttga atgatgttac
 1080
 tgttcttttg agaaccctat agttaccaga gtatagacta aataatatat aggtgatggg
 1140
 tcagagaatg agtacttatg tcatgagttg tgtctgtata atatgttttc tcaattctta
 1200
 tatgttaaat tgctaatgtt aacttcaata ttatcagcc agtatgtttt ttttaataaa
 1260
 atattgaagc aaaaaaaaaa aaaaaaaaaa aaaaaaaagt actctgcgtt gttaccactg
 1320
 cttaatcgaa ttc
 1333

<210> 326
 <211> 320
 <212> PRT
 <213> Trifolium repens

<400> 326

Met Ser Lys Leu Val Cys Val Thr Gly Gly Ser Gly Cys Ile Gly Ser
 1 5 10 15

Trp Leu Val His Leu Leu Leu Leu Arg Gly Tyr Thr Val His Ala Thr
 20 25 30

Val Gln Asn Leu Asn Asp Glu Asn Glu Thr Lys His Leu Glu Ala Leu
 35 40 45

Glu Gly Ala Gln Thr Asn Leu Arg Leu Phe Gln Ile Asp Leu Leu Asn
 50 55 60

Tyr Asp Thr Ile Leu Ala Ala Val Arg Gly Cys Val Gly Ile Phe His
 65 70 75 80

Leu Ala Ser Pro Cys Thr Val Asp Lys Val His Asp Pro Gln Lys Glu
 85 90 95

Leu Leu Asp Pro Ala Ile Lys Gly Thr Leu Asn Val Leu Thr Ala Ala
 100 105 110

Lys Glu Val Gly Val Lys Arg Val Val Val Thr Ser Ser Val Ser Ala
115 120 125

Ile Thr Pro Ser Pro Asp Trp Pro Ser Asp Val Val Lys Arg Glu Asp
130 135 140

Cys Trp Thr Asp Val Glu Tyr Cys Lys Lys Lys Glu Leu Trp Tyr Pro
145 150 155 160

Leu Ser Lys Thr Leu Ala Glu Lys Ala Ala Trp Asp Phe Ser Lys Glu
165 170 175

Asn Gly Leu Asp Val Val Val Val Asn Pro Gly Thr Val Met Gly Pro
180 185 190

Val Ile Pro Pro Arg His Asn Ala Ser Met Leu Met Leu Val Arg Leu
195 200 205

Leu Glu Gly Cys Ala Glu Thr Phe Glu Asp Tyr Phe Met Gly Leu Val
210 215 220

His Phe Lys Asp Val Ala Leu Ala His Ile Leu Val Tyr Glu Asn Lys
225 230 235 240

Glu Ala Ser Gly Arg His Val Cys Val Glu Thr Ile Ser His Tyr Gly
245 250 255

Asp Phe Val Ala Lys Val Ala Glu Leu Tyr Pro Glu Tyr Ser Val Pro
260 265 270

Arg Met Gln Arg Asp Thr Gln Pro Gly Leu Leu Arg Ala Asn Asp Gly
275 280 285

Ser Lys Lys Leu Ile Asp Leu Gly Leu Glu Phe Ile Pro Met Glu Gln
290 295 300

Ile Ile Lys Asp Ala Val Glu Ser Leu Lys Asn Lys Gly Phe Ile Ser
305 310 315 320

<210> 327
<211> 1470
<212> DNA
<213> Trifolium repens

<400> 327
gaattcgatt aagcagtggt aacaacgcag agtacgcggg gaccactcta tttatttcta
60

cttaaacctc acaaaaaata aaccacacaa cacacaaaaca ccaaaaaacag agcaccgttt
120

ccatcatcaa acaatggcac cagccaaaac tctaagttat ctctcacaac aaaacactct
180

cgagtcgaagt ttcggttaggg aagaagatga gcgtccaaaa gttgcctaca ataacttcag
240

caacgagatt ccaatcattt ctcttgctgg aattgatgag gttgatggtc gtgaacaga
300

gatatgtaac aagattgttg aagcttgta gaattggggg attttccagg ttgttgatca
360

tggtgttgat acaaaaacttg tttctgagat gaccogttt gctagagagt tttttgcttt
420

gccacccgaa gagaagctcc ggtttgacat gtccgggtgt aaaaagggtg gtttcattgt
480

ctctagtcat cttcaaggag aagcagtga ggattggaga gagctagtga catatttttc
540

atacccaatt aaacaaagag attattcaag gtggccagac aagccagaag gatggaaaga
600

ggtaacagaa aaatacagtg aaacctaata gaatttagct tgcaagctat tggaagtttt
660

atcagaagca atgggttttag aaaagaagc tctaacaaaa gcattgtgtg atatggatca
720

aaaagtgtgt ataaattatt acccaaaatg ccctgaacct gacctcacac ttggccttaa
780

acgtcacact gaccttgga caattactct tttgcttcaa gatcaagttg gtgggtctca
840

agctaccaa gataatggta agacgtggat tacagttcaa ccagttgaag gtgcttttgt
900

tgттаатстт ggagaccatg gtcactatct aagtaatgga cggttcaaaa atgctgacca
960

tcaagcagtg gtgaattoga actacagccg tttatcaata gcaacatttc aaaatccagc
1020

tccagatgca actgtgtacc ctttgaagat tagagatggg gaaaaactcg tgttggaaga
1080

accaatcact tttgctgaaa tgtatagaag gaagatgacc aaagaccttg aaattgctag
1140

gatgaagaag ttggctaagg aacaacaact tagggacttg gaggagaaca agactaataa
1200

tgaggccaaa cctttgaatg agatctttgc ttaattaatt agtcttaatt tasataataa
1260

attttagact taatttcatc атаатаатт таатттттг ttcaattaat ctatgtttaa
1320

tttgtcgta ttgtccacgt gtattaaagct gcttggttgt gtgtgccttg gagaataatc
1380

aataatatta catctatggt taattataaa aaaaaaaaaa aaaaaaaaaa gtatctgcgt
1440

tgttaccact gcttaatcac tagtgaattc
1470

<210> 328
 <211> 366
 <212> PRT
 <213> Trifolium repens

<400> 328

Met Ala Pro Ala Lys Thr Leu Ser Tyr Leu Ser Gln Gln Asn Thr Leu
 1 5 10 15

Glu Ser Ser Phe Val Arg Glu Glu Asp Glu Arg Pro Lys Val Ala Tyr
 20 25 30

Asn Asn Phe Ser Asn Glu Ile Pro Ile Ile Ser Leu Ala Gly Ile Asp
 35 40 45

Glu Val Asp Gly Arg Arg Thr Glu Ile Cys Asn Lys Ile Val Glu Ala
 50 55 60

Cys Glu Asn Trp Gly Ile Phe Gln Val Val Asp His Gly Val Asp Thr
 65 70 75 80

Lys Leu Val Ser Glu Met Thr Arg Phe Ala Arg Glu Phe Phe Ala Leu
 85 90 95

Pro Pro Glu Glu Lys Leu Arg Phe Asp Met Ser Gly Gly Lys Lys Gly
 100 105 110

Gly Phe Ile Val Ser Ser His Leu Gln Gly Glu Ala Val Lys Asp Trp
 115 120 125

Arg Glu Leu Val Thr Tyr Phe Ser Tyr Pro Ile Lys Gln Arg Asp Tyr
 130 135 140

Ser Arg Trp Pro Asp Lys Pro Glu Gly Trp Lys Glu Val Thr Glu Lys
 145 150 155 160

Tyr Ser Glu Asn Leu Met Asn Leu Ala Cys Lys Leu Leu Glu Val Leu
 165 170 175

Ser Glu Ala Met Gly Leu Glu Lys Glu Ala Leu Thr Lys Ala Cys Val
 180 185 190

Asp Met Asp Gln Lys Val Val Ile Asn Tyr Tyr Pro Lys Cys Pro Glu
 195 200 205

Pro Asp Leu Thr Leu Gly Leu Lys Arg His Thr Asp Pro Gly Thr Ile
 210 215 220

Thr Leu Leu Leu Gln Asp Gln Val Gly Gly Leu Gln Ala Thr Lys Asp

225 230 235 240

Asn Gly Lys Thr Trp Ile Thr Val Gln Pro Val Glu Gly Ala Phe Val
245 250 255

Val Asn Leu Gly Asp His Gly His Tyr Leu Ser Asn Gly Arg Phe Lys
260 265 270

Asn Ala Asp His Gln Ala Val Val Asn Ser Asn Tyr Ser Arg Leu Ser
275 280 285

Ile Ala Thr Phe Gln Asn Pro Ala Pro Asp Ala Thr Val Tyr Pro Leu
290 295 300

Lys Ile Arg Asp Gly Glu Lys Ser Val Leu Glu Glu Pro Ile Thr Phe
305 310 315 320

Ala Glu Met Tyr Arg Arg Lys Met Thr Lys Asp Leu Glu Ile Ala Arg
325 330 335

Met Lys Lys Leu Ala Lys Glu Gln Gln Leu Arg Asp Leu Glu Glu Asn
340 345 350

Lys Thr Lys Tyr Glu Ala Lys Pro Leu Asn Glu Ile Phe Ala
355 360 365

<210> 329
<211> 2515
<212> DNA
<213> *Trifolium repens*

<400> 329
gaattcgatt aagcagtggg aacaacgcag agtacgcggg gaggaaatc acaactcaaa
60
tattctctta attctttcat ataactatt gaatttcatt tctccctaaa aattctatag
120
ctaccacatc acacaacata acaaatattg aaatatttat tactatatata agatatggaa
180
gtatagtcag cagcaatcac aaaaaacaat ggcaagattg attcattttg cttgaatcat
240
gctaattgcta ataacatgaa agtgaattgg gctgacccct tgaattgggg tgtggctgct
300
gaggcaatga aggggaagtca cttggatgag gtgaagcgta tgggtggaggaa ataccggaaa
360
ccggttgctc gtcttggctg cgagacacta accatttctc aggtggctgc cattgctgca
420
cagatgggtg caacgggtgga gctatcggaa tctgctagag ccggcggttaa ggcaagcagt
480
gaactgcgtta tggagagtat gaacaaagggt accgacagct acggtgtctcc aacagggtt

540

ggcgctacct cgcaccgcgc aaccaaaca ggtggtgctt tgcagaaaga gtcataaagg
600

tttttgatg ctggaatatt tggaaatgga actgagtcaa gccacacact accacacaca
660

gccacaagag ctgccaatgct agtgagaatc aacacacttc tccaaggcta ttcagggaatt
720

agatttgaaa tcttagaagc tatcacaagc ctctttaaca acaatgtcac cccatgttta
780

ccgcttcgag gtacaatcac agcttcagga gatttagtcc ctctttctta cattgctggg
840

ttactaacgc gacgacaaa ttccaaggct catggacott ctggagaagt acttaatgca
900

aaacaagctt ttcaatcagc tggaatcgat gcgagttct ttgaattaca accaaaagaa
960

ggccttgccc ttgttaacgc aaccgctggt ggttctgggt tagcttctat tgtcttttt
1020

gaggctaata tattggcggg gttgtctgaa gttctatctg caattttcgc tgaagttatg
1080

caagggaagc ccgaatttac cgatcatttg acacataagt tgaaacatca cctgggtcaa
1140

attgaggctg ctgctattat ggaacacatt ttggatggga gtgcttatgt taaagacgct
1200

aagaagttgc atgagatgga tcctttacag aagccaaaac aagatagata tgcacttagg
1260

acttcgccac aatggcttgg tcctttgatt gaagtgatta gattctctac caagtcaatt
1320

gagagagaga tcaactctgt caatgacaat cctttgattg atgtttcaag gaacaaggct
1380

ttgcatgggt gaaattttca aggaacacct atcggagtat ccatggataa tacacgtttg
1440

gctcttgcat caattggcaa acttatgttt gctcaattct ctgagcttgt caatgatttt
1500

tacaacaatg gattgccatc aaatctctct gctagtagaa atccgagctt ggattatggg
1560

ttcaagggat ccgaaattgc catggcttct tattgttccg agtgcaata tcttgcaaat
1620

ccggttacaa ctcatgtcca aagtgcggaa caacacaacc aagatgtcaa ctctttgggt
1680

ttgatttctt ctagaaaaac ttatgaagca attgagatcc ttcaattgat gtcttccaca
1740

ttcttgattg cactttgtca agcaattgat ttaagacatt tggaggagaa ttgaaaaac
1800

tcggtcaaaa ataccgtaag ccaagtggcc aaaaagacac taaccatagg tgtcaatgga

1860

gaacttcac cttcaagatt ttgtgaaaa gacttattga aagtgggtga tagggaacat
1920

gtctttgcct acattgatga tctttagtagt gctacatacc cattgatgca aaaactcagg
1980

caagtactag tggatcatgc attagttaat ggagaaagtg agaagaattt gaacacatca
2040

atcttccaaa agattgcaac ttttgaggaa gaggtgaaaa acctttgccca aaagagggtg
2100

aaagtgcag gattgcatat gaaagtggaa attcaacaat tccaacaag atcaatggat
2160

gcagatctta tccactctac aattttgtga gaaaggagtt ggggaactggt ttgctaactg
2220

gagaaaatgt catttcaccg ggtgaagagt gtgacaaact attcacagct atgtgtcaag
2280

gaaaaatcat tgatcctctt cttgaatgct tgggagagtg gaacggtgct cctcttccaa
2340

tttgtttaact ttgattgtta gttcataaaa tgttttattt gtatttatca ttgtatttta
2400

tcgagctgta gtaataatga ttaggtgttt tgtgccttta atgaaaaaaa aaaaaaaaaa
2460

aaaaaaaaa aaaagtactc tgcgttgta ccaactgctta atcactagtg aattc
2515

<210> 330

<211> 671

<212> PRT

<213> Trifolium repens

<400> 330

Met Glu Val Val Ala Ala Ala Ile Thr Lys Asn Asn Gly Lys Ile Asp
1 5 10 15

Ser Phe Cys Leu Asn His Ala Asn Ala Asn Asn Met Lys Val Asn Gly
20 25 30

Ala Asp Pro Leu Asn Trp Gly Val Ala Ala Glu Ala Met Lys Gly Ser
35 40 45

His Leu Asp Glu Val Lys Arg Met Val Glu Glu Tyr Arg Lys Pro Val
50 55 60

Val Arg Leu Gly Gly Glu Thr Leu Thr Ile Ser Gln Val Ala Ala Ile
65 70 75 80

Ala Ala His Asp Gly Ala Thr Val Glu Leu Ser Glu Ser Ala Arg Ala
85 90 95

Gly Val Lys Ala Ser Ser Asp Trp Val Met Glu Ser Met Asn Lys Gly
 100 105 110

Thr Asp Ser Tyr Gly Val Pro Thr Gly Phe Gly Ala Thr Ser His Arg
 115 120 125

Arg Thr Lys Gln Gly Gly Ala Leu Gln Lys Glu Leu Ile Arg Phe Leu
 130 135 140

Asn Ala Gly Ile Phe Gly Asn Gly Thr Glu Ser Ser His Thr Leu Pro
 145 150 155 160

His Thr Ala Thr Arg Ala Ala Met Leu Val Arg Ile Asn Thr Leu Leu
 165 170 175

Gln Gly Tyr Ser Gly Ile Arg Phe Glu Ile Leu Glu Ala Ile Thr Lys
 180 185 190

Leu Leu Asn Asn Asn Val Thr Pro Cys Leu Pro Leu Arg Gly Thr Ile
 195 200 205

Thr Ala Ser Gly Asp Leu Val Pro Leu Ser Tyr Ile Ala Gly Leu Leu
 210 215 220

Thr Gly Arg Pro Asn Ser Lys Ala His Gly Pro Ser Gly Glu Val Leu
 225 230 235 240

Asn Ala Lys Gln Ala Phe Gln Ser Ala Gly Ile Asp Ala Glu Phe Phe
 245 250 255

Glu Leu Gln Pro Lys Glu Gly Leu Ala Leu Val Asn Gly Thr Ala Val
 260 265 270

Gly Ser Gly Leu Ala Ser Ile Val Leu Phe Glu Ala Asn Ile Leu Ala
 275 280 285

Val Leu Ser Glu Val Leu Ser Ala Ile Phe Ala Glu Val Met Gln Gly
 290 295 300

Lys Pro Glu Phe Thr Asp His Leu Thr His Lys Leu Lys His His Pro
 305 310 315 320

Gly Gln Ile Glu Ala Ala Ala Ile Met Glu His Ile Leu Asp Gly Ser
 325 330 335

Ala Tyr Val Lys Asp Ala Lys Lys Leu His Glu Met Asp Pro Leu Gln
 340 345 350

Lys Pro Lys Gln Asp Arg Tyr Ala Leu Arg Thr Ser Pro Gln Trp Leu

355	360	365
Gly Pro Leu Ile Glu Val Ile Arg Phe Ser Thr Lys Ser Ile Glu Arg		
370	375	380
Glu Ile Asn Ser Val Asn Asp Asn Pro Leu Ile Asp Val Ser Arg Asn		
385	390	395 400
Lys Ala Leu His Gly Gly Asn Phe Gln Gly Thr Pro Ile Gly Val Ser		
	405	410 415
Met Asp Asn Thr Arg Leu Ala Leu Ala Ser Ile Gly Lys Leu Met Phe		
	420	425 430
Ala Gln Phe Ser Glu Leu Val Asn Asp Phe Tyr Asn Asn Gly Leu Pro		
	435	440 445
Ser Asn Leu Ser Ala Ser Arg Asn Pro Ser Leu Asp Tyr Gly Phe Lys		
	450	455 460
Gly Ser Glu Ile Ala Met Ala Ser Tyr Cys Ser Glu Leu Gln Tyr Leu		
465	470	475 480
Ala Asn Pro Val Thr Thr His Val Gln Ser Ala Glu Gln His Asn Gln		
	485	490 495
Asp Val Asn Ser Leu Gly Leu Ile Ser Ser Arg Lys Thr Tyr Glu Ala		
	500	505 510
Ile Glu Ile Leu Gln Leu Met Ser Ser Thr Phe Leu Ile Ala Leu Cys		
	515	520 525
Gln Ala Ile Asp Leu Arg His Leu Glu Glu Asn Leu Lys Asn Ser Val		
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Lys Asn Thr Val Ser Gln Val Ala Lys Lys Thr Leu Thr Ile Gly Val		
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Asn Gly Glu Leu His Pro Ser Arg Phe Cys Glu Lys Asp Leu Leu Lys		
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Val Val Asp Arg Glu His Val Phe Ala Tyr Ile Asp Asp Pro Cys Ser		
	580	585 590
Ala Thr Tyr Pro Leu Met Gln Lys Leu Arg Gln Val Leu Val Asp His		
	595	600 605
Ala Leu Val Asn Gly Glu Ser Glu Lys Asn Leu Asn Thr Ser Ile Phe		
	610	615 620

Gln Lys Ile Ala Thr Phe Glu Glu Glu Leu Lys Asn Leu Cys Gln Lys
625 630 635 640

Arg Leu Lys Val Gln Gly Leu His Met Lys Val Glu Ile Gln Gln Phe
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720
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1260

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1560

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1680

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1740

gaaaatctga ggaacactgt caagaacacg gtaagccaag tagcgaagag aacactcacc
1800

accgggtgta atggagaact tcactcttct agatttttgt agaaagattt gctcaaagtt
1860

gttgatagg agtatgtatt tgctatgtc gacgatcctt gtctagctac ataccctttg
1920

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1980

aatttgaaca catcaatctt tcaaaagatt gcaacttttg aggtgaatt gaaagctatc
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2100

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2160

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2280

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2520

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<211> 712

<212> PRT

<213> *Trifolium repens*

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20 25 30

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35 40 45

Asn Pro Leu Val Lys Ile Gly Gly Glu Thr Leu Thr Ile Ala Gln Val
50 55 60

Ala Gly Ile Ala Ser His Asp Ser Gly Val Arg Val Glu Leu Ser Glu
65 70 75 80

Ser Ala Arg Ala Gly Val Lys Ala Ser Ser Gly Trp Val Met Asp Ser
85 90 95

Met Asn Asn Gly Thr Asp Ser Tyr Gly Val Thr Thr Gly Phe Gly Ala
100 105 110

Thr Ser His Arg Arg Thr Lys Gln Gly Gly Ala Leu Gln Lys Glu Leu
115 120 125

Ile Arg Phe Leu Asn Ala Gly Ile Phe Gly Asn Gly Thr Glu Ser Asn
130 135 140

Cys Thr Leu Pro His Thr Ala Thr Arg Ala Ala Met Leu Val Arg Ile
 145 150 155 160

Asn Thr Leu Leu Gln Gly Tyr Ser Gly Ile Arg Phe Glu Ile Leu Glu
 165 170 175

Ala Ile Thr Lys Leu Leu Asn Asn Asn Ile Thr Pro Cys Leu Pro Leu
 180 185 190

Arg Gly Thr Ile Thr Ala Ser Gly Asp Leu Val Pro Leu Ser Tyr Ile
 195 200 205

Ala Gly Leu Leu Thr Gly Arg Pro Asn Ser Lys Ala Val Gly Pro Ser
 210 215 220

Gly Glu Ile Leu Asn Ala Lys Glu Ala Phe Gln Leu Ala Gly Ile Gly
 225 230 235 240

Ser Glu Phe Phe Glu Leu Gln Pro Lys Glu Gly Leu Ala Leu Val Asn
 245 250 255

Gly Thr Ala Val Gly Ser Gly Leu Ala Ser Ile Val Leu Phe Glu Ala
 260 265 270

Asn Val Leu Ala Val Leu Ser Glu Val Met Ser Ala Ile Phe Ala Glu
 275 280 285

Val Met Gln Gly Lys Pro Glu Phe Thr Asp His Leu Thr His Lys Leu
 290 295 300

Lys His His Pro Gly Gln Ile Glu Ala Ala Ala Ile Met Glu His Ile
 305 310 315 320

Leu Asp Gly Ser Ala Tyr Val Lys Ala Ala Lys Lys Leu His Glu Thr
 325 330 335

Asp Pro Leu Gln Lys Pro Lys Gln Asp Arg Tyr Ala Leu Arg Thr Ser
 340 345 350

Pro Gln Trp Leu Gly Pro Leu Ile Glu Val Ile Arg Phe Ser Thr Lys
 355 360 365

Ser Ile Glu Arg Glu Ile Asn Ser Val Asn Asp Asn Pro Leu Ile Asp
 370 375 380

Val Ser Arg Asn Lys Ala Ile His Gly Gly Asn Phe Gln Gly Thr Pro
 385 390 395 400

Ile Gly Val Ser Met Asp Asn Thr Arg Leu Ala Leu Ala Ser Ile Gly
 405 410 415

Lys Leu Met Phe Ala Gln Phe Ser Glu Leu Val Asn Asp Phe Tyr Asn
 420 425 430

Asn Gly Leu Pro Ser Asn Leu Thr Ala Ser Arg Asn Pro Ser Leu Asp
 435 440 445

Tyr Gly Phe Lys Gly Ser Glu Ile Ala Met Ala Ser Tyr Cys Ser Glu
 450 455 460

Leu Gln Tyr Leu Ala Asn Pro Val Thr Thr His Val Gln Ser Ala Glu
 465 470 475 480

Gln His Asn Gln Asp Val Asn Ser Leu Gly Leu Ile Ser Ser Arg Lys
 485 490 495

Thr Asn Glu Ala Ile Glu Ile Leu Lys Leu Met Ser Ser Thr Phe Leu
 500 505 510

Ile Ala Leu Cys Gln Ala Ile Asp Leu Arg His Leu Glu Glu Asn Leu
 515 520 525

Arg Asn Thr Val Lys Asn Thr Val Ser Gln Val Ala Lys Arg Thr Leu
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 545 550 555 560

Asp Leu Leu Lys Val Val Asp Arg Glu Tyr Val Phe Ala Tyr Val Asp
 565 570 575

Asp Pro Cys Leu Ala Thr Tyr Pro Leu Met Gln Lys Leu Arg Gln Val
 580 585 590

Leu Val Asp His Ala Leu Val Asn Ala Asp Gly Glu Lys Asn Leu Asn
 595 600 605

Thr Ser Ile Phe Gln Lys Ile Ala Thr Phe Glu Asp Glu Leu Lys Ala
 610 615 620

Ile Leu Pro Lys Glu Val Glu Ser Thr Arg Thr Ala Tyr Glu Asn Gly
 625 630 635 640

Gln Cys Gly Ile Ser Asn Lys Ile Lys Glu Cys Arg Ser Tyr Pro Leu
 645 650 655

Tyr Lys Phe Val Arg Glu Glu Leu Gly Thr Ala Leu Leu Thr Gly Glu
 660 665 670

Lys Thr Ile Ser Leu Gly Glu Glu Cys Asp Lys Leu Phe Thr Ala Met
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Asn Gly Ala Pro Leu Pro Ile Cys
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 <211> 2664
 <212> DNA
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1920

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<211> 712

<212> PRT

<213> *Trifolium repens*

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Asn Pro Leu Ala Lys Ile Gly Gly Glu Thr Leu Thr Ile Ala Gln Val
50 55 60

Ala Gly Ile Ala Ser His Asp Ser Gly Val Arg Val Glu Leu Ser Glu
65 70 75 80

Ser Ala Arg Ala Gly Val Lys Ala Ser Ser Asp Trp Val Met Asp Ser
85 90 95

Met Asn Asn Gly Thr Asp Ser Tyr Gly Val Thr Thr Gly Phe Gly Ala
100 105 110

Thr Ser His Arg Arg Thr Lys Gln Gly Gly Ala Leu Gln Lys Glu Leu
115 120 125

Ile Arg Phe Leu Asn Ala Gly Ile Phe Gly Asn Gly Thr Glu Ser Asn
130 135 140

Cys Thr Leu Pro His Thr Ala Thr Arg Ala Ala Met Leu Val Arg Ile

145	150	155	160
Asn Thr Leu Leu Gln Gly Tyr Ser Gly Ile Arg Phe Glu Ile Leu Glu	165	170	175
Ala Ile Thr Lys Leu Pro Asn Asn Asn Ile Thr Pro Cys Leu Pro Leu	180	185	190
Arg Gly Thr Ile Thr Ala Ser Gly Asp Leu Val Pro Leu Ser Tyr Ile	195	200	205
Ala Gly Leu Leu Thr Gly Arg Pro Asn Ser Lys Ala Val Gly Pro Ser	210	215	220
Gly Glu Ile Leu Ser Ala Lys Glu Ala Phe Gln Leu Ala Gly Ile Gly	225	230	240
Ser Glu Phe Phe Glu Leu Gln Pro Lys Glu Gly Leu Ala Leu Val Asn	245	250	255
Gly Thr Ala Val Gly Ser Gly Leu Ala Ser Ile Val Leu Phe Glu Ala	260	265	270
Asn Val Leu Ala Val Leu Ser Glu Val Met Ser Ala Ile Phe Ala Glu	275	280	285
Val Met Gln Gly Lys Pro Glu Phe Thr Asp His Leu Thr His Lys Leu	290	295	300
Lys His His Pro Gly Gln Ile Glu Ala Ala Ile Met Glu His Ile	305	310	315
Leu Asp Gly Ser Ala Tyr Val Lys Ala Ala Lys Lys Leu His Glu Thr	325	330	335
Asp Pro Leu Gln Lys Pro Lys Gln Asp Arg Tyr Ala Leu Arg Thr Ser	340	345	350
Pro Gln Trp Leu Gly Pro Leu Ile Glu Val Ile Arg Phe Ser Thr Lys	355	360	365
Ser Ile Glu Arg Glu Ile Asn Ser Val Asn Asp Asn Pro Leu Ile Asp	370	375	380
Val Ser Arg Asn Lys Ala Ile His Gly Gly Asn Phe Gln Gly Thr Pro	385	390	400
Ile Gly Val Ser Met Asp Asn Thr Arg Leu Ala Leu Ala Ser Ile Gly	405	410	415

Lys Leu Met Phe Ala Gln Phe Ser Glu Leu Val Asn Asp Phe Tyr Asn
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Asn Gly Leu Pro Ser Tyr Leu Thr Ala Ser Arg Asn Pro Ser Leu Asp
 435 440 445

Tyr Gly Phe Lys Gly Ser Glu Ile Ala Met Ala Ser Tyr Cys Ser Glu
 450 455 460

Leu Gln Tyr Leu Ala Asn Pro Val Thr Thr His Val Gln Ser Ala Glu
 465 470 475 480

Gln His Asn Gln Asp Val Asn Ser Leu Gly Leu Ile Ser Ser Arg Lys
 485 490 495

Thr Asn Glu Ala Ile Glu Ile Leu Lys Leu Met Ser Ser Thr Phe Leu
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Ile Ala Leu Cys Gln Ala Ile Asp Leu Arg His Leu Glu Glu Asn Leu
 515 520 525

Arg Asn Thr Val Lys Asn Thr Val Ser Gln Val Ala Lys Arg Thr Leu
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Thr Thr Gly Val Asn Gly Glu Leu His Ser Ser Arg Phe Cys Glu Lys
 545 550 555 560

Asp Leu Leu Lys Val Val Asp Arg Glu Tyr Val Phe Ala Tyr Ala Asp
 565 570 575

Asp Pro Cys Leu Ala Thr Tyr Pro Leu Met Gln Lys Leu Arg Gln Val
 580 585 590

Leu Val Asp His Ala Leu Val Asn Val Asp Gly Glu Lys Asn Leu Asn
 595 600 605

Thr Ser Ile Phe Gln Lys Ile Ala Thr Phe Glu Asp Glu Leu Lys Ala
 610 615 620

Ile Leu Pro Lys Glu Val Glu Ser Thr Arg Thr Ala Tyr Glu Asn Gly
 625 630 635 640

Gln Cys Gly Ile Ser Asn Lys Ile Lys Glu Cys Arg Ser Tyr Pro Leu
 645 650 655

Tyr Lys Phe Val Arg Glu Glu Leu Gly Thr Ala Leu Leu Thr Gly Glu
 660 665 670

Lys Thr Ile Ser Pro Gly Glu Glu Cys Asp Lys Leu Phe Thr Ala Met

675

680

685

Cys Gln Gly Lys Ile Val Asp Pro Leu Met Glu Cys Leu Gly Glu Trp
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Asn Gly Ala Pro Leu Pro Ile Cys
 705 710

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 <211> 1296
 <212> DNA
 <213> Trifolium repens

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1020

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1080

ctaagtattg gtttgaaaaa aattccatga agctgagaaa acaataatat gcctaaaaatc
1140

aatgatggct aatgaaatgt acaagtttat gcataaagtt atttgatgat aatcaaaataa
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<211> 326

<212> PRT

<213> *Trifolium repens*

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20 25 30

Asn Thr Thr Ile Arg Ala Asp Pro Glu Arg Lys Arg Asp Val Ser Phe
35 40 45

Leu Thr Asn Leu Pro Gly Ala Ser Glu Arg Leu His Phe Phe Asn Ala
50 55 60

Asp Leu Asp Asp Pro Glu Ser Phe Asn Glu Ala Ile Glu Gly Cys Val
65 70 75 80

Gly Ile Phe His Thr Ala Ser Pro Ile Asp Phe Ala Val Ser Glu Pro
85 90 95

Glu Glu Ile Val Thr Lys Arg Thr Val Asp Gly Ala Leu Gly Ile Leu
100 105 110

Lys Ala Cys Val Asn Ser Lys Thr Val Lys Arg Phe Ile Tyr Thr Ser
115 120 125

Ser Gly Ser Ala Val Ser Phe Asn Gly Lys Asn Lys Asp Val Leu Asp
130 135 140

Glu Ser Asp Trp Ser Asp Val Asp Leu Leu Arg Ser Val Lys Pro Phe
145 150 155 160

Gly Trp Ser Tyr Gly Val Ser Lys Thr Leu Ala Glu Lys Ala Val Leu

165										170					175								
Glu	Phe	Gly	Gln	Gln	Asn	Gly	Ile	Asp	Val	Val	Thr	Leu	Ile	Leu	Pro								
180								185					190										
Phe	Ile	Val	Gly	Ser	Phe	Val	Cys	Pro	Lys	Leu	Pro	Asp	Ser	Val	Glu								
195								200					205										
Lys	Ala	Leu	Val	Leu	Val	Leu	Gly	Lys	Lys	Glu	Gln	Ile	Gly	Ile	Ile								
210								215					220										
Ser	Phe	His	Met	Val	His	Val	Asp	Asp	Val	Ala	Arg	Ala	His	Ile	Tyr								
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Leu	Leu	Glu	Asn	Pro	Val	Pro	Gly	Gly	Arg	Tyr	Asn	Cys	Ser	Pro	Phe								
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INTERNATIONAL SEARCH REPORT

International application No.

PCT/AU02/01345

A. CLASSIFICATION OF SUBJECT MATTER

Int. Cl. ⁷: C12N 15/29, 15/52, 15/53, 15/55, 15/60, 15/61; A01H 5/00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

SEE ELECTRONIC DATABASE BOX BELOW

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

SEE ELECTRONIC DATABASE BOX BELOW

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

PEPTIDE DATABASES (SWISSPROT, GENBANK, EMBL, PIR) DGENE: SEQ ID NOS

2,9,14,18,24,65,70,79,92,96,109,111,118,136,148,154,156,160,162,164,169,186,195,197,203,246,248,250,279,287,29
4,299,304,308,310,312,314,318,320,322,324,326,328,334

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
PX	WO 02 18604 A (THE SALK INSTITUTE FOR BIOLOGICAL STUDIES) 7 March 2002 Fig 1D shares ~92% identity with SEQ ID NOS 2, 9, 14, 308	1-3, 13-19, 25, 27
X	US 6 054 636 A (FADER GM) 25 April 2000 Fig 2 shares ~81% identity with SEQ ID NOS 2, 9, 14, 308	1-3, 13-27

☒ Further documents are listed in the continuation of Box C

☒ See patent family annex

* Special categories of cited documents:	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A" document defining the general state of the art which is not considered to be of particular relevance	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"B" earlier application or patent but published on or after the international filing date	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"&" document member of the same patent family
"O" document referring to an oral disclosure, use, exhibition or other means	
"P" document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search
28 November 2002

Date of mailing of the international search report

05 DEC 2002

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INTERNATIONAL SEARCH REPORT

International application No.

PCT/AU02/01345

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 99 36543 A (PIONEER HI-BRED INTERNATIONAL, INC.) 22 July 1999 SEQ ID NO 2 shares ~81% identity with SEQ ID NOS 2, 9, 14, 308	1-3, 13-17, 21, 22, 24-27
X	Genbank Acc No AAB41524 chalcone isomerase (<i>Medicago sativa</i>) 29 January 1997 (See also Medline Abstract 8193301) 92% identity with SEQ ID NOS 18, 310	1-3, 13-18, 24-27
X	Genbank Acc No CAA74847 anther-specific protein (<i>Nicotiana sylvestris</i>) (See also Medline Abstract 99084767) 83% identity with SEQ ID NOS 96, 322 and 67% identity with SEQ ID NOS 318, 70	1, 2, 4, 13-18, 24-26, 28
X	Genbank Acc No CAC14061 chalcone synthase (<i>Ruta graveolens</i>) 27 October 2000 ~87% identity with SEQ ID NOS 24, 65, 79, 92, 102, 107, 314, 316, 320, 324	1, 2, 4, 13-18, 24-26, 28
X	Genbank Acc No AAB41556 chalcone reductase (<i>Medicago sativa</i>) 30 January 1997 ~95% identity with SEQ ID NOS 109, 118, 312	1, 2, 5, 13-18, 20, 24-26, 29
X	Genbank Acc No CAA11226 chalcone reductase (<i>Sesbania rostrata</i>) 3 July 2001 90% identity with SEQ ID NO 111	1, 2, 5, 13-18, 24-26, 29
X	Genbank Acc No AAK52955 dihydro-flavonoid reductase-like protein (<i>Zea mays</i>) 14 May 2001 69% identity with SEQ ID NOS 287, 160 and 53% identity with SEQ ID NO 148	1, 2, 6, 13-18, 24-26, 30
PX	WO 02 063021 A (PIONEER HI-BRED INTERNATIONAL, INC.) 15 August 2002 SEQ ID NO 1 shares 74% identity with SEQ ID NOS 148, 160, 287	1, 2, 6, 13-18, 24-26, 30
X	Genbank Acc No AAD54273 dihydroflavonol-4-reductase DFR1 (<i>Glycine max</i>) 10 September 1999 81 % identity with SEQ ID NO 169	1, 2, 6, 13-18, 24-26, 30
X	WO 95 27790 A (CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE) 19 October 1995 SEQ ID NO 1 shares 43% identity with SEQ ID NOS 136, 156, 326, 39% identity with SEQ ID NO 154 and 51% identity with SEQ ID NO 294.	1, 2, 6, 13-18, 24-26, 30
PX	WO 02 10210 A (BAYER AKTIENGESSELLSCHAFT) 7 February 2002 SEQ ID NO 2329 shares 51% identity with SEQ ID NO 164, SEQ ID NO 636 shares 62% identity with SEQ ID NO 186, SEQ ID NO 1573 shares 49% identity with SEQ ID NOS 246, 248, SEQ ID NO 2091 shares 57% identity with SEQ ID NOS 304, 299	1, 2, 7, 9, 13-17, 24-26, 31, 32
X	WO 99 14351 (E.I. DU PONT DE NEMOURS AND COMPANY) 25 March 1999 SEQ ID NO 1 shares 56% identity with SEQ ID NO 162	1, 2, 6, 13-17, 21, 22, 24-26, 30

INTERNATIONAL SEARCH REPORT

International application No.

PCT/AU02/01345

C (Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
PX	WO 02 26994 A (AGRICULTURE VICTORIA SERVICES PTY LTD) 4 April 2002 Fig 39 shares 72% identity with SEQ ID NO 294	1, 2, 6, 13-18, 21, 22, 24-26, 30
X	WO 97 12982 A (CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE) 10 April 1997 SEQ ID NO 5 shares 55% identity with SEQ ID NO 294	1, 2, 6, 13-17, 24-26, 30
X	Genbank Acc No CAA80265 flavonoid 3',5'-hydroxylase (<i>Petunia x hybrida</i>) 7 December 1993 70% identity with SEQ ID NO 197	1, 2, 8, 13-18, 24-26, 32
X	EP 1 033 405 (CERES INCORPORATED) 6 September 2000 SEQ ID NO 49742 shares 57% identity with SEQ ID NO 195	1, 2, 8, 13-18, 24-26, 32
X	Genbank Acc No AAF23859 DFR-like protein (<i>Arabidopsis thaliana</i>) 11 January 2000 61% identity with SEQ ID NO 186	1, 2, 7, 13-18, 24-26, 31
X	Genbank Acc No BAB01697 oxidase-like protein (<i>Arabidopsis thaliana</i>) 27 December 2000 50% identity with SEQ ID NOS 246, 248	1, 2, 9, 13-18, 24-26, 33
X	TREMBL Acc No CAB63776 F3'H1 protein (<i>Glycine max</i>) 1 May 2000 85% identity with SEQ ID NO 328, 203	1, 2, 9, 13-18, 24-26, 33
X	Genbank Acc No CAB78172 flavanone 3-beta-hydroxylase (<i>Arabidopsis thaliana</i>) 16 March 2000 57% identity with SEQ ID NOS 304, 299	1, 2, 9, 13-17, 24-26, 33
X	Genbank Acc No AAG49298 Flavonoid 3'-hydroxylase (<i>Callistephus chinensis</i>) 16 January 2001 68% identity with SEQ ID NO 250	1, 2, 10, 13- 18, 20, 24-26, 34
X	Genbank Acc No AAA99500 Phenylalanine ammonia lyase (<i>Stylosanthes humilis</i>) 15 May 1996 88% identity with SEQ ID NOS 254, 259, 269, 271, 273, 275, 330, 332, 334	1, 2, 11, 13- 18, 24-26, 35
X	Genbank Acc No CAA41169 phenylalanine ammonia lyase (<i>Medicago sativa</i>) 5 May 1995 87% identity with SEQ ID NOS 254, 259, 269, 271, 273, 275, 330, 332, 334	1, 2, 11, 13- 18, 24-26, 35
X	Genbank Acc No AAB41550 vestitone reductase (<i>Medicago sativa</i>) 30 January 1997 (See also Medline abstract 7625843) 95% identity with SEQ ID NOS 336, 279	1, 2, 12-18, 21, 22, 24-26, 36

INTERNATIONAL SEARCH REPORT

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Box I Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos :
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos :
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos :
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a)

Box II Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

See supplemental Box

1. ☒ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☒ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

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Supplemental Box 1

(To be used when the space in any of Boxes I to VIII is not sufficient)

Continuation of Box No: II (lack of unity)

The international application does not comply with the requirements of unity of invention because it does not relate to one invention or to a group of inventions so linked as to form a single general inventive concept. The fundamental test for unity of invention is specified in Rule 13.2 of the Regulations under the PCT.

"Where a group of inventions is claimed in one and the same international application, the requirement of unity of invention referred to in Rule 13.1 shall be fulfilled only where there is a technical relationship among those inventions involving one or more of the same or corresponding special technical features. The expression "special technical feature" shall mean those technical features that define a contribution which each of the claimed inventions, considered as a whole, make over the prior art."

The problem addressed by the application is the modification of flavonoid biosynthesis (see page 2, line 29-page 3, line 7). The solution provided by the claims resides in the use of 56 specific polypeptides from clover, medic, ryegrass or fescue species (claim 25) and the nucleic acids or fragments coding for these polypeptides (claim 1). These 56 specific polypeptides fall within the following ten groups:

- | | |
|---|---|
| 1. Chalcone isomerases (CHI) | (SEQ IDS 2,9,14,18,308,310) |
| 2. Chalcone synthase (CHS) | (SEQ IDS 24,65,70,79,92,96,102,107,314,316,318,322,324) |
| 3. Chalcone reductase (CHR) | (SEQ IDS 109,111,118,312) |
| 4. Dihydroflavonol 4-reductase (DFR) | (SEQ IDS 136,148,154,156,160,162,164,169,287,294,326) |
| 5. Leucoanthocyanidin reductase (LCR) | (SEQ ID 186) |
| 6. Flavonoid 3',5'-hydroxylase (F3'5'H) | (SEQ IDS 195,197) |
| 7. Flavonone 3-hydroxylase (F3H) | (SEQ IDS 203,246,248,299,304,328) |
| 8. Flavonoid 3'-hydroxylase (F3'H) | (SEQ ID 250) |
| 9. Phenylalanine ammonia-lyase (PAL) | (SEQ IDS 254,259,269,271,273,275,330,332,334) |
| 10. Vestitone reductase (VR) | (SEQ IDS 279,336) |

The application acknowledges that representatives of these enzyme species, and the nucleotides that encode them, are known and have been isolated from other plant species (see page 2 lines 29-31). This is supported by the following documents, which disclose the isolation and characterisation of a number of these enzymes from a range of species, including clover and medic and rye.

EMBL CAA63306	<i>Secale cereale</i> chalcone synthase (CHS) (5 March 1999)
GENBANK AAA17993	<i>Trifolium subterraneum</i> phenylalanine ammonia-lyase (PAL) (10 May 1994)
PIR S66262	<i>Medicago sativa</i> vestitone reductase (VS) (12 November 1999)
SWISSPROT P51109	<i>Medicago sativa</i> dihydroflavonol 4-reductase (DHR) (1 October 1996)
SWISSPROT P51088	<i>Trifolium subterraneum</i> chalcone synthase (CHS) (15 July 1999)
PIR S44371	<i>Medicago sativa</i> chalcone isomerase (CHI) (16 July 1999)
Medline Abstract 11164576	altered pigmentation using CHS and DFR
Medline Abstract: 7981963	altered plant stress response using CHS and PAL

These documents disclose not only flavonoid biosynthesis enzymes in a range of plant species they also disclose manipulation of these sequences to modify features such as pigmentation and stress responses. Thus features such as the 10 listed enzyme families, the isolation of representative of these families from a range of plant species and modification of flavonoid pathway enzymes are known. Furthermore, the enzymes isolated from the 4 specific species: clover, medic, ryegrass and fescue, do not appear to contribute any advantage or produce any unexpected result in comparison to known members of the same families isolated from other species. Thus these features are known or are obvious and cannot be regarded as "special technical features" conferring unity on the separate inventions.

INTERNATIONAL SEARCH REPORT

International application No.

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Supplemental Box 1

(To be used when the space in any of Boxes I to VIII is not sufficient)

Continuation of Box No: II (lack of unity)

In the absence of an obvious special technical feature, it is appropriate to use the Markush approach.

Claims 1 and 26 are written as claims directed to alternatives, in a so-called Markush style of drafting. The application of the test for Markush claims gives the following result:

(A) the common property is modification of the flavonoid biosynthesis pathway.

(B) (1) no common structure is evident as the structures of the polypeptides are not revealed

(B) (2) there is no single recognised class of compounds embracing all the polypeptides, as the polypeptides belong to different classes ie CHI, CHS, CHR, DFR, LCR F3'5'H, F3H, F3'H, PAL, VR, each carrying out different biological functions.

The species of origin of the polypeptides does not provide a legitimate classification as proteins are primarily classified by their activity not their origin. Thus the polypeptides can be grouped into 10 classes CHI, CHS, CHR, DFR, LCR F3'5'H, F3H, F3'H, PAL, VR, based on their activities, and represent 10 different inventions. Each of these inventions can only be searched using independent search strategies and thus each search requires significant additional effort.

As a service to the Applicant, multiple inventions, as specified by the Applicant, were searched for a single search fee with the proviso that the total number of amino acid sequences associated with the combination of inventions was no greater than 10. This offer was independent of unity consideration and was provided solely as a service to the Applicant. For five additional search fees all the inventions, totalling 56 sequences were searched.

This Annex lists the known "A" publication level patent family members relating to the patent documents cited in the above-mentioned international search report. The Australian Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

Patent Document Cited in Search Report				Patent Family Member			
US	6 054 636	AU	94934/98	EP	1 015 614	WO	99 14351
WO	99 36543	AU	22321/99	EP	1 045 909		
WO	99 14351	AU	94934/98				
WO	97 12892	EP	0 853 672	FR	2739395		
							END OF ANNEX